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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

(57) Abstract: The present invention relates to compositions containing novel proteins and methods of using those compositions for the diagnosis and treatment of immune related diseases.

COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

Field of the Invention

The present invention relates to compositions and methods useful for the diagnosis and treatment of immune related diseases.

Background of the Invention

Immune related and inflammatory diseases are the manifestation or consequence of fairly complex, often multiple interconnected biological pathways which in normal physiology are critical to respond to insult or injury, initiate repair from insult or injury, and mount innate and acquired defense against foreign organisms. Disease or pathology occurs when these normal physiological pathways cause additional insult or injury either as directly related to the intensity of the response, as a consequence of abnormal regulation or excessive stimulation, as a reaction to self, or as a combination of these.

Though the genesis of these diseases often involves multistep pathways and often multiple different biological systems/pathways, intervention at critical points in one or more of these pathways can have an ameliorative or therapeutic effect. Therapeutic intervention can occur by either antagonism of a detrimental process/pathway or stimulation of a beneficial process/pathway.

Many immune related diseases are known and have been extensively studied. Such diseases include immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, *etc.*

T lymphocytes (T cells) are an important component of a mammalian immune response. T cells recognize antigens which are associated with a self-molecule encoded by genes within the major histocompatibility complex (MHC). The antigen may be displayed together with MHC molecules on the surface of antigen presenting cells, virus infected cells, cancer cells, grafts, *etc.* The T cell system eliminates these altered cells which pose a health threat to the host mammal. T cells include helper T cells and cytotoxic T cells. Helper T cells proliferate extensively following recognition of an antigen -MHC complex on an antigen presenting cell. Helper T cells also secrete a variety of cytokines, *i.e.*, lymphokines, which play a central role in the activation of B cells, cytotoxic T cells and a variety of other cells which participate in the immune response.

Immune related diseases could be treated by suppressing the immune response. Using neutralizing antibodies that inhibit molecules having immune stimulatory activity would be beneficial in the treatment of immune-mediated and inflammatory diseases. Molecules which inhibit the immune response can be utilized (proteins directly or via the use of antibody agonists) to inhibit the immune response and thus ameliorate immune related disease.

CD4+ T cells are known to be important regulators of inflammation. Herein, CD4+ T cells were activated and the profile of genes differentially expressed upon activation was analyzed. As such, the activation specific genes may be potential therapeutic targets. *In vivo* co-stimulation is necessary for a productive immune proliferative response. The list of costimulatory molecules is quite extensive and it is

still unclear just which co-stimulatory molecules play critical roles in different types and stages of inflammation. In this application the focus is on genes which are specifically upregulated by stimulation with ICAM, anti-CD28 or ICAM/anti-CD28 in combination and may be useful in targeting inflammatory processes which are associated with these different molecules.

Summary of the Invention

A. Embodiments

The present invention concerns compositions and methods useful for the diagnosis and treatment of immune related disease in mammals, including humans. The present invention is based on the identification of proteins (including agonist and antagonist antibodies) which are a result of stimulation of the immune response in mammals. Immune related diseases can be treated by suppressing or enhancing the immune response. Molecules that enhance the immune response stimulate or potentiate the immune response to an antigen. Molecules which stimulate the immune response can be used therapeutically where enhancement of the immune response would be beneficial. Alternatively, molecules that suppress the immune response attenuate or reduce the immune response to an antigen (*e.g.*, neutralizing antibodies) can be used therapeutically where attenuation of the immune response would be beneficial (*e.g.*, inflammation). Accordingly, the PRO polypeptides, agonists and antagonists thereof are also useful to prepare medicines and medicaments for the treatment of immune-related and inflammatory diseases. In a specific aspect, such medicines and medicaments comprise a therapeutically effective amount of a PRO polypeptide, agonist or antagonist thereof with a pharmaceutically acceptable carrier. Preferably, the admixture is sterile.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprises contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native sequence PRO polypeptide. In a specific aspect, the PRO agonist or antagonist is an anti-PRO antibody.

In another embodiment, the invention concerns a composition of matter comprising a PRO polypeptide or an agonist or antagonist antibody which binds the polypeptide in admixture with a carrier or excipient. In one aspect, the composition comprises a therapeutically effective amount of the polypeptide or antibody. In another aspect, when the composition comprises an immune stimulating molecule, the composition is useful for: (a) increasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) stimulating or enhancing an immune response in a mammal in need thereof, (c) increasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen, (d) stimulating the activity of T-lymphocytes or (e) increasing the vascular permeability. In a further aspect, when the composition comprises an immune inhibiting molecule, the composition is useful for: (a) decreasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) inhibiting or reducing an immune response in a mammal in need thereof, (c) decreasing the activity of T-lymphocytes or (d) decreasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen. In another aspect, the composition comprises a further active ingredient, which may, for example, be a further antibody or a cytotoxic or chemotherapeutic agent. Preferably, the composition is sterile.

In another embodiment, the invention concerns a method of treating an immune related disorder in

a mammal in need thereof, comprising administering to the mammal an effective amount of a PRO polypeptide, an agonist thereof, or an antagonist thereto. In a preferred aspect, the immune related disorder is selected from the group consisting of: systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody. In one aspect, the present invention concerns an isolated antibody which binds a PRO polypeptide. In another aspect, the antibody mimics the activity of a PRO polypeptide (an agonist antibody) or conversely the antibody inhibits or neutralizes the activity of a PRO polypeptide (an antagonist antibody). In another aspect, the antibody is a monoclonal antibody, which preferably has nonhuman complementarity determining region (CDR) residues and human framework region (FR) residues. The antibody may be labeled and may be immobilized on a solid support. In a further aspect, the antibody is an antibody fragment, a monoclonal antibody, a single-chain antibody, or an anti-idiotypic antibody.

In yet another embodiment, the present invention provides a composition comprising an anti-PRO antibody in admixture with a pharmaceutically acceptable carrier. In one aspect, the composition comprises a therapeutically effective amount of the antibody. Preferably, the composition is sterile. The composition may be administered in the form of a liquid pharmaceutical formulation, which may be preserved to achieve extended storage stability. Alternatively, the antibody is a monoclonal antibody, an antibody fragment, a humanized antibody, or a single-chain antibody.

In a further embodiment, the invention concerns an article of manufacture, comprising:

(a) a composition of matter comprising a PRO polypeptide or agonist or antagonist thereof;

(b) a container containing said composition; and

(c) a label affixed to said container, or a package insert included in said container referring to the use of said PRO polypeptide or agonist or antagonist thereof in the treatment of an immune related disease. The composition may comprise a therapeutically effective amount of the PRO polypeptide or the agonist or antagonist thereof.

In yet another embodiment, the present invention concerns a method of diagnosing an immune related disease in a mammal, comprising detecting the level of expression of a gene encoding a PRO

polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower expression level in the test sample as compared to the control sample indicates the presence of immune related disease in the mammal from which the test tissue cells were obtained.

In another embodiment, the present invention concerns a method of diagnosing an immune disease in a mammal, comprising (a) contacting an anti-PRO antibody with a test sample of tissue cells obtained from the mammal, and (b) detecting the formation of a complex between the antibody and a PRO polypeptide, in the test sample; wherein the formation of said complex is indicative of the presence or absence of said disease. The detection may be qualitative or quantitative, and may be performed in comparison with monitoring the complex formation in a control sample of known normal tissue cells of the same cell type. A larger quantity of complexes formed in the test sample indicates the presence or absence of an immune disease in the mammal from which the test tissue cells were obtained. The antibody preferably carries a detectable label. Complex formation can be monitored, for example, by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. The test sample is usually obtained from an individual suspected of having a deficiency or abnormality of the immune system.

In another embodiment, the invention provides a method for determining the presence of a PRO polypeptide in a sample comprising exposing a test sample of cells suspected of containing the PRO polypeptide to an anti-PRO antibody and determining the binding of said antibody to said cell sample. In a specific aspect, the sample comprises a cell suspected of containing the PRO polypeptide and the antibody binds to the cell. The antibody is preferably detectably labeled and/or bound to a solid support.

In another embodiment, the present invention concerns an immune-related disease diagnostic kit, comprising an anti-PRO antibody and a carrier in suitable packaging. The kit preferably contains instructions for using the antibody to detect the presence of the PRO polypeptide. Preferably the carrier is pharmaceutically acceptable.

In another embodiment, the present invention concerns a diagnostic kit, containing an anti-PRO antibody in suitable packaging. The kit preferably contains instructions for using the antibody to detect the PRO polypeptide.

In another embodiment, the invention provides a method of diagnosing an immune-related disease in a mammal which comprises detecting the presence or absence or a PRO polypeptide in a test sample of tissue cells obtained from said mammal, wherein the presence or absence of the PRO polypeptide in said test sample is indicative of the presence of an immune-related disease in said mammal.

In another embodiment, the present invention concerns a method for identifying an agonist of a PRO polypeptide comprising:

(a) contacting cells and a test compound to be screened under conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and

(b) determining the induction of said cellular response to determine if the test compound is an effective agonist, wherein the induction of said cellular response is indicative of said test compound being an effective agonist.

In another embodiment, the invention concerns a method for identifying a compound capable of inhibiting the activity of a PRO polypeptide comprising contacting a candidate compound with a PRO

polypeptide under conditions and for a time sufficient to allow these two components to interact and determining whether the activity of the PRO polypeptide is inhibited. In a specific aspect, either the candidate compound or the PRO polypeptide is immobilized on a solid support. In another aspect, the non-immobilized component carries a detectable label. In a preferred aspect, this method comprises the steps of:

(a) contacting cells and a test compound to be screened in the presence of a PRO polypeptide under conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and

(b) determining the induction of said cellular response to determine if the test compound is an effective antagonist.

In another embodiment, the invention provides a method for identifying a compound that inhibits the expression of a PRO polypeptide in cells that normally express the polypeptide, wherein the method comprises contacting the cells with a test compound and determining whether the expression of the PRO polypeptide is inhibited. In a preferred aspect, this method comprises the steps of:

(a) contacting cells and a test compound to be screened under conditions suitable for allowing expression of the PRO polypeptide; and

(b) determining the inhibition of expression of said polypeptide.

In yet another embodiment, the present invention concerns a method for treating an immune-related disorder in a mammal that suffers therefrom comprising administering to the mammal a nucleic acid molecule that codes for either (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide or (c) an antagonist of a PRO polypeptide, wherein said agonist or antagonist may be an anti-PRO antibody. In a preferred embodiment, the mammal is human. In another preferred embodiment, the nucleic acid is administered via *ex vivo* gene therapy. In a further preferred embodiment, the nucleic acid is comprised within a vector, more preferably an adenoviral, adeno-associated viral, lentiviral or retroviral vector.

In yet another aspect, the invention provides a recombinant viral particle comprising a viral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide, or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein the viral vector is in association with viral structural proteins. Preferably, the signal sequence is from a mammal, such as from a native PRO polypeptide.

In a still further embodiment, the invention concerns an *ex vivo* producer cell comprising a nucleic acid construct that expresses retroviral structural proteins and also comprises a retroviral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein said producer cell packages the retroviral vector in association with the structural proteins to produce recombinant retroviral particles.

In a still further embodiment, the invention provides a method of increasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in

the mammal is decreased.

In a still further embodiment, the invention provides a method of increasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is decreased.

B. Additional Embodiments

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences.

In other embodiments, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid

sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences herein above identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about

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In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as herein before described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as herein before described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO69457 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA287163".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO69458 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA287164".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO52268 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA287165".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO69459 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA287166".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO62927 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA275240".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO59136 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA287167".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO37121 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA226658".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:14 shown in Figure 14.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO69460 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA287168".

Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO60475 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA272213".

Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO34451 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA218655".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO38070 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA227607".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO23756 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA194378".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO10404 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA287169".

Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO69461 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA288240".

Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO70006 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA288241".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO69462 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA287171".

Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO2081 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA287620".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

Figure 35A-B shows a nucleotide sequence (SEQ ID NO:35A-B) of a native sequence PRO70007 cDNA, wherein SEQ ID NO:35A-B is a clone designated herein as "DNA288242".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35A-B shown in Figure 35A-B.

Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO69463 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA287173".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO62908 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA275214".

Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO69464 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA287174".

Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO52804 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA287175".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO60438 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA272171".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO69465 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA287176".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO37421 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA226958".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO37596 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA227133".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO36124 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA225661".

Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO69466 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA287177".

Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO60499 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA272237".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO69467 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA287178".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO61824 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA273865".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO69468 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA287179".

Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO21341 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA287180".

Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67A-B shows a nucleotide sequence (SEQ ID NO:67A-B) of a native sequence PRO38213 cDNA, wherein SEQ ID NO:67A-B is a clone designated herein as "DNA227750".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67A-B shown in Figure 67A-B.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO69469 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA287181".

Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO37172 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA226709".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO35991 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA225528".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

Figure 75A-B shows a nucleotide sequence (SEQ ID NO:75A-B) of a native sequence PRO36905 cDNA, wherein SEQ ID NO:75A-B is a clone designated herein as "DNA226442".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75A-B shown in Figure 75A-B.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO69470 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA287182".

Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO36451 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA288243".

Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO69471 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA287184".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO37492 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA227029".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

Figure 85A-B shows a nucleotide sequence (SEQ ID NO:85A-B) of a native sequence PRO70008 cDNA, wherein SEQ ID NO:85A-B is a clone designated herein as "DNA288244".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85A-B shown in Figure 85A-B.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO69472 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA287186".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO69473 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA287187".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO36996 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA226533".

Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO22613 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA189698".

Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO69475 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA287189".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO61755 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA273794".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO70009 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA288245".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO69476 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA287190".

Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO4881 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA103554".

Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105A-B shows a nucleotide sequence (SEQ ID NO:105A-B) of a native sequence PRO12876 cDNA, wherein SEQ ID NO:105A-B is a clone designated herein as "DNA151420".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105A-B shown in Figure 105A-B.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO70010 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA288246".

Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO37534 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA227071".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

Figure 111A-B shows a nucleotide sequence (SEQ ID NO:111A-B) of a native sequence PRO21928 cDNA, wherein SEQ ID NO:111A-B is a clone designated herein as "DNA188400".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111A-B shown in Figure 111A-B.

Figure 113A-B shows a nucleotide sequence (SEQ ID NO:113A-B) of a native sequence PRO69478 cDNA, wherein SEQ ID NO:113A-B is a clone designated herein as "DNA287192".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113A-B shown in Figure 113A-B.

Figure 115A-B shows a nucleotide sequence (SEQ ID NO:115A-B) of a native sequence PRO69479 cDNA, wherein SEQ ID NO:115A-B is a clone designated herein as "DNA287193".

Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115A-B shown in Figure 115A-B.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO69480 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA287194".

Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO69481 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA287195".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO69482 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA287196".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO69483 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA287197".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO38642 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA228179".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO69484 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA287198".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO66269 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA287199".

Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1723 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA82376".

Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO22297 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA287623".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO61349 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA273346".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO69485 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA287201".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO69486 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA287202".

Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO69487 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA287203".

Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO36963 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA226500".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO23814 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA287204".

Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO57980 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA287205".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO20128 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA171400".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4551 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA103221".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO69488 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA287206".

Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO39268 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA287207".

Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO69489 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA287208".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO69490 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA287209".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO69491 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA287625".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO69492 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA287211".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO37713 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA227250".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO58993cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA287212".

Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO69493 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA287213".

Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO69494 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA287214".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO69495 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA287215".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO70011 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA288247".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO62861 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA275157".

Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO36640 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA226177".

Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181A-B shows a nucleotide sequence (SEQ ID NO:181A-B) of a native sequence PRO36766 cDNA, wherein SEQ ID NO:181A-B is a clone designated herein as "DNA287217".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181A-B shown in Figure 181A-B.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO69497 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA287218".

Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO69498 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA287219".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO69499 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA287220".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO69500 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA287221".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO69501 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA287222".

Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO70012 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA288248".

Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO69503 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA287224".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO69474 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA287188".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO69505 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA287226".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO69506 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA287227".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO69507 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA288249".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO51301 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA256257".

Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO69508 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA287229".

Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO69509 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA287230".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO69510 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA287231".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO69511 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA287232".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO51309 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA256265".

Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217A-B shows a nucleotide sequence (SEQ ID NO:217A-B) of a native sequence PRO50578 cDNA, wherein SEQ ID NO:217A-B is a clone designated herein as "DNA255513".

Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217A-B shown in Figure 217A-B.

Figure 219A-B shows a nucleotide sequence (SEQ ID NO:219A-B) of a native sequence PRO69512 cDNA, wherein SEQ ID NO:219A-B is a clone designated herein as "DNA287233".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219A-B shown in Figure 219A-B.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO69513 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA287234".

Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO69514 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA287235".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

Figure 225A-B shows a nucleotide sequence (SEQ ID NO:225A-B) of a native sequence PRO10607 cDNA, wherein SEQ ID NO:225A-B is a clone designated herein as "DNA287236".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225A-B shown in Figure 225A-B.

Figure 227A-B shows a nucleotide sequence (SEQ ID NO:227A-B) of a native sequence PRO61705 cDNA, wherein SEQ ID NO:227A-B is a clone designated herein as "DNA273742".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227A-B shown in Figure 227A-B.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO49214 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA253811".

Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO39648 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA287237".

Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO69515 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA287238".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO38497 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA287239".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO29371 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA287240".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO70013 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA288250".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO69516 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA287241".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO69517 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA287242".

Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO69518 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA287243".

Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO70014 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA288251".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO69520 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA287245".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO69521 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA287246".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO69522 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA287247".

Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO69523 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA287628".

Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO60513 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA272251".

Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO2512 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA288252".

Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO69524 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA287250".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO12569 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA150989".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO69525 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA287251".

Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO69526 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA287252".

Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO69527 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA287253".

Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO69528 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA287254".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO69529 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA287255".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO12166 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA151021".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO2154 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA287630".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO69530 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA287257".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO51916 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA257326".

Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO52174 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA287258".

Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO69531 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA287259".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO69532 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA287260".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

Figure 289 shows a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO69533 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA287261".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figure 289.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO69534 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA287262".

Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO54728 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA260982".

Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO70015 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA288253".

Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO69536 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA288254".

Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO69537 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA287265".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO37498 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA227035".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

Figure 303A-B shows a nucleotide sequence (SEQ ID NO:303A-B) of a native sequence PRO22175 cDNA, wherein SEQ ID NO:303A-B is a clone designated herein as "DNA189214".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303A-B shown in Figure 303A-B.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO69538 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA287266".

Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO37015 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA287267".

Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO12187 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA151799".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

Figure 311 shows a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO69539 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA287268".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figure 311.

Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO69880 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA287632".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO69541 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA287270".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO69542 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA287271".

Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO69543 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA287272".

Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO70016 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA288255".

Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

Figure 323A-B shows a nucleotide sequence (SEQ ID NO:323A-B) of a native sequence PRO69545 cDNA, wherein SEQ ID NO:323A-B is a clone designated herein as "DNA287273".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323A-B shown in Figure 323A-B.

Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO50197 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA255115".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO69546 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA287274".

Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO69547 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA287275".

Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO69548 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA287276".

Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO69549 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA287277".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO69550 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA287278".

Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO69551 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA287279".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO69552 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA287280".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO37460 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA226997".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO42223 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA242927".

Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345A-B shows a nucleotide sequence (SEQ ID NO:345A-B) of a native sequence PRO69553 cDNA, wherein SEQ ID NO:345A-B is a clone designated herein as "DNA287281".

Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345A-B shown in Figure 345A-B.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO69554 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA287282".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO69555 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA287283".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

Figure 351 shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO61014 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA272930".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figure 351.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO59915 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA287284".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

Figure 355A-B shows a nucleotide sequence (SEQ ID NO:355A-B) of a native sequence PRO37891 cDNA, wherein SEQ ID NO:355A-B is a clone designated herein as "DNA227428".

Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355A-B shown in Figure 355A-B.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO69556 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA287285".

Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO12875 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA151237".

Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO70017 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA288256".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO70018 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA288257".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO4426 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA287287".

Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO69558 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA287288".

Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO69559 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA287289".

Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO37676 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA227213".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO69560 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA287290".

Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO69561 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA287291".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO69562 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA287292".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO63204 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA287293".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO70019 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA288258".

Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO69564 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA287295".

Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO62830 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA287296".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO69565 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA287297".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO69566 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA287298".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO69567 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA287299".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO49675 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA254572".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO69568 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA287300".

Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO2013 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA75526".

Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO69569 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA287302".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO69570 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA287303".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO69571 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA287304".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405A-B shows a nucleotide sequence (SEQ ID NO:405A-B) of a native sequence PRO36403 cDNA, wherein SEQ ID NO:405A-B is a clone designated herein as "DNA225940".

Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405A-B shown in Figure 405A-B.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO4676 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA288259".

Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO37657 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA227194".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO62097 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA274167".

Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO38081 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA227618".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO69572 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA287306".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO69573 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA287307".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO69574 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA287308".

Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO69883 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA287635".

Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO69576 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA287310".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO37584 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA227121".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO11603 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA151007".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO70020 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA288260".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO51695 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA256762".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO69579 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA287314".

Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO69580 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA287315".

Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO69581 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA287316".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO69582 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA287317".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO69583 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA287318".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO69584 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA287319".

Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO69585 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA287320".

Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO69586 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA287321".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO69587 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA287322".

Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO69588 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA287323".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO69589 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA287637".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

Figure 455A-B shows a nucleotide sequence (SEQ ID NO:455A-B) of a native sequence PRO70021 cDNA, wherein SEQ ID NO:455A-B is a clone designated herein as "DNA288261".

Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455A-B shown in Figure 455A-B.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO69590 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA288262".

Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO70022 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA288263".

Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

Figure 461A-B shows a nucleotide sequence (SEQ ID NO:461A-B) of a native sequence PRO69592 cDNA, wherein SEQ ID NO:461A-B is a clone designated herein as "DNA287327".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461A-B shown in Figure 461A-B.

Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO37029 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA287328".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO69593 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA287329".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467A-B shows a nucleotide sequence (SEQ ID NO:467A-B) of a native sequence PRO69594 cDNA, wherein SEQ ID NO:467A-B is a clone designated herein as "DNA287330".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467A-B shown in Figure 467A-B.

Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO69595 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA287331".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO1207 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA66480".

Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO69596 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA287332".

Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO69597 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA287333".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO51139 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA256089".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO62545 cDNA, wherein SEQ ID NO: 479 is a clone designated herein as "DNA274778".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO3615 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA287334".

Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO38036 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA227573".

Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO69598 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA287335".

Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4701 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA103371".

Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO69599 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA287336".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO69600 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA287337".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO69601 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA287338".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO69887 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA287640".

Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO69603 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA287340".

Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO69604 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA287341".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO70023 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA288264".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO69606 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA287343".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO69607 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA287344".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO69608 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA287345".

Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO69609 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA287346".

Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO69610 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA287347".

Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO9902 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA287642".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO69611 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA287349".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO69612 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA287350".

Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO69613 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA287351".

Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO69614 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA287352".

Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO69615 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA287643".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figure 525 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO70024 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA288265".

Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figure 525.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO69616 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA287354".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO49619 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA254512".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO69617 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA287355".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO69618 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA287356".

Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO38040 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA227577".

Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO69619 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA287357".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO69620 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA287358".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO69621 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA287359".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543A-B shows a nucleotide sequence (SEQ ID NO:543A-B) of a native sequence PRO69622 cDNA, wherein SEQ ID NO:543A-B is a clone designated herein as "DNA287360".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543A-B shown in Figure 543A-B.

Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO4401 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA287362".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO70025 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA288266".

Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO69625 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA287364".

Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

Figure 551 shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO12025 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA288267".

Figure 552 shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in Figure 551.

Figure 553 shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO70026 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA288268".

Figure 554 shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in Figure 553.

Figure 555 shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO69627 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA287367".

Figure 556 shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in Figure 555.

Figure 557 shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO69628 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA287368".

Figure 558 shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in Figure 557.

Figure 559 shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO22637 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA189703".

Figure 560 shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in Figure 559.

Figure 561A-B shows a nucleotide sequence (SEQ ID NO:561A-B) of a native sequence PRO69629 cDNA, wherein SEQ ID NO:561A-B is a clone designated herein as "DNA287369".

Figure 562 shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561A-B shown in Figure 561A-B.

Figure 563 shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO70027 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA288269".

Figure 564 shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in Figure 563.

Figure 565 shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO70028 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA288270".

Figure 566 shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in Figure 565.

Figure 567 shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO69632 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA287372".

Figure 568 shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in Figure 567.

Figure 569 shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO69634 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA287374".

Figure 570 shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in Figure 569.

Figure 571 shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO36857 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA226394".

Figure 572 shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in Figure 571.

Figure 573 shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO69893 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA287648".

Figure 574 shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in Figure 573.

Figure 575 shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO69635 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA287375".

Figure 576 shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in Figure 575.

Figure 577 shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO6180 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA287376".

Figure 578 shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in Figure 577.

Figure 579 shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO69637 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA287378".

Figure 580 shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in Figure 579.

Figure 581 shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO69638 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA287379".

Figure 582 shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in Figure 581.

Figure 583 shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO69639 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA287380".

Figure 584 shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in Figure 583.

Figure 585 shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO69640 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA287381".

Figure 586 shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in Figure 585.

Figure 587 shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO69641 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA287382".

Figure 588 shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in Figure 587.

Figure 589 shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO62766 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA275043".

Figure 590 shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in Figure 589.

Figure 591 shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO53782 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA287383".

Figure 592 shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in Figure 591.

Figure 593 shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO61472 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA273489".

Figure 594 shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in Figure 593.

Figure 595 shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO38179 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA227716".

Figure 596 shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in Figure 595.

Figure 597 shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO69642 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA287384".

Figure 598 shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in Figure 597.

Figure 599 shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO69643 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA287385".

Figure 600 shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in Figure 599.

Figure 601 shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO69644 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA287386".

Figure 602 shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in Figure 601.

Figure 603 shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO69645 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA287387".

Figure 604 shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in Figure 603.

Figure 605 shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO11608 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA151077".

Figure 606 shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in Figure 605.

Figure 607 shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO69646 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA287388".

Figure 608 shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in Figure 607.

Figure 609 shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO59825 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA271536".

Figure 610 shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in Figure 609.

Figure 611 shows a nucleotide sequence (SEQ ID NO:611) of a native sequence PRO69647 cDNA, wherein SEQ ID NO:611 is a clone designated herein as "DNA287389".

Figure 612 shows the amino acid sequence (SEQ ID NO:612) derived from the coding sequence of SEQ ID NO:611 shown in Figure 611.

Figure 613 shows a nucleotide sequence (SEQ ID NO:613) of a native sequence PRO69648 cDNA, wherein SEQ ID NO:613 is a clone designated herein as "DNA287390".

Figure 614 shows the amino acid sequence (SEQ ID NO:614) derived from the coding sequence of SEQ ID NO:613 shown in Figure 613.

Figure 615 shows a nucleotide sequence (SEQ ID NO:615) of a native sequence PRO70029 cDNA, wherein SEQ ID NO:615 is a clone designated herein as "DNA288271".

Figure 616 shows the amino acid sequence (SEQ ID NO:616) derived from the coding sequence of SEQ ID NO:615 shown in Figure 615.

Figure 617 shows a nucleotide sequence (SEQ ID NO:617) of a native sequence PRO1213 cDNA, wherein SEQ ID NO:617 is a clone designated herein as "DNA66487".

Figure 618 shows the amino acid sequence (SEQ ID NO:618) derived from the coding sequence of SEQ ID NO:617 shown in Figure 617.

Figure 619 shows a nucleotide sequence (SEQ ID NO:619) of a native sequence PRO70030 cDNA, wherein SEQ ID NO:619 is a clone designated herein as "DNA288272".

Figure 620 shows the amino acid sequence (SEQ ID NO:620) derived from the coding sequence of SEQ ID NO:619 shown in Figure 619.

Figure 621 shows a nucleotide sequence (SEQ ID NO:621) of a native sequence PRO50195 cDNA, wherein SEQ ID NO:621 is a clone designated herein as "DNA255113".

Figure 622 shows the amino acid sequence (SEQ ID NO:622) derived from the coding sequence of SEQ ID NO:621 shown in Figure 621.

Figure 623 shows a nucleotide sequence (SEQ ID NO:623) of a native sequence PRO69651 cDNA, wherein SEQ ID NO:623 is a clone designated herein as "DNA287393".

Figure 624 shows the amino acid sequence (SEQ ID NO:624) derived from the coding sequence of SEQ ID NO:623 shown in Figure 623.

Figure 625A-B shows a nucleotide sequence (SEQ ID NO:625A-B) of a native sequence PRO37538 cDNA, wherein SEQ ID NO:625A-B is a clone designated herein as "DNA227075".

Figure 626 shows the amino acid sequence (SEQ ID NO:626) derived from the coding sequence of SEQ ID NO:625A-B shown in Figure 625A-B.

Figure 627 shows a nucleotide sequence (SEQ ID NO:627) of a native sequence PRO69652 cDNA, wherein SEQ ID NO:627 is a clone designated herein as "DNA287394".

Figure 628 shows the amino acid sequence (SEQ ID NO:628) derived from the coding sequence of SEQ ID NO:627 shown in Figure 627.

Figure 629 shows a nucleotide sequence (SEQ ID NO:629) of a native sequence PRO59210 cDNA, wherein SEQ ID NO:629 is a clone designated herein as "DNA270875".

Figure 630 shows the amino acid sequence (SEQ ID NO:630) derived from the coding sequence of SEQ ID NO:629 shown in Figure 629.

Figure 631 shows a nucleotide sequence (SEQ ID NO:631) of a native sequence PRO23374 cDNA, wherein SEQ ID NO:631 is a clone designated herein as "DNA193967".

Figure 632 shows the amino acid sequence (SEQ ID NO:632) derived from the coding sequence of SEQ ID NO:631 shown in Figure 631.

Figure 633 shows a nucleotide sequence (SEQ ID NO:633) of a native sequence PRO24844 cDNA, wherein SEQ ID NO:633 is a clone designated herein as "DNA288273".

Figure 634 shows the amino acid sequence (SEQ ID NO:634) derived from the coding sequence of SEQ ID NO:633 shown in Figure 633.

Figure 635 shows a nucleotide sequence (SEQ ID NO:635) of a native sequence PRO70031 cDNA, wherein SEQ ID NO:635 is a clone designated herein as "DNA288274".

Figure 636 shows the amino acid sequence (SEQ ID NO:636) derived from the coding sequence of SEQ ID NO:635 shown in Figure 635.

Figure 637 shows a nucleotide sequence (SEQ ID NO:637) of a native sequence PRO69653 cDNA, wherein SEQ ID NO:637 is a clone designated herein as "DNA287396".

Figure 638 shows the amino acid sequence (SEQ ID NO:638) derived from the coding sequence of SEQ ID NO:637 shown in Figure 637.

Figure 639 shows a nucleotide sequence (SEQ ID NO:639) of a native sequence PRO69654 cDNA, wherein SEQ ID NO:639 is a clone designated herein as "DNA287397".

Figure 640 shows the amino acid sequence (SEQ ID NO:640) derived from the coding sequence of SEQ ID NO:639 shown in Figure 639.

Figure 641 shows a nucleotide sequence (SEQ ID NO:641) of a native sequence PRO69655 cDNA, wherein SEQ ID NO:641 is a clone designated herein as "DNA287398".

Figure 642 shows the amino acid sequence (SEQ ID NO:642) derived from the coding sequence of SEQ ID NO:641 shown in Figure 641.

Figure 643 shows a nucleotide sequence (SEQ ID NO:643) of a native sequence PRO69656 cDNA, wherein SEQ ID NO:643 is a clone designated herein as "DNA287399".

Figure 644 shows the amino acid sequence (SEQ ID NO:644) derived from the coding sequence of SEQ ID NO:643 shown in Figure 643.

Figure 645 shows a nucleotide sequence (SEQ ID NO:645) of a native sequence PRO70032 cDNA, wherein SEQ ID NO:645 is a clone designated herein as "DNA288275".

Figure 646 shows the amino acid sequence (SEQ ID NO:646) derived from the coding sequence of SEQ ID NO:645 shown in Figure 645.

Figure 647 shows a nucleotide sequence (SEQ ID NO:647) of a native sequence PRO69659 cDNA, wherein SEQ ID NO:647 is a clone designated herein as "DNA287402".

Figure 648 shows the amino acid sequence (SEQ ID NO:648) derived from the coding sequence of SEQ ID NO:647 shown in Figure 647.

Figure 649 shows a nucleotide sequence (SEQ ID NO:649) of a native sequence PRO69660 cDNA, wherein SEQ ID NO:649 is a clone designated herein as "DNA287403".

Figure 650 shows the amino acid sequence (SEQ ID NO:650) derived from the coding sequence of SEQ ID NO:649 shown in Figure 649.

Figure 651A-B shows a nucleotide sequence (SEQ ID NO:651A-B) of a native sequence PRO58054 cDNA, wherein SEQ ID NO:651A-B is a clone designated herein as "DNA269642".

Figure 652 shows the amino acid sequence (SEQ ID NO:652) derived from the coding sequence of SEQ ID NO:651A-B shown in Figure 651A-B.

Figure 653 shows a nucleotide sequence (SEQ ID NO:653) of a native sequence PRO69661 cDNA, wherein SEQ ID NO:653 is a clone designated herein as "DNA287404".

Figure 654 shows the amino acid sequence (SEQ ID NO:654) derived from the coding sequence of SEQ ID NO:653 shown in Figure 653.

Figure 655 shows a nucleotide sequence (SEQ ID NO:655) of a native sequence PRO69662 cDNA, wherein SEQ ID NO:655 is a clone designated herein as "DNA287405".

Figure 656 shows the amino acid sequence (SEQ ID NO:656) derived from the coding sequence of SEQ ID NO:655 shown in Figure 655.

Figure 657 shows a nucleotide sequence (SEQ ID NO:657) of a native sequence PRO69898 cDNA, wherein SEQ ID NO:657 is a clone designated herein as "DNA287653".

Figure 658 shows the amino acid sequence (SEQ ID NO:658) derived from the coding sequence of SEQ ID NO:657 shown in Figure 657.

Figure 659 shows a nucleotide sequence (SEQ ID NO:659) of a native sequence PRO69664 cDNA, wherein SEQ ID NO:659 is a clone designated herein as "DNA287407".

Figure 660 shows the amino acid sequence (SEQ ID NO:660) derived from the coding sequence of SEQ ID NO:659 shown in Figure 659.

Figure 661 shows a nucleotide sequence (SEQ ID NO:661) of a native sequence PRO69665 cDNA, wherein SEQ ID NO:661 is a clone designated herein as "DNA287408".

Figure 662 shows the amino acid sequence (SEQ ID NO:662) derived from the coding sequence of SEQ ID NO:661 shown in Figure 661.

Figure 663 shows a nucleotide sequence (SEQ ID NO:663) of a native sequence PRO69666 cDNA, wherein SEQ ID NO:663 is a clone designated herein as "DNA287409".

Figure 664 shows the amino acid sequence (SEQ ID NO:664) derived from the coding sequence of SEQ ID NO:663 shown in Figure 663.

Figure 665 shows a nucleotide sequence (SEQ ID NO:665) of a native sequence PRO69667 cDNA, wherein SEQ ID NO:665 is a clone designated herein as "DNA287410".

Figure 666 shows the amino acid sequence (SEQ ID NO:666) derived from the coding sequence of SEQ ID NO:665 shown in Figure 665.

Figure 667 shows a nucleotide sequence (SEQ ID NO:667) of a native sequence PRO69669 cDNA, wherein SEQ ID NO:667 is a clone designated herein as "DNA287412".

Figure 668 shows the amino acid sequence (SEQ ID NO:668) derived from the coding sequence of SEQ ID NO:667 shown in Figure 667.

Figure 669 shows a nucleotide sequence (SEQ ID NO:669) of a native sequence PRO69671 cDNA, wherein SEQ ID NO:669 is a clone designated herein as "DNA287414".

Figure 670 shows the amino acid sequence (SEQ ID NO:670) derived from the coding sequence of SEQ ID NO:669 shown in Figure 669.

Figure 671 shows a nucleotide sequence (SEQ ID NO:671) of a native sequence PRO69672 cDNA, wherein SEQ ID NO:671 is a clone designated herein as "DNA287415".

Figure 672 shows the amino acid sequence (SEQ ID NO:672) derived from the coding sequence of SEQ ID NO:671 shown in Figure 671.

Figure 673A-B shows a nucleotide sequence (SEQ ID NO:673A-B) of a native sequence PRO58204 cDNA, wherein SEQ ID NO:673A-B is a clone designated herein as "DNA269799".

Figure 674 shows the amino acid sequence (SEQ ID NO:674) derived from the coding sequence of SEQ ID NO:673A-B shown in Figure 673A-B.

Figure 675 shows a nucleotide sequence (SEQ ID NO:675) of a native sequence PRO49419 cDNA, wherein SEQ ID NO:675 is a clone designated herein as "DNA254308".

Figure 676 shows the amino acid sequence (SEQ ID NO:676) derived from the coding sequence of SEQ ID NO:675 shown in Figure 675.

Figure 677 shows a nucleotide sequence (SEQ ID NO:677) of a native sequence PRO69673 cDNA, wherein SEQ ID NO:677 is a clone designated herein as "DNA287416".

Figure 678 shows the amino acid sequence (SEQ ID NO:678) derived from the coding sequence of SEQ ID NO:677 shown in Figure 677.

Figure 679 shows a nucleotide sequence (SEQ ID NO:679) of a native sequence PRO69674 cDNA, wherein SEQ ID NO:679 is a clone designated herein as "DNA287417".

Figure 680 shows the amino acid sequence (SEQ ID NO:680) derived from the coding sequence of SEQ ID NO:679 shown in Figure 679.

Figure 681 shows a nucleotide sequence (SEQ ID NO:681) of a native sequence PRO49810 cDNA, wherein SEQ ID NO:681 is a clone designated herein as "DNA254710".

Figure 682 shows the amino acid sequence (SEQ ID NO:682) derived from the coding sequence of SEQ ID NO:681 shown in Figure 681.

Figure 683 shows a nucleotide sequence (SEQ ID NO:683) of a native sequence PRO70033 cDNA, wherein SEQ ID NO:683 is a clone designated herein as "DNA288276".

Figure 684 shows the amino acid sequence (SEQ ID NO:684) derived from the coding sequence of SEQ ID NO:683 shown in Figure 683.

Figure 685 shows a nucleotide sequence (SEQ ID NO:685) of a native sequence PRO69676 cDNA, wherein SEQ ID NO:685 is a clone designated herein as "DNA287419".

Figure 686 shows the amino acid sequence (SEQ ID NO:686) derived from the coding sequence of SEQ ID NO:685 shown in Figure 685.

Figure 687 shows a nucleotide sequence (SEQ ID NO:687) of a native sequence PRO58076 cDNA, wherein SEQ ID NO:687 is a clone designated herein as "DNA269665".

Figure 688 shows the amino acid sequence (SEQ ID NO:688) derived from the coding sequence of SEQ ID NO:687 shown in Figure 687.

Figure 689 shows a nucleotide sequence (SEQ ID NO:689) of a native sequence PRO69677 cDNA, wherein SEQ ID NO:689 is a clone designated herein as "DNA287420".

Figure 690 shows the amino acid sequence (SEQ ID NO:690) derived from the coding sequence of SEQ ID NO:689 shown in Figure 689.

Figure 691 shows a nucleotide sequence (SEQ ID NO:691) of a native sequence PRO69678 cDNA, wherein SEQ ID NO:691 is a clone designated herein as "DNA287421".

Figure 692 shows the amino acid sequence (SEQ ID NO:692) derived from the coding sequence of SEQ ID NO:691 shown in Figure 691.

Figure 693 shows a nucleotide sequence (SEQ ID NO:693) of a native sequence PRO69679 cDNA, wherein SEQ ID NO:693 is a clone designated herein as "DNA287422".

Figure 694 shows the amino acid sequence (SEQ ID NO:694) derived from the coding sequence of SEQ ID NO:693 shown in Figure 693.

Figure 695 shows a nucleotide sequence (SEQ ID NO:695) of a native sequence PRO1718 cDNA, wherein SEQ ID NO:695 is a clone designated herein as "DNA82362".

Figure 696 shows the amino acid sequence (SEQ ID NO:696) derived from the coding sequence of SEQ ID NO:695 shown in Figure 695.

Figure 697 shows a nucleotide sequence (SEQ ID NO:697) of a native sequence PRO51161 cDNA, wherein SEQ ID NO:697 is a clone designated herein as "DNA256112".

Figure 698 shows the amino acid sequence (SEQ ID NO:698) derived from the coding sequence of SEQ ID NO:697 shown in Figure 697.

Figure 699 shows a nucleotide sequence (SEQ ID NO:699) of a native sequence PRO69680 cDNA, wherein SEQ ID NO:699 is a clone designated herein as "DNA287423".

Figure 700 shows the amino acid sequence (SEQ ID NO:700) derived from the coding sequence of SEQ ID NO:699 shown in Figure 699.

Figure 701 shows a nucleotide sequence (SEQ ID NO:701) of a native sequence PRO59281 cDNA, wherein SEQ ID NO:701 is a clone designated herein as "DNA270950".

Figure 702 shows the amino acid sequence (SEQ ID NO:702) derived from the coding sequence of SEQ ID NO:701 shown in Figure 701.

Figure 703 shows a nucleotide sequence (SEQ ID NO:703) of a native sequence PRO36102 cDNA, wherein SEQ ID NO:703 is a clone designated herein as "DNA225639".

Figure 704 shows the amino acid sequence (SEQ ID NO:704) derived from the coding sequence of SEQ ID NO:703 shown in Figure 703.

Figure 705 shows a nucleotide sequence (SEQ ID NO:705) of a native sequence PRO61799 cDNA, wherein SEQ ID NO:705 is a clone designated herein as "DNA273839".

Figure 706 shows the amino acid sequence (SEQ ID NO:706) derived from the coding sequence of SEQ ID NO:705 shown in Figure 705.

Figure 707 shows a nucleotide sequence (SEQ ID NO:707) of a native sequence PRO69681 cDNA, wherein SEQ ID NO:707 is a clone designated herein as "DNA287424 ".

Figure 708 shows the amino acid sequence (SEQ ID NO:708) derived from the coding sequence of SEQ ID NO:707 shown in Figure 707.

Figure 709 shows a nucleotide sequence (SEQ ID NO:709) of a native sequence PRO69682 cDNA, wherein SEQ ID NO:709 is a clone designated herein as "DNA287425".

Figure 710 shows the amino acid sequence (SEQ ID NO:710) derived from the coding sequence of SEQ ID NO:710 shown in Figure 710.

Figure 711 shows a nucleotide sequence (SEQ ID NO:711) of a native sequence PRO69901 cDNA, wherein SEQ ID NO:711 is a clone designated herein as "DNA287656".

Figure 712 shows the amino acid sequence (SEQ ID NO:712) derived from the coding sequence of SEQ ID NO:711 shown in Figure 711.

Figure 713 shows a nucleotide sequence (SEQ ID NO:713) of a native sequence PRO69684 cDNA, wherein SEQ ID NO:713 is a clone designated herein as "DNA287427".

Figure 714 shows the amino acid sequence (SEQ ID NO:714) derived from the coding sequence of SEQ ID NO:713 shown in Figure 713.

Figure 715 shows a nucleotide sequence (SEQ ID NO:715) of a native sequence PRO69685 cDNA, wherein SEQ ID NO:715 is a clone designated herein as "DNA287428".

Figure 716 shows the amino acid sequence (SEQ ID NO:716) derived from the coding sequence of SEQ ID NO:715 shown in Figure 715.

Figure 717 shows a nucleotide sequence (SEQ ID NO:717) of a native sequence PRO69686 cDNA, wherein SEQ ID NO:717 is a clone designated herein as "DNA287429".

Figure 718 shows the amino acid sequence (SEQ ID NO:718) derived from the coding sequence of SEQ ID NO:717 shown in Figure 717.

Figure 719 shows a nucleotide sequence (SEQ ID NO:719) of a native sequence PRO69687 cDNA, wherein SEQ ID NO:719 is a clone designated herein as "DNA287430".

Figure 720 shows the amino acid sequence (SEQ ID NO:720) derived from the coding sequence of SEQ ID NO:719 shown in Figure 719.

Figure 721 shows a nucleotide sequence (SEQ ID NO:721) of a native sequence PRO38469 cDNA, wherein SEQ ID NO:721 is a clone designated herein as "DNA228006".

Figure 722 shows the amino acid sequence (SEQ ID NO:722) derived from the coding sequence of SEQ ID NO:721 shown in Figure 721.

Figure 723 shows a nucleotide sequence (SEQ ID NO:723) of a native sequence PRO69688 cDNA, wherein SEQ ID NO:723 is a clone designated herein as "DNA287657".

Figure 724 shows the amino acid sequence (SEQ ID NO:724) derived from the coding sequence of SEQ ID NO:723 shown in Figure 723.

Figure 725 shows a nucleotide sequence (SEQ ID NO:725) of a native sequence PRO70034 cDNA, wherein SEQ ID NO:725 is a clone designated herein as "DNA288277".

Figure 726 shows the amino acid sequence (SEQ ID NO:726) derived from the coding sequence of SEQ ID NO:725 shown in Figure 725.

Figure 727 shows a nucleotide sequence (SEQ ID NO:727) of a native sequence PRO59354 cDNA, wherein SEQ ID NO:727 is a clone designated herein as "DNA271026".

Figure 728 shows the amino acid sequence (SEQ ID NO:728) derived from the coding sequence of SEQ ID NO:727 shown in Figure 727.

Figure 729 shows a nucleotide sequence (SEQ ID NO:729) of a native sequence PRO59189 cDNA, wherein SEQ ID NO:729 is a clone designated herein as "DNA270851".

Figure 730 shows the amino acid sequence (SEQ ID NO:730) derived from the coding sequence of SEQ ID NO:729 shown in Figure 729.

Figure 731 shows a nucleotide sequence (SEQ ID NO:731) of a native sequence PRO38197 cDNA, wherein SEQ ID NO:731 is a clone designated herein as "DNA227734".

Figure 732 shows the amino acid sequence (SEQ ID NO:732) derived from the coding sequence of SEQ ID NO:731 shown in Figure 731.

Figure 733 shows a nucleotide sequence (SEQ ID NO:733) of a native sequence PRO69902 cDNA, wherein SEQ ID NO:733 is a clone designated herein as "DNA287658".

Figure 734 shows the amino acid sequence (SEQ ID NO:734) derived from the coding sequence of SEQ ID NO:733 shown in Figure 733.

Figure 735 shows a nucleotide sequence (SEQ ID NO:735) of a native sequence PRO69690 cDNA, wherein SEQ ID NO:735 is a clone designated herein as "DNA287433".

Figure 736 shows the amino acid sequence (SEQ ID NO:736) derived from the coding sequence of SEQ ID NO:735 shown in Figure 735.

Figure 737A-B shows a nucleotide sequence (SEQ ID NO:737A-B) of a native sequence PRO61569 cDNA, wherein SEQ ID NO:737A-B is a clone designated herein as "DNA273593".

Figure 738 shows the amino acid sequence (SEQ ID NO:738) derived from the coding sequence of SEQ ID NO:737A-B shown in Figure 737A-B.

Figure 739 shows a nucleotide sequence (SEQ ID NO:739) of a native sequence PRO69903 cDNA, wherein SEQ ID NO:739 is a clone designated herein as "DNA287659".

Figure 740 shows the amino acid sequence (SEQ ID NO:740) derived from the coding sequence of SEQ ID NO:739 shown in Figure 739.

Figure 741 shows a nucleotide sequence (SEQ ID NO:741) of a native sequence PRO1970 cDNA, wherein SEQ ID NO:741 is a clone designated herein as "DNA287434".

Figure 742 shows the amino acid sequence (SEQ ID NO:742) derived from the coding sequence of SEQ ID NO:741 shown in Figure 741.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In

various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about

86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B

(which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid

sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least

about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word

threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1)

to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative

temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

The term "immune related disease" means a disease in which a component of the immune system of a mammal causes, mediates or otherwise contributes to a morbidity in the mammal. Also included are diseases in which stimulation or intervention of the immune response has an ameliorative effect on progression of the disease. Included within this term are immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, *etc.*

The term "T cell mediated disease" means a disease in which T cells directly or indirectly mediate or otherwise contribute to a morbidity in a mammal. The T cell mediated disease may be associated with cell mediated effects, lymphokine mediated effects, *etc.*, and even effects associated with B cells if the B cells are stimulated, for example, by the lymphokines secreted by T cells.

Examples of immune-related and inflammatory diseases, some of which are immune or T cell mediated, which can be treated according to the invention include systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease. Infectious diseases including viral diseases such as AIDS (HIV infection), hepatitis A, B, C, D, and E, herpes, *etc.*, bacterial infections, fungal infections, protozoal infections and parasitic infections.

The term "effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which results in achieving a particular stated purpose. An "effective amount" of a PRO polypeptide or agonist or antagonist thereof may be determined empirically. Furthermore, a "therapeutically effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which is effective for achieving a stated therapeutic effect. This amount may also be determined empirically.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (*e.g.*, I^{131}, I^{125}, Y^{90} and Re^{186}), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiotepa, busulfan, cytoxin, taxoids, *e.g.*, paclitaxel (Taxol, Bristol-Myers Squibb Oncology, Princeton, NJ), and doxetaxel (Taxotere, Rhône-Poulenc Rorer, Antony, France), toxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin, mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), melphalan and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially cancer cell overexpressing any of the genes identified herein, either *in vitro* or *in*

vivo. Thus, the growth inhibitory agent is one which significantly reduces the percentage of cells overexpressing such genes in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxol, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in *The Molecular Basis of Cancer*, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogens, and antineoplastic drugs" by Murakami *et al.* (WB Saunders: Philadelphia, 1995), especially p. 13.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-α and -β; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-β; platelet-growth factor; transforming growth factors (TGFs) such as TGF-α and TGF-β; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-α, -β, and -γ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1α, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF-α or TNF-β; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (*i.e.*, is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

As used herein, the term "inflammatory cells" designates cells that enhance the inflammatory response such as mononuclear cells, eosinophils, macrophages, and polymorphonuclear neutrophils (PMN).

Table 1

```
/*
*
* C-C increased from 12 to 15
* Z is average of EQ
* B is average of ND
* match with stop is _M; stop-stop = 0; J (joker) match = 0
*/
#define  _M      -8        /* value of a match with a stop */

int      _day[26][26] = {
/*     A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */   { 2, 0,-2, 0, 0,-4, 1,-1,-1, 0,-1,-2,-1, 0,_M, 1, 0,-2, 1, 1, 0, 0,-6, 0,-3, 0},
/* B */   { 0, 3,-4, 3, 2,-5, 0, 1,-2, 0, 0,-3,-2, 2,_M,-1, 1, 0, 0, 0, 0,-2,-5, 0,-3, 1},
/* C */   {-2,-4,15,-5,-5,-4,-3,-3,-2, 0,-5,-6,-5,-4,_M,-3,-5,-4, 0,-2, 0,-2,-8, 0, 0,-5},
/* D */   { 0, 3,-5, 4, 3,-6, 1, 1,-2, 0, 0,-4,-3, 2,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 2},
/* E */   { 0, 2,-5, 3, 4,-5, 0, 1,-2, 0, 0,-3,-2, 1,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 3},
/* F */   {-4,-5,-4,-6,-5, 9,-5,-2, 1, 0,-5, 2, 0,-4,_M,-5,-5,-4,-3,-3, 0,-1, 0, 0, 7,-5},
/* G */   { 1, 0,-3, 1, 0,-5, 5,-2,-3, 0,-2,-4,-3, 0,_M,-1,-1,-3, 1, 0, 0,-1,-7, 0,-5, 0},
/* H */   {-1, 1,-3, 1, 1,-2,-2, 6,-2, 0, 0,-2,-2, 2,_M, 0, 3, 2,-1,-1, 0,-2,-3, 0, 0, 2},
/* I */   {-1,-2,-2,-2,-2, 1,-3,-2, 5, 0,-2, 2, 2,-2,_M,-2,-2,-2,-1, 0, 0, 4,-5, 0,-1,-2},
/* J */   { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */   {-1, 0,-5, 0, 0,-5,-2, 0,-2, 0, 5,-3, 0, 1,_M,-1, 1, 3, 0, 0, 0,-2,-3, 0,-4, 0},
/* L */   {-2,-3,-6,-4,-3, 2,-4,-2, 2, 0,-3, 6, 4,-3,_M,-3,-2,-3,-3,-1, 0, 2,-2, 0,-1,-2},
/* M */   {-1,-2,-5,-3,-2, 0,-3,-2, 2, 0, 0, 4, 6,-2,_M,-2,-1, 0,-2,-1, 0, 2,-4, 0,-2,-1},
/* N */   { 0, 2,-4, 2, 1,-4, 0, 2,-2, 0, 1,-3,-2, 2,_M,-1, 1, 0, 1, 0, 0,-2,-4, 0,-2, 1},
/* O */   {_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M, 0,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M},
/* P */   { 1,-1,-3,-1,-1,-5,-1, 0,-2, 0,-1,-3,-2,-1,_M, 6, 0, 0, 1, 0, 0,-1,-6, 0,-5, 0},
/* Q */   { 0, 1,-5, 2, 2,-5,-1, 3,-2, 0, 1,-2,-1, 1,_M, 0, 4, 1,-1,-1, 0,-2,-5, 0,-4, 3},
/* R */   {-2, 0,-4,-1,-1,-4,-3, 2,-2, 0, 3,-3, 0, 0,_M, 0, 1, 6, 0,-1, 0,-2, 2, 0,-4, 0},
/* S */   { 1, 0, 0, 0, 0,-3, 1,-1,-1, 0, 0.-3,-2, 1,_M, 1,-1, 0, 2, 1, 0,-1,-2, 0,-3, 0},
/* T */   { 1, 0,-2, 0, 0,-3, 0,-1, 0, 0, 0,-1,-1, 0,_M, 0,-1,-1, 1, 3, 0, 0,-5, 0,-3, 0},
/* U */   { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */   { 0,-2,-2,-2,-2,-1,-1,-2, 4, 0,-2, 2, 2,-2,_M,-1,-2,-2,-1, 0, 0, 4,-6, 0,-2,-2},
/* W */   {-6,-5,-8,-7,-7, 0,-7,-3,-5, 0,-3,-2,-4,-4,_M,-6,-5, 2,-2,-5, 0,-6,17, 0, 0,-6},
/* X */   { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */   {-3,-3, 0,-4,-4, 7,-5, 0,-1, 0,-4,-1,-2,-2,_M,-5,-4,-4,-3,-3, 0,-2, 0, 0,10,-4},
/* Z */   { 0, 1,-5, 2, 3,-5, 0, 2,-2, 0, 0,-2,-1, 1,_M, 0, 3, 0, 0, 0, 0,-2,-6, 0,-4, 4}
};
```

Table 1 (cont')

```
/*
 */
#include <stdio.h>
#include <ctype.h>

#define MAXJMP    16     /* max jumps in a diag */
#define MAXGAP    24     /* don't continue to penalize gaps larger than this */
#define JMPS      1024   /* max jmps in an path */
#define MX        4      /* save if there's at least MX-1 bases since last jmp */

#define DMAT      3      /* value of matching bases */
#define DMIS      0      /* penalty for mismatched bases */
#define DINS0     8      /* penalty for a gap */
#define DINS1     1      /* penalty per base */
#define PINS0     8      /* penalty for a gap */
#define PINS1     4      /* penalty per residue */

struct jmp {
        short           n[MAXJMP];      /* size of jmp (neg for dely) */
        unsigned short  x[MAXJMP];      /* base no. of jmp in seq x */
};                                      /* limits seq to 2^16 -1 */

struct diag {
        int             score;          /* score at last jmp */
        long            offset;         /* offset of prev block */
        short           ijmp;           /* current jmp index */
        struct jmp      jp;             /* list of jmps */
};

struct path {
        int     spc;            /* number of leading spaces */
        short   n[JMPS]; /* size of jmp (gap) */
        int     x[JMPS]; /* loc of jmp (last elem before gap) */
};

char            *ofile;                 /* output file name */
char            *namex[2];              /* seq names: getseqs() */
char            *prog;                  /* prog name for err msgs */
char            *seqx[2];               /* seqs: getseqs() */
int             dmax;                   /* best diag: nw() */
int             dmax0;                  /* final diag */
int             dna;                    /* set if dna: main() */
int             endgaps;                /* set if penalizing end gaps */
int             gapx, gapy;             /* total gaps in seqs */
int             len0, len1;             /* seq lens */
int             ngapx, ngapy;           /* total size of gaps */
int             smax;                   /* max score: nw() */
int             *xbm;                   /* bitmap for matching */
long            offset;                 /* current offset in jmp file */
struct  diag    *dx;                    /* holds diagonals */
struct  path    pp[2];                  /* holds path for seqs */

char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_calloc();
```

Table 1 (cont')

```
/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *   where file1 and file2 are two dna or two protein sequences.
 *   The sequences can be in upper- or lower-case an may contain ambiguity
 *   Any lines beginning with ';', '>' or '<' are ignored
 *   Max file length is 65535 (limited by unsigned short x in the jmp struct)
 *   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 *   Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static    _dbval[26] = {
          1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static    _pbval[26] = {
          1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
          128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
          1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
          1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
          main
          int       ac;
          char      *av[ ];
{
          prog = av[0];
          if (ac != 3) {
                    fprintf(stderr,"usage: %s file1 file2\n", prog);
                    fprintf(stderr,"where file1 and file2 are two dna or two protein sequences.\n");
                    fprintf(stderr,"The sequences can be in upper- or lower-case\n");
                    fprintf(stderr,"Any lines beginning with ';' or '<' are ignored\n");
                    fprintf(stderr,"Output is in the file \"align.out\"\n");
                    exit(1);
          }
          namex[0] = av[1];
          namex[1] = av[2];
          seqx[0] = getseq(namex[0], &len0);
          seqx[1] = getseq(namex[1], &len1);
          xbm = (dna)? _dbval : _pbval;

          endgaps = 0;                    /* 1 to penalize endgaps */
          ofile = "align.out";            /* output file */

          nw();               /* fill in the matrix, get the possible jmps */
          readjmps();         /* get the actual jmps */
          print();            /* print stats, alignment */

          cleanup(0);         /* unlink any tmp files */
}
```

Table 1 (cont')

```
/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
        nw
{
        char            *px, *py;       /* seqs and ptrs */
        int             *ndely, *dely;  /* keep track of dely */
        int             ndelx, delx;    /* keep track of delx */
        int             *tmp;           /* for swapping row0, row1 */
        int             mis;            /* score for each type */
        int             ins0, ins1;     /* insertion penalties */
        register        id;             /* diagonal index */
        register        ij;             /* jmp index */
        register        *col0, *col1;   /* score for curr, last row */
        register        xx, yy;         /* index into seqs */

        dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
        col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;

        smax = -10000;
        if (endgaps) {
                for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                        col0[yy] = dely[yy] = col0[yy-1] - ins1;
                        ndely[yy] = yy;
                }
                col0[0] = 0;    /* Waterman Bull Math Biol 84 */
        }
        else
                for (yy = 1; yy <= len1; yy++)
                        dely[yy] = -ins0;

        /* fill in match matrix
         */
        for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
                /* initialize first entry in col
                 */
                if (endgaps) {
                        if (xx == 1)
                                col1[0] = delx = -(ins0+ins1);
                        else
                                col1[0] = delx = col0[0] - ins1;
                        ndelx = xx;
                }
                else {
                        col1[0] = 0;
                        delx = -ins0;
                        ndelx = 0;
                }
```

Table 1 (cont')

...nw

```
for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
	mis = col0[yy-1];
	if (dna)
		mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
	else
		mis += _day[*px-'A'][*py-'A'];

	/* update penalty for del in x seq;
	 * favor new del over ongong del
	 * ignore MAXGAP if weighting endgaps
	 */
	if (endgaps || ndely[yy] < MAXGAP) {
		if (col0[yy] - ins0 >= dely[yy]) {
			dely[yy] = col0[yy] - (ins0+ins1);
			ndely[yy] = 1;
		} else {
			dely[yy] -= ins1;
			ndely[yy]++;
		}
	} else {
		if (col0[yy] - (ins0+ins1) >= dely[yy]) {
			dely[yy] = col0[yy] - (ins0+ins1);
			ndely[yy] = 1;
		} else
			ndely[yy]++;
	}

	/* update penalty for del in y seq;
	 * favor new del over ongong del
	 */
	if (endgaps || ndelx < MAXGAP) {
		if (col1[yy-1] - ins0 >= delx) {
			delx = col1[yy-1] - (ins0+ins1);
			ndelx = 1;
		} else {
			delx -= ins1;
			ndelx++;
		}
	} else {
		if (col1[yy-1] - (ins0+ins1) >= delx) {
			delx = col1[yy-1] - (ins0+ins1);
			ndelx = 1;
		} else
			ndelx++;
	}

	/* pick the maximum score; we're favoring
	 * mis over any del and delx over dely
	 */
```

Table 1 (cont')

...nw

```
id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
        col1[yy] = mis;
else if (delx >= dely[yy]) {
        col1[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                        writejmps(id);
                        ij = dx[id].ijmp = 0;
                        dx[id].offset = offset;
                        offset += sizeof(struct jmp) + sizeof(offset);
                }
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
}
else {
        col1[yy] = dely[yy];
        ij = dx[id].ijmp;
if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                        writejmps(id);
                        ij = dx[id].ijmp = 0;
                        dx[id].offset = offset;
                        offset += sizeof(struct jmp) + sizeof(offset);
                }
        }
        dx[id].jp.n[ij] = -ndely[yy];
        dx[id].jp.x[ij] = xx;
        dx[id].score = dely[yy];
}
if (xx == len0 && yy < len1) {
        /* last col
         */
        if (endgaps)
                col1[yy] -= ins0+ins1*(len1-yy);
        if (col1[yy] > smax) {
                smax = col1[yy];
                dmax = id;
        }
}
    }
    if (endgaps && xx < len0)
            col1[yy-1] -= ins0+ins1*(len0-xx);
    if (col1[yy-1] > smax) {
            smax = col1[yy-1];
            dmax = id;
    }
    tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);                }
```

Table 1 (cont')

```
/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[ ]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() - -put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC      3
#define P_LINE   256     /* maximum output line */
#define P_SPC    3       /* space between name or num and seq */

extern   _day[26][26];
int      olen;           /* set output line length */
FILE     *fx;            /* output file */

print()
        print
{
        int     lx, ly, firstgap, lastgap;      /* overlap */

        if ((fx = fopen(ofile, "w")) == 0) {
                fprintf(stderr,"%s: can't write %s\n", prog, ofile);
                cleanup(1);
        }
        fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
        fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
        olen = 60;
        lx = len0;
        ly = len1;
        firstgap = lastgap = 0;
        if (dmax < len1 - 1) {          /* leading gap in x */
                pp[0].spc = firstgap = len1 - dmax - 1;
                ly -= pp[0].spc;
        }
        else if (dmax > len1 - 1) {     /* leading gap in y */
                pp[1].spc = firstgap = dmax - (len1 - 1);
                lx -= pp[1].spc;
        }
        if (dmax0 < len0 - 1) {         /* trailing gap in x */
                lastgap = len0 - dmax0 -1;
                lx -= lastgap;
        }
        else if (dmax0 > len0 - 1) {    /* trailing gap in y */
                lastgap = dmax0 - (len0 - 1);
                ly -= lastgap;
        }
        getmat(lx, ly, firstgap, lastgap);
        pr_align();
}
```

Table 1 (cont')

getmat

```
/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
	int	lx, ly;			/* "core" (minus endgaps) */
	int	firstgap, lastgap;	/* leading trailing overlap */
{
	int		nm, i0, i1, siz0, siz1;
	char		outx[32];
	double		pct;
	register	n0, n1;
	register char	*p0, *p1;

	/* get total matches, score
	 */
	i0 = i1 = siz0 = siz1 = 0;
	p0 = seqx[0] + pp[1].spc;
	p1 = seqx[1] + pp[0].spc;
	n0 = pp[1].spc + 1;
	n1 = pp[0].spc + 1;

	nm = 0;
	while ( *p0 && *p1 ) {
		if (siz0) {
			p1++;
			n1++;
			siz0--;
		}
		else if (siz1) {
			p0++;
			n0++;
			siz1--;
		}
		else {
			if (xbm[*p0-'A']&xbm[*p1-'A'])
				nm++;
			if (n0++ == pp[0].x[i0])
				siz0 = pp[0].n[i0++];
			if (n1++ == pp[1].x[i1])
				siz1 = pp[1].n[i1++];
			p0++;
			p1++;
		}
	}

	/* pct homology:
	 * if penalizing endgaps, base is the shorter seq
	 * else, knock off overhangs and take shorter core
	 */
	if (endgaps)
		lx = (len0 < len1)? len0 : len1;
	else
		lx = (lx < ly)? lx : ly;
	pct = 100.*(double)nm/(double)lx;
	fprintf(fx, "\n");
	fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
		nm, (nm == 1)? "" : "es", lx, pct);
```

Table 1 (cont')

...getmat

```
        fprintf(fx, "<gaps in first sequence: %d", gapx);
        if (gapx) {
                (void) sprintf(outx, " (%d %s%s)",
                        ngapx, (dna)? "base":"residue", (ngapx == 1)? "":"s");
                fprintf(fx,"%s", outx);

        fprintf(fx, ", gaps in second sequence: %d", gapy);
        if (gapy) {
                (void) sprintf(outx, " (%d %s%s)",
                        ngapy, (dna)? "base":"residue", (ngapy == 1)? "":"s");
                fprintf(fx,"%s", outx);
        }
        if (dna)
                fprintf(fx,
                "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
                smax, DMAT, DMIS, DINS0, DINS1);
        else
                fprintf(fx,
                "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
                smax, PINS0, PINS1);
        if (endgaps)
                fprintf(fx,
                "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
                firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
                lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
        else
                fprintf(fx, "<endgaps not penalized\n");
}
static          nm;             /* matches in core -- for checking */
static          lmax;           /* lengths of stripped file names */
static          ij[2];          /* jmp index for a path */
static          nc[2];          /* number at start of current line */
static          ni[2];          /* current elem number -- for gapping */
static          siz[2];
static char     *ps[2];         /* ptr to current element */
static char     *po[2];         /* ptr to next output char slot */
static char     out[2][P_LINE]; /* output line */
static char     star[P_LINE];   /* set by stars() */

/*
 * print alignment of described in struct path pp[ ]
 */
static
pr_align()
{
        int             nn;     /* char count */
        int             more;
        register        i;

        for (i = 0, lmax = 0; i < 2; i++) {
                nn = stripname(namex[i]);
                if (nn > lmax)
                        lmax = nn;

                nc[i] = 1;
                ni[i] = 1;
                siz[i] = ij[i] = 0;
                ps[i] = seqx[i];
                po[i] = out[i];         }
```

pr_align

Table 1 (cont')

...pr_align

```
	for (nn = nm = 0, more = 1; more; ) {
		for (i = more = 0; i < 2; i++) {
			/*
			 * do we have more of this sequence?
			 */
			if (!*ps[i])
				continue;

			more++;

			if (pp[i].spc) {	/* leading space */
				*po[i]++ = ' ';
				pp[i].spc--;
			}
			else if (siz[i]) {	/* in a gap */
				*po[i]++ = '-';
				siz[i]--;
			}
			else {			/* we're putting a seq element
						 */
				*po[i] = *ps[i];
				if (islower(*ps[i]))
					*ps[i] = toupper(*ps[i]);
				po[i]++;
				ps[i]++;

				/*
				 * are we at next gap for this seq?
				 */
				if (ni[i] == pp[i].x[ij[i]]) {
					/*
					 * we need to merge all gaps
					 * at this location
					 */
					siz[i] = pp[i].n[ij[i]++];
					while (ni[i] == pp[i].x[ij[i]])
						siz[i] += pp[i].n[ij[i]++];
				}
				ni[i]++;
			}
		}
		if (++nn == olen || !more && nn) {
			dumpblock();
			for (i = 0; i < 2; i++)
				po[i] = out[i];
			nn = 0;
		}
	}
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
```

dumpblock

```
{
	register	i;
	for (i = 0; i < 2; i++)
		*po[i]-- = '\0';
```

Table 1 (cont')

...dumpblock

```
		(void) putc('\n', fx);
		for (i = 0; i < 2; i++) {
			if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
				if (i == 0)
					nums(i);
				if (i == 0 && *out[1])
					stars();
				putline(i);
				if (i == 0 && *out[1])
					fprintf(fx, star);
				if (i == 1)
					nums(i);
			}
		}
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
		int	ix;	/* index in out[ ] holding seq line */
{
		char		nline[P_LINE];
		register	i, j;
		register char	*pn, *px, *py;

		for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
			*pn = ' ';
		for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
			if (*py == ' ' || *py == '-')
				*pn = ' ';
			else {
				if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
					j = (i < 0)? -i : i;
					for (px = pn; j; j /= 10, px--)
						*px = j%10 + '0';
					if (i < 0)
						*px = '-';
				}
				else
					*pn = ' ';
				i++;
			}
		}
		*pn = '\0';
		nc[ix] = i;
		for (pn = nline; *pn; pn++)
			(void) putc(*pn, fx);
		(void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
		int	ix;			{
```

nums

putline

Table 1 (cont')

...putline

```
        int             i;
        register char   *px;

        for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
                (void) putc(*px, fx);
        for (; i < lmax+P_SPC; i++)
                (void) putc(' ', fx);

        /* these count from 1:
         * ni[ ] is current element (from 1)
         * nc[ ] is number at start of current line
         */
        for (px = out[ix]; *px; px++)
                (void) putc(*px&0x7F, fx);
        (void) putc('\n', fx);
}


/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
```

stars

```
{
        int             i;
        register char   *p0, *p1, cx, *px;

        if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
           !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
                return;
        px = star;
        for (i = lmax+P_SPC; i; i--)
                *px++ = ' ';

        for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
                if (isalpha(*p0) && isalpha(*p1)) {

                        if (xbm[*p0-'A']&xbm[*p1-'A']) {
                                cx = '*';
                                nm++;
                        }
                        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                                cx = '.';
                        else
                                cx = ' ';
                }
                else
                        cx = ' ';
                *px++ = cx;
        }
        *px++ = '\n';
        *px = '\0';
}
```

Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
        stripname
        char    *pn;     /* file name (may be path) */
{
        register char    *px, *py;

        py = 0;
        for (px = pn; *px; px++)
                if (*px == '/')
                        py = px + 1;
        if (py)
                (void) strcpy(pn, py);
        return(strlen(pn));
}
```

Table 1 (cont')

```
/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 * readjmps() -- get the good jmps, from tmp file if necessary
 * writejmps() -- write a filled array of jmps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jmps */
FILE    *fj;

int     cleanup();                           /* cleanup tmp file */
long    lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)                                                              cleanup
        int     i;
{
        if (fj)
                (void) unlink(jname);
        exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)                                                       getseq
        char    *file;  /* file name */
        int     *len;   /* seq len */
{
        char            line[1024], *pseq;
        register char   *px, *py;
        int             natgc, tlen;
        FILE            *fp;

        if ((fp = fopen(file,"r")) == 0) {
                fprintf(stderr,"%s: can't read %s\n", prog, file);
                exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++)
                        if (isupper(*px) || islower(*px))
                                tlen++;
        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
                fprintf(stderr,"%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
                exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
```

Table 1 (cont')

...getseq

```
        py = pseq + 4;
        *len = tlen;
        rewind(fp);

        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++) {
                        if (isupper(*px))
                                *py++ = *px;
                        else if (islower(*px))
                                *py++ = toupper(*px);
                        if (index("ATGCU",*(py-1)))
                                natgc++;
                }
        }
        *py++ = '\0';
        *py = '\0';
        (void) fclose(fp);
        dna = natgc > (tlen/3);
        return(pseq+4);
}
```

g_calloc

```
char    *
g_calloc(msg, nx, sz)
        char    *msg;           /* program, calling routine */
        int     nx, sz;         /* number and size of elements */
{
        char            *px, *calloc();

        if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
                if (*msg) {
                        fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                        exit(1);
                }
        }
        return(px);
}

/*
 * get final jmps from dx[ ] or tmp file, set pp[ ], reset dmax: main()
 */
readjmps()
```

readjmps

```
{
        int             fd = -1;
        int             siz, i0, i1;
        register  i, j, xx;

        if (fj) {
                (void) fclose(fj);
                if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                        fprintf(stderr, "%s: can't open() %s\n", prog, jname);
                        cleanup(1);
                }
        }
        for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
                while (1) {
                        for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                                ;
```

Table 1 (cont')

...readjmps

```
                        if (j < 0 && dx[dmax].offset && fj) {
                                (void) lseek(fd, dx[dmax].offset, 0);
                                (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
                                (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
                                dx[dmax].ijmp = MAXJMP-1;
                        }
                        else
                                break;
                }
                if (i >= JMPS) {
                        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
                        cleanup(1);
                }
                if (j >= 0) {
                        siz = dx[dmax].jp.n[j];
                        xx = dx[dmax].jp.x[j];
                        dmax += siz;
                        if (siz < 0) {                  /* gap in second seq */
                                pp[1].n[i1] = -siz;
                                xx += siz;
                                /* id = xx - yy + len1 - 1
                                 */
                                pp[1].x[i1] = xx - dmax + len1 - 1;
                                gapy++;
                                ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
                                siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
                                i1++;
                        }
                        else if (siz > 0) {     /* gap in first seq */
                                pp[0].n[i0] = siz;
                                pp[0].x[i0] = xx;
                                gapx++;
                                ngapx += siz;
/* ignore MAXGAP when doing endgaps */
                                siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
                                i0++;
                        }
                }
                else
                        break;
        }

        /* reverse the order of jmps
         */
        for (j = 0, i0--; j < i0; j++, i0--) {
                i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
                i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
        }
        for (j = 0, i1--; j < i1; j++, i1--) {
                i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
                i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
        }
        if (fd >= 0)
                (void) close(fd);
        if (fj) {
                (void) unlink(jname);
                fj = 0;
                offset = 0;
        }                                       }
```

Table 1 (cont')

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejmps(ix)
        writejmps
        int     ix;
{
        char    *mktemp();

        if (!fj) {
                if (mktemp(jname) < 0) {
                        fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                        cleanup(1);
                }
                if ((fj = fopen(jname, "w")) == 0) {
                        fprintf(stderr, "%s: can't write %s\n", prog, jname);
                        exit(1);
                }
        }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
        }
```

Table 2

PRO	XXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 10 = 50%

Table 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =
4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally, the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions

or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an alpha-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, $CaCl_2$, $CaPO_4$, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r*; *E. coli* W3110 strain 40B4, which is strain

37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora, Penicillium, Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis,* and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination

sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp*1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be

employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Tissue Distribution

The location of tissues expressing the PRO can be identified by determining mRNA expression in various human tissues. The location of such genes provides information about which tissues are most likely to be affected by the stimulating and inhibiting activities of the PRO polypeptides. The location of a gene in a specific tissue also provides sample tissue for the activity blocking assays discussed below.

As noted before, gene expression in various tissues may be measured by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA (Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 [1980]), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

Gene expression in various tissues, alternatively, may be measured by immunological methods, such as immunohistochemical staining of tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining

and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence of a PRO polypeptide or against a synthetic peptide based on the DNA sequences encoding the PRO polypeptide or against an exogenous sequence fused to a DNA encoding a PRO polypeptide and encoding a specific antibody epitope. General techniques for generating antibodies, and special protocols for Northern blotting and *in situ* hybridization are provided below.

F. Antibody Binding Studies

The activity of the PRO polypeptides can be further verified by antibody binding studies, in which the ability of anti-PRO antibodies to inhibit the effect of the PRO polypeptides, respectively, on tissue cells is tested. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies, the preparation of which will be described hereinbelow.

Antibody binding studies may be carried out in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp.147-158 (CRC Press, Inc., 1987).

Competitive binding assays rely on the ability of a labeled standard to compete with the test sample analyte for binding with a limited amount of antibody. The amount of target protein in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies preferably are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies may conveniently be separated from the standard and analyte which remain unbound.

Sandwich assays involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three-part complex. See, *e.g.*, US Pat No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

For immunohistochemistry, the tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin, for example.

G. Cell-Based Assays

Cell-based assays and animal models for immune related diseases can be used to further understand the relationship between the genes and polypeptides identified herein and the development and pathogenesis of immune related disease.

In a different approach, cells of a cell type known to be involved in a particular immune related disease are transfected with the cDNAs described herein, and the ability of these cDNAs to stimulate or inhibit immune function is analyzed. Suitable cells can be transfected with the desired gene, and monitored for immune function activity. Such transfected cell lines can then be used to test the ability of poly- or monoclonal antibodies or antibody compositions to inhibit or stimulate immune function, for example to modulate T-cell proliferation or inflammatory cell infiltration. Cells transfected with the coding sequences of the genes identified herein can further be used to identify drug candidates for the treatment of immune

related diseases.

In addition, primary cultures derived from transgenic animals (as described below) can be used in the cell-based assays herein, although stable cell lines are preferred. Techniques to derive continuous cell lines from transgenic animals are well known in the art (see, *e.g.*, Small *et al.*, *Mol. Cell. Biol.* 5: 642-648 [1985]).

One suitable cell based assay is the mixed lymphocyte reaction (MLR). *Current Protocols in Immunology*, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc. In this assay, the ability of a test compound to stimulate or inhibit the proliferation of activated T cells is assayed. A suspension of responder T cells is cultured with allogeneic stimulator cells and the proliferation of T cells is measured by uptake of tritiated thymidine. This assay is a general measure of T cell reactivity. Since the majority of T cells respond to and produce IL-2 upon activation, differences in responsiveness in this assay in part reflect differences in IL-2 production by the responding cells. The MLR results can be verified by a standard lymphokine (IL-2) detection assay. *Current Protocols in Immunology*, above, 3.15, 6.3.

A proliferative T cell response in an MLR assay may be due to direct mitogenic properties of an assayed molecule or to external antigen induced activation. Additional verification of the T cell stimulatory activity of the PRO polypeptides can be obtained by a costimulation assay. T cell activation requires an antigen specific signal mediated through the T-cell receptor (TCR) and a costimulatory signal mediated through a second ligand binding interaction, for example, the B7 (CD80, CD86)/CD28 binding interaction. CD28 crosslinking increases lymphokine secretion by activated T cells. T cell activation has both negative and positive controls through the binding of ligands which have a negative or positive effect. CD28 and CTLA-4 are related glycoproteins in the Ig superfamily which bind to B7. CD28 binding to B7 has a positive costimulation effect of T cell activation; conversely, CTLA-4 binding to B7 has a T cell deactivating effect. Chambers, C. A. and Allison, *J. P., Curr. Opin. Immunol.* (1997) 9:396. Schwartz, R. H., *Cell* (1992) 71:1065; Linsey, P. S. and Ledbetter, J. A., *Annu. Rev. Immunol.* (1993) 11:191; June, C. H. *et al, Immunol. Today* (1994) 15:321; Jenkins, M. K., *Immunity* (1994) 1:405. In a costimulation assay, the PRO polypeptides are assayed for T cell costimulatory or inhibitory activity.

Direct use of a stimulating compound as in the invention has been validated in experiments with 4-1BB glycoprotein, a member of the tumor necrosis factor receptor family, which binds to a ligand (4-1BBL) expressed on primed T cells and signals T cell activation and growth. Alderson, M. E. *et al., J. Immunol.* (1994) 24:2219.

The use of an agonist stimulating compound has also been validated experimentally. Activation of 4-1BB by treatment with an agonist anti-4-1BB antibody enhances eradication of tumors. Hellstrom, I. and Hellstrom, K. E., *Crit. Rev. Immunol.* (1998) 18:1. Immunoadjuvant therapy for treatment of tumors, described in more detail below, is another example of the use of the stimulating compounds of the invention.

Alternatively, an immune stimulating or enhancing effect can also be achieved by administration of a PRO which has vascular permeability enhancing properties. Enhanced vascular permeability would be beneficial to disorders which can be attenuated by local infiltration of immune cells (*e.g.*, monocytes, eosinophils, PMNs) and inflammation.

On the other hand, PRO polypeptides, as well as other compounds of the invention, which are direct inhibitors of T cell proliferation/activation, lymphokine secretion, and/or vascular permeability can be directly used to suppress the immune response. These compounds are useful to reduce the degree of the immune response and to treat immune related diseases characterized by a hyperactive, superoptimal, or autoimmune response. This use of the compounds of the invention has been validated by the experiments described above in which CTLA-4 binding to receptor B7 deactivates T cells. The direct inhibitory compounds of the invention function in an analogous manner. The use of compound which suppress vascular permeability would be expected to reduce inflammation. Such uses would be beneficial in treating conditions associated with excessive inflammation.

Alternatively, compounds, *e.g.*, antibodies, which bind to stimulating PRO polypeptides and block the stimulating effect of these molecules produce a net inhibitory effect and can be used to suppress the T cell mediated immune response by inhibiting T cell proliferation/activation and/or lymphokine secretion. Blocking the stimulating effect of the polypeptides suppresses the immune response of the mammal. This use has been validated in experiments using an anti-IL2 antibody. In these experiments, the antibody binds to IL2 and blocks binding of IL2 to its receptor thereby achieving a T cell inhibitory effect.

H. Animal Models

The results of the cell based in vitro assays can be further verified using *in vivo* animal models and assays for T-cell function. A variety of well known animal models can be used to further understand the role of the genes identified herein in the development and pathogenesis of immune related disease, and to test the efficacy of candidate therapeutic agents, including antibodies, and other antagonists of the native polypeptides, including small molecule antagonists. The *in vivo* nature of such models makes them predictive of responses in human patients. Animal models of immune related diseases include both non-recombinant and recombinant (transgenic) animals. Non-recombinant animal models include, for example, rodent, *e.g.*, murine models. Such models can be generated by introducing cells into syngeneic mice using standard techniques, *e.g.*, subcutaneous injection, tail vein injection, spleen implantation, intraperitoneal implantation, implantation under the renal capsule, *etc.*

Graft-versus-host disease occurs when immunocompetent cells are transplanted into immunosuppressed or tolerant patients. The donor cells recognize and respond to host antigens. The response can vary from life threatening severe inflammation to mild cases of diarrhea and weight loss. Graft-versus-host disease models provide a means of assessing T cell reactivity against MHC antigens and minor transplant antigens. A suitable procedure is described in detail in Current Protocols in Immunology, above, unit 4.3.

An animal model for skin allograft rejection is a means of testing the ability of T cells to mediate *in vivo* tissue destruction and a measure of their role in transplant rejection. The most common and accepted models use murine tail-skin grafts. Repeated experiments have shown that skin allograft rejection is mediated by T cells, helper T cells and killer-effector T cells, and not antibodies. Auchincloss, H. Jr. and Sachs, D. H., *Fundamental Immunology*, 2nd ed., W. E. Paul ed., Raven Press, NY, 1989, 889-992. A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.4. Other transplant rejection models which can be used to test the compounds of the invention are the allogeneic heart

transplant models described by Tanabe, M. *et al, Transplantation* (1994) 58:23 and Tinubu, S. A. *et al, J. Immunol.* (1994) 4330-4338.

Animal models for delayed type hypersensitivity provides an assay of cell mediated immune function as well. Delayed type hypersensitivity reactions are a T cell mediated *in vivo* immune response characterized by inflammation which does not reach a peak until after a period of time has elapsed after challenge with an antigen. These reactions also occur in tissue specific autoimmune diseases such as multiple sclerosis (MS) and experimental autoimmune encephalomyelitis (EAE, a model for MS). A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.5.

EAE is a T cell mediated autoimmune disease characterized by T cell and mononuclear cell inflammation and subsequent demyelination of axons in the central nervous system. EAE is generally considered to be a relevant animal model for MS in humans. Bolton, C., *Multiple Sclerosis* (1995) 1:143. Both acute and relapsing-remitting models have been developed. The compounds of the invention can be tested for T cell stimulatory or inhibitory activity against immune mediated demyelinating disease using the protocol described in *Current Protocols in Immunology*, above, units 15.1 and 15.2. See also the models for myelin disease in which oligodendrocytes or Schwann cells are grafted into the central nervous system as described in Duncan, I. D. *et al, Molec. Med. Today* (1997) 554-561.

Contact hypersensitivity is a simple delayed type hypersensitivity *in vivo* assay of cell mediated immune function. In this procedure, cutaneous exposure to exogenous haptens which gives rise to a delayed type hypersensitivity reaction which is measured and quantitated. Contact sensitivity involves an initial sensitizing phase followed by an elicitation phase. The elicitation phase occurs when the T lymphocytes encounter an antigen to which they have had previous contact. Swelling and inflammation occur, making this an excellent model of human allergic contact dermatitis. A suitable procedure is described in detail in *Current Protocols in Immunology*, Eds. J. E. Cologan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach and W. Strober, John Wiley & Sons, Inc., 1994, unit 4.2. See also Grabbe, S. and Schwarz, T, *Immun. Today* 19 (1): 37-44 (1998).

An animal model for arthritis is collagen-induced arthritis. This model shares clinical, histological and immunological characteristics of human autoimmune rheumatoid arthritis and is an acceptable model for human autoimmune arthritis. Mouse and rat models are characterized by synovitis, erosion of cartilage and subchondral bone. The compounds of the invention can be tested for activity against autoimmune arthritis using the protocols described in *Current Protocols in Immunology*, above, units 15.5. See also the model using a monoclonal antibody to CD18 and VLA-4 integrins described in Issekutz, A.C. *et al., Immunology* (1996) 88:569.

A model of asthma has been described in which antigen-induced airway hyper-reactivity, pulmonary eosinophilia and inflammation are induced by sensitizing an animal with ovalbumin and then challenging the animal with the same protein delivered by aerosol. Several animal models (guinea pig, rat, non-human primate) show symptoms similar to atopic asthma in humans upon challenge with aerosol antigens. Murine models have many of the features of human asthma. Suitable procedures to test the compounds of the invention for activity and effectiveness in the treatment of asthma are described by Wolyniec, W. W. *et al, Am. J. Respir. Cell Mol. Biol.* (1998) 18:777 and the references cited therein.

Additionally, the compounds of the invention can be tested on animal models for psoriasis like diseases. Evidence suggests a T cell pathogenesis for psoriasis. The compounds of the invention can be tested in the scid/scid mouse model described by Schon, M. P. *et al, Nat. Med.* (1997) 3:183, in which the mice demonstrate histopathologic skin lesions resembling psoriasis. Another suitable model is the human skin/scid mouse chimera prepared as described by Nickoloff, B. J. *et al, Am. J. Path.* (1995) 146:580.

Recombinant (transgenic) animal models can be engineered by introducing the coding portion of the genes identified herein into the genome of animals of interest, using standard techniques for producing transgenic animals. Animals that can serve as a target for transgenic manipulation include, without limitation, mice, rats, rabbits, guinea pigs, sheep, goats, pigs, and non-human primates, *e.g.*, baboons, chimpanzees and monkeys. Techniques known in the art to introduce a transgene into such animals include pronucleic microinjection (Hoppe and Wanger, U.S. Patent No. 4,873,191); retrovirus-mediated gene transfer into germ lines (*e.g.*, Van der Putten *et al., Proc. Natl. Acad. Sci. USA* 82, 6148-615 [1985]); gene targeting in embryonic stem cells (Thompson *et al., Cell* 56, 313-321 [1989]); electroporation of embryos (Lo, *Mol. Cel. Biol.* 3, 1803-1814 [1983]); sperm-mediated gene transfer (Lavitrano *et al., Cell* 57, 717-73 [1989]). For review, see, for example, U.S. Patent No. 4,736,866.

For the purpose of the present invention, transgenic animals include those that carry the transgene only in part of their cells ("mosaic animals"). The transgene can be integrated either as a single transgene, or in concatamers, *e.g.*, head-to-head or head-to-tail tandems. Selective introduction of a transgene into a particular cell type is also possible by following, for example, the technique of Lasko *et al., Proc. Natl. Acad. Sci. USA* 89, 6232-636 (1992).

The expression of the transgene in transgenic animals can be monitored by standard techniques. For example, Southern blot analysis or PCR amplification can be used to verify the integration of the transgene. The level of mRNA expression can then be analyzed using techniques such as *in situ* hybridization, Northern blot analysis, PCR, or immunocytochemistry.

The animals may be further examined for signs of immune disease pathology, for example by histological examination to determine infiltration of immune cells into specific tissues. Blocking experiments can also be performed in which the transgenic animals are treated with the compounds of the invention to determine the extent of the T cell proliferation stimulation or inhibition of the compounds. In these experiments, blocking antibodies which bind to the PRO polypeptide, prepared as described above, are administered to the animal and the effect on immune function is determined.

Alternatively, "knock out" animals can be constructed which have a defective or altered gene encoding a polypeptide identified herein, as a result of homologous recombination between the endogenous gene encoding the polypeptide and altered genomic DNA encoding the same polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a particular polypeptide can be used to clone genomic DNA encoding that polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a particular polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see *e.g.*, Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced DNA

has homologously recombined with the endogenous DNA are selected [see *e.g.*, Li *et al.*, *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse or rat) to form aggregation chimeras [see *e.g.*, Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the polypeptide.

I. ImmunoAdjuvant Therapy

In one embodiment, the immunostimulating compounds of the invention can be used in immunoadjuvant therapy for the treatment of tumors (cancer). It is now well established that T cells recognize human tumor specific antigens. One group of tumor antigens, encoded by the MAGE, BAGE and GAGE families of genes, are silent in all adult normal tissues , but are expressed in significant amounts in tumors, such as melanomas, lung tumors, head and neck tumors, and bladder carcinomas. DeSmet, C. *et al.*, (1996) *Proc. Natl. Acad. Sci. USA*, 93:7149. It has been shown that costimulation of T cells induces tumor regression and an antitumor response both *in vitro* and *in vivo*. Melero, I. *et al.*, *Nature Medicine* (1997) 3:682; Kwon, E. D. *et al.*, *Proc. Natl. Acad. Sci. USA* (1997) 94: 8099; Lynch, D. H. *et al*, *Nature Medicine* (1997) 3:625; Finn, O. J. and Lotze, M. T., *J. Immunol.* (1998) 21:114. The stimulatory compounds of the invention can be administered as adjuvants, alone or together with a growth regulating agent, cytotoxic agent or chemotherapeutic agent, to stimulate T cell proliferation/activation and an antitumor response to tumor antigens. The growth regulating, cytotoxic, or chemotherapeutic agent may be administered in conventional amounts using known administration regimes. Immunostimulating activity by the compounds of the invention allows reduced amounts of the growth regulating, cytotoxic, or chemotherapeutic agents thereby potentially lowering the toxicity to the patient.

J. Screening Assays for Drug Candidates

Screening assays for drug candidates are designed to identify compounds that bind to or complex with the polypeptides encoded by the genes identified herein or a biologically active fragment thereof, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds, including peptides, preferably soluble peptides, (poly)peptide-immunoglobulin fusions, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art. All assays are common in that they call for contacting the drug candidate with a polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to

interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, *e.g.*, on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the polypeptide and drying. Alternatively, an immobilized antibody, *e.g.*, a monoclonal antibody, specific for the polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, *e.g.*, the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, *e.g.*, by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labelled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular protein encoded by a gene identified herein, its interaction with that protein can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers [Fields and Song, *Nature (London)* 340, 245-246 (1989); Chien *et al., Proc. Natl. Acad. Sci. USA* 88, 9578-9582 (1991)] as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA* 89, 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, while the other one functioning as the transcription activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lac*Z reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β-galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

In order to find compounds that interfere with the interaction of a gene identified herein and other intra- or extracellular components can be tested, a reaction mixture is usually prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a test compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described above.

The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

K. Compositions and Methods for the Treatment of Immune Related Diseases

The compositions useful in the treatment of immune related diseases include, without limitation, proteins, antibodies, small organic molecules, peptides, phosphopeptides, antisense and ribozyme molecules, triple helix molecules, *etc.* that inhibit or stimulate immune function, for example, T cell proliferation/activation, lymphokine release, or immune cell infiltration.

For example, antisense RNA and RNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation initiation site, *e.g.*, between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, *e.g.*, Rossi, *Current Biology* 4, 469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, *e.g.*, PCT publication No. WO 97/33551, *supra*.

These molecules can be identified by any or any combination of the screening assays discussed above and/or by any other screening techniques well known for those skilled in the art.

L. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, Bio/Technology 10, 779-783 (1992); Lonberg *et al.*, Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild *et al.*, Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by

affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form

the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*; J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody.. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al* ., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

M. Pharmaceutical Compositions

The active PRO molecules of the invention (*e.g.*, PRO polypeptides, anti-PRO antibodies, and/or variants of each) as well as other molecules identified by the screening assays disclosed above, can be administered for the treatment of immune related diseases, in the form of pharmaceutical compositions.

Therapeutic formulations of the active PRO molecule, preferably a polypeptide or antibody of the invention, are prepared for storage by mixing the active molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

Compounds identified by the screening assays disclosed herein can be formulated in an analogous manner, using standard techniques well known in the art.

Lipofections or liposomes can also be used to deliver the PRO molecule into cells. Where antibody fragments are used, the smallest inhibitory fragment which specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable region sequences of an antibody, peptide molecules can be designed which retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (see, *e.g.*, Marasco *et al.*, *Proc. Natl. Acad. Sci. USA* 90, 7889-7893 [1993]).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine or growth inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active PRO molecules may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980).

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations or the PRO molecules may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ-ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

N. Methods of Treatment

It is contemplated that the polypeptides, antibodies and other active compounds of the present invention may be used to treat various immune related diseases and conditions, such as T cell mediated diseases, including those characterized by infiltration of inflammatory cells into a tissue, stimulation of T-cell proliferation, inhibition of T-cell proliferation, increased or decreased vascular permeability or the inhibition thereof.

Exemplary conditions or disorders to be treated with the polypeptides, antibodies and other compounds of the invention, include, but are not limited to systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, osteoarthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease.

In systemic lupus erythematosus, the central mediator of disease is the production of auto-reactive antibodies to self proteins/tissues and the subsequent generation of immune-mediated inflammation. Antibodies either directly or indirectly mediate tissue injury. Though T lymphocytes have not been shown to be directly involved in tissue damage, T lymphocytes are required for the development of auto-reactive antibodies. The genesis of the disease is thus T lymphocyte dependent. Multiple organs and systems are affected clinically including kidney, lung, musculoskeletal system, mucocutaneous, eye, central nervous system, cardiovascular system, gastrointestinal tract, bone marrow and blood.

Rheumatoid arthritis (RA) is a chronic systemic autoimmune inflammatory disease that mainly involves the synovial membrane of multiple joints with resultant injury to the articular cartilage. The pathogenesis is T lymphocyte dependent and is associated with the production of rheumatoid factors, auto-antibodies directed against self IgG, with the resultant formation of immune complexes that attain high levels in joint fluid and blood. These complexes in the joint may induce the marked infiltrate of lymphocytes and monocytes into the synovium and subsequent marked synovial changes; the joint space/fluid if infiltrated by similar cells with the addition of numerous neutrophils. Tissues affected are primarily the joints, often in symmetrical pattern. However, extra-articular disease also occurs in two major forms. One form is the development of extra-articular lesions with ongoing progressive joint disease and typical lesions of pulmonary fibrosis, vasculitis, and cutaneous ulcers. The second form of extra-articular disease is the so called Felty's syndrome which occurs late in the RA disease course, sometimes after joint disease has become quiescent, and involves the presence of neutropenia, thrombocytopenia and splenomegaly. This can be accompanied by vasculitis in multiple organs with formations of infarcts, skin ulcers and gangrene. Patients often also develop rheumatoid nodules in the subcutis tissue overlying affected joints; the nodules late stage have necrotic centers surrounded by a mixed inflammatory cell infiltrate. Other manifestations which can occur in RA include: pericarditis, pleuritis, coronary arteritis, intestitial pneumonitis with pulmonary fibrosis, keratoconjunctivitis sicca, and rhematoid nodules.

Juvenile chronic arthritis is a chronic idiopathic inflammatory disease which begins often at less than 16 years of age. Its phenotype has some similarities to RA; some patients which are rhematoid factor positive are classified as juvenile rheumatoid arthritis. The disease is sub-classified into three major categories: pauciarticular, polyarticular, and systemic. The arthritis can be severe and is typically destructive and leads to joint ankylosis and retarded growth. Other manifestations can include chronic anterior uveitis and systemic amyloidosis.

Spondyloarthropathies are a group of disorders with some common clinical features and the common association with the expression of HLA-B27 gene product. The disorders include: ankylosing sponylitis, Reiter's syndrome (reactive arthritis), arthritis associated with inflammatory bowel disease, spondylitis associated with psoriasis, juvenile onset spondyloarthropathy and undifferentiated spondyloarthropathy. Distinguishing features include sacroileitis with or without spondylitis; inflammatory asymmetric arthritis; association with HLA-B27 (a serologically defined allele of the HLA-B locus of class I MHC); ocular inflammation, and absence of autoantibodies associated with other rheumatoid disease. The cell most implicated as key to induction of the disease is the CD8+ T lymphocyte, a cell which targets antigen presented by class I MHC molecules. CD8+ T cells may react against the class I MHC allele HLA-B27 as if it were a foreign peptide expressed by MHC class I molecules. It has been hypothesized that an

epitope of HLA-B27 may mimic a bacterial or other microbial antigenic epitope and thus induce a CD8+ T cells response.

Systemic sclerosis (scleroderma) has an unknown etiology. A hallmark of the disease is induration of the skin; likely this is induced by an active inflammatory process. Scleroderma can be localized or systemic; vascular lesions are common and endothelial cell injury in the microvasculature is an early and important event in the development of systemic sclerosis; the vascular injury may be immune mediated. An immunologic basis is implied by the presence of mononuclear cell infiltrates in the cutaneous lesions and the presence of anti-nuclear antibodies in many patients. ICAM-1 is often upregulated on the cell surface of fibroblasts in skin lesions suggesting that T cell interaction with these cells may have a role in the pathogenesis of the disease. Other organs involved include: the gastrointestinal tract: smooth muscle atrophy and fibrosis resulting in abnormal peristalsis/motility; kidney: concentric subendothelial intimal proliferation affecting small arcuate and interlobular arteries with resultant reduced renal cortical blood flow, results in proteinuria, azotemia and hypertension; skeletal muscle: atrophy, interstitial fibrosis; inflammation; lung: interstitial pneumonitis and interstitial fibrosis; and heart: contraction band necrosis, scarring/fibrosis.

Idiopathic inflammatory myopathies including dermatomyositis, polymyositis and others are disorders of chronic muscle inflammation of unknown etiology resulting in muscle weakness. Muscle injury/inflammation is often symmetric and progressive. Autoantibodies are associated with most forms. These myositis-specific autoantibodies are directed against and inhibit the function of components, proteins and RNA's, involved in protein synthesis.

Sjögren's syndrome is due to immune-mediated inflammation and subsequent functional destruction of the tear glands and salivary glands. The disease can be associated with or accompanied by inflammatory connective tissue diseases. The disease is associated with autoantibody production against Ro and La antigens, both of which are small RNA-protein complexes. Lesions result in keratoconjunctivitis sicca, xerostomia, with other manifestations or associations including bilary cirrhosis, peripheral or sensory neuropathy, and palpable purpura.

Systemic vasculitis are diseases in which the primary lesion is inflammation and subsequent damage to blood vessels which results in ischemia/necrosis/degeneration to tissues supplied by the affected vessels and eventual end-organ dysfunction in some cases. Vasculitides can also occur as a secondary lesion or sequelae to other immune-inflammatory mediated diseases such as rheumatoid arthritis, systemic sclerosis, *etc.*, particularly in diseases also associated with the formation of immune complexes. Diseases in the primary systemic vasculitis group include: systemic necrotizing vasculitis: polyarteritis nodosa, allergic angiitis and granulomatosis, polyangiitis; Wegener's granulomatosis; lymphomatoid granulomatosis; and giant cell arteritis. Miscellaneous vasculitides include: mucocutaneous lymph node syndrome (MLNS or Kawasaki's disease), isolated CNS vasculitis, Behet's disease, thromboangiitis obliterans (Buerger's disease) and cutaneous necrotizing venulitis. The pathogenic mechanism of most of the types of vasculitis listed is believed to be primarily due to the deposition of immunoglobulin complexes in the vessel wall and subsequent induction of an inflammatory response either via ADCC, complement activation, or both.

Sarcoidosis is a condition of unknown etiology which is characterized by the presence of epithelioid granulomas in nearly any tissue in the body; involvement of the lung is most common. The pathogenesis

involves the persistence of activated macrophages and lymphoid cells at sites of the disease with subsequent chronic sequelae resultant from the release of locally and systemically active products released by these cell types.

Autoimmune hemolytic anemia including autoimmune hemolytic anemia, immune pancytopenia, and paroxysmal noctural hemoglobinuria is a result of production of antibodies that react with antigens expressed on the surface of red blood cells (and in some cases other blood cells including platelets as well) and is a reflection of the removal of those antibody coated cells via complement mediated lysis and/or ADCC/Fc-receptor-mediated mechanisms.

In autoimmune thrombocytopenia including thrombocytopenic purpura, and immune-mediated thrombocytopenia in other clinical settings, platelet destruction/removal occurs as a result of either antibody or complement attaching to platelets and subsequent removal by complement lysis, ADCC or FC-receptor mediated mechanisms.

Thyroiditis including Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, and atrophic thyroiditis, are the result of an autoimmune response against thyroid antigens with production of antibodies that react with proteins present in and often specific for the thyroid gland. Experimental models exist including spontaneous models: rats (BUF and BB rats) and chickens (obese chicken strain); inducible models: immunization of animals with either thyroglobulin, thyroid microsomal antigen (thyroid peroxidase).

Type I diabetes mellitus or insulin-dependent diabetes is the autoimmune destruction of pancreatic islet β cells; this destruction is mediated by auto-antibodies and auto-reactive T cells. Antibodies to insulin or the insulin receptor can also produce the phenotype of insulin-non-responsiveness.

Immune mediated renal diseases, including glomerulonephritis and tubulointerstitial nephritis, are the result of antibody or T lymphocyte mediated injury to renal tissue either directly as a result of the production of autoreactive antibodies or T cells against renal antigens or indirectly as a result of the deposition of antibodies and/or immune complexes in the kidney that are reactive against other, non-renal antigens. Thus other immune-mediated diseases that result in the formation of immune-complexes can also induce immune mediated renal disease as an indirect sequelae. Both direct and indirect immune mechanisms result in inflammatory response that produces/induces lesion development in renal tissues with resultant organ function impairment and in some cases progression to renal failure. Both humoral and cellular immune mechanisms can be involved in the pathogenesis of lesions.

Demyelinating diseases of the central and peripheral nervous systems, including Multiple Sclerosis; idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome; and Chronic Inflammatory Demyelinating Polyneuropathy, are believed to have an autoimmune basis and result in nerve demyelination as a result of damage caused to oligodendrocytes or to myelin directly. In MS there is evidence to suggest that disease induction and progression is dependent on T lymphocytes. Multiple Sclerosis is a demyelinating disease that is T lymphocyte-dependent and has either a relapsing-remitting course or a chronic progressive course. The etiology is unknown; however, viral infections, genetic predisposition, environment, and autoimmunity all contribute. Lesions contain infiltrates of predominantly T lymphocyte mediated, microglial cells and infiltrating macrophages; CD4+ T lymphocytes are the predominant cell type at lesions.

The mechanism of oligodendrocyte cell death and subsequent demyelination is not known but is likely T lymphocyte driven.

Inflammatory and Fibrotic Lung Disease, including Eosinophilic Pneumonias; Idiopathic Pulmonary Fibrosis, and Hypersensitivity Pneumonitis may involve a disregulated immune-inflammatory response. Inhibition of that response would be of therapeutic benefit.

Autoimmune or Immune-mediated Skin Disease including Bullous Skin Diseases, Erythema Multiforme, and Contact Dermatitis are mediated by auto-antibodies, the genesis of which is T lymphocyte-dependent.

Psoriasis is a T lymphocyte-mediated inflammatory disease. Lesions contain infiltrates of T lymphocytes, macrophages and antigen processing cells, and some neutrophils.

Allergic diseases, including asthma; allergic rhinitis; atopic dermatitis; food hypersensitivity; and urticaria are T lymphocyte dependent. These diseases are predominantly mediated by T lymphocyte induced inflammation, IgE mediated-inflammation or a combination of both.

Transplantation associated diseases, including Graft rejection and Graft-Versus-Host-Disease (GVHD) are T lymphocyte-dependent; inhibition of T lymphocyte function is ameliorative.

Other diseases in which intervention of the immune and/or inflammatory response have benefit are infectious disease including but not limited to viral infection (including but not limited to AIDS, hepatitis A, B, C, D, E and herpes) bacterial infection, fungal infections, and protozoal and parasitic infections (molecules (or derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response to infectious agents), diseases of immunodeficiency (molecules/derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response for conditions of inherited, acquired, infectious induced (as in HIV infection), or iatrogenic (*i.e.*, as from chemotherapy) immunodeficiency, and neoplasia.

It has been demonstrated that some human cancer patients develop an antibody and/or T lymphocyte response to antigens on neoplastic cells. It has also been shown in animal models of neoplasia that enhancement of the immune response can result in rejection or regression of that particular neoplasm. Molecules that enhance the T lymphocyte response in the MLR have utility *in vivo* in enhancing the immune response against neoplasia. Molecules which enhance the T lymphocyte proliferative response in the MLR (or small molecule agonists or antibodies that affected the same receptor in an agonistic fashion) can be used therapeutically to treat cancer. Molecules that inhibit the lymphocyte response in the MLR also function *in vivo* during neoplasia to suppress the immune response to a neoplasm; such molecules can either be expressed by the neoplastic cells themselves or their expression can be induced by the neoplasm in other cells. Antagonism of such inhibitory molecules (either with antibody, small molecule antagonists or other means) enhances immune-mediated tumor rejection.

Additionally, inhibition of molecules with proinflammatory properties may have therapeutic benefit in reperfusion injury; stroke; myocardial infarction; atherosclerosis; acute lung injury; hemorrhagic shock; burn; sepsis/septic shock; acute tubular necrosis; endometriosis; degenerative joint disease and pancreatis.

The compounds of the present invention, *e.g.*, polypeptides or antibodies, are administered to a mammal, preferably a human, in accord with known methods, such as intravenous administration as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal,

subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation (intranasal, intrapulmonary) routes. Intravenous or inhaled administration of polypeptides and antibodies is preferred.

In immunoadjuvant therapy, other therapeutic regimens, such administration of an anti-cancer agent, may be combined with the administration of the proteins, antibodies or compounds of the instant invention. For example, the patient to be treated with a the immunoadjuvant of the invention may also receive an anti-cancer agent (chemotherapeutic agent) or radiation therapy. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in *Chemotherapy Service* Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992). The chemotherapeutic agent may precede, or follow administration of the immunoadjuvant or may be given simultaneously therewith. Additionally, an anti-estrogen compound such as tamoxifen or an anti-progesterone such as onapristone (see, EP 616812) may be given in dosages known for such molecules.

It may be desirable to also administer antibodies against other immune disease associated or tumor associated antigens, such as antibodies which bind to CD20, CD11a, CD18, ErbB2, EGFR, ErbB3, ErbB4, or vascular endothelial factor (VEGF). Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein may be coadministered to the patient. Sometimes, it may be beneficial to also administer one or more cytokines to the patient. In one embodiment, the PRO polypeptides are coadministered with a growth inhibitory agent. For example, the growth inhibitory agent may be administered first, followed by a PRO polypeptide. However, simultaneous administration or administration first is also contemplated. Suitable dosages for the growth inhibitory agent are those presently used and may be lowered due to the combined action (synergy) of the growth inhibitory agent and the PRO polypeptide.

For the treatment or reduction in the severity of immune related disease, the appropriate dosage of an a compound of the invention will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the agent is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the compound, and the discretion of the attending physician. The compound is suitably administered to the patient at one time or over a series of treatments.

For example, depending on the type and severity of the disease, about 1 μg/kg to 15 mg/kg (*e.g.*, 0.1-20 mg/kg) of polypeptide or antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

O. Articles of Manufacture

In another embodiment of the invention, an article of manufacture containing materials (*e.g.*, comprising a PRO molecule) useful for the diagnosis or treatment of the disorders described above is provided. The article of manufacture comprises a container and an instruction. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of

materials such as glass or plastic. The container holds a composition which is effective for diagnosing or treating the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is usually a polypeptide or an antibody of the invention. An instruction or label on, or associated with, the container indicates that the composition is used for diagnosing or treating the condition of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

P. <u>Diagnosis and Prognosis of Immune Related Disease</u>

Cell surface proteins, such as proteins which are overexpressed in certain immune related diseases, are excellent targets for drug candidates or disease treatment. The same proteins along with secreted proteins encoded by the genes amplified in immune related disease states find additional use in the diagnosis and prognosis of these diseases. For example, antibodies directed against the protein products of genes amplified in multiple sclerosis, rheumatoid arthritis, or another immune related disease, can be used as diagnostics or prognostics.

For example, antibodies, including antibody fragments, can be used to qualitatively or quantitatively detect the expression of proteins encoded by amplified or overexpressed genes ("marker gene products"). The antibody preferably is equipped with a detectable, *e.g.*, fluorescent label, and binding can be monitored by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. These techniques are particularly suitable, if the overexpressed gene encodes a cell surface protein Such binding assays are performed essentially as described above.

In situ detection of antibody binding to the marker gene products can be performed, for example, by immunofluorescence or immunoelectron microscopy. For this purpose, a histological specimen is removed from the patient, and a labeled antibody is applied to it, preferably by overlaying the antibody on a biological sample. This procedure also allows for determining the distribution of the marker gene product in the tissue examined. It will be apparent for those skilled in the art that a wide variety of histological methods are readily available for *in situ* detection.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

<u>EXAMPLES</u>

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Microarray analysis of stimulated T-cells

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (in this instance, activated CD4+ T cells) sample is greater than hybridization signal of a probe from a control (in this instance, non-stimulated CD4 + T cells) sample, the gene or genes overexpressed in the test tissue are identified. The implication of this result is that an overexpressed protein in a test tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In one example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in PCT Patent Application Serial No. PCT/US01/10482, filed on March 30, 2001 and which is herein incorporated by reference.

In this experiment, CD4+ T cells were purified from a single donor using the RossetteSep™ protocol from (Stem Cell Technologies, Vancouver BC) which contains anti-CD8, anti-CD16, anti-CD19, anti-CD36 and anti-CD56 antibodies used to produce a population of isolated CD4 + T cells. Isolated CD4+ T cells were activated with an anti-CD3 antibody (used at a concentration that does not stimulate proliferation) together with either ICAM-1, anti-CD28 antibody or a combination of both ICAM-1, anti-CD28. At 24 or 72 hours cells were harvested, RNA extracted and analysis run on Affimax (Affymetrix Inc., Santa Clara, CA) U95A chips. Non-stimulated (resting) cells were harvested immediately after purification, and subjected to the same analysis. Genes were compared whose expression was upregulated at either of the two timepoints in activated vs. resting cells. These genes were also compared to a panel of normal tissues. A normal "universal" tissue control sample was prepared by pooling non-cancerous, human tissues including liver, kidney, and lung. Microarray hybridization experiments using the universal control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the universal control sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

Below are the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in isolated CD4 + T cells activated by ICAM-1, anti-CD 28, or a combination of ICAM-1/anti-CD28 as compared to isolated resting CD4+ T cells. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more immune disorders, but also serve as therapeutic targets for the treatment of those immune disorders.

Figures 1-280 are the PRO polypeptides increased by ICAM-1/anti-CD28.

Figures 281-496 are the PRO polypeptides increased by ICAM-1.

Figures 497-742 are the PRO polypeptides increased by anti-CD28.

EXAMPLE 2: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the

solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g $(NH_4)_2SO_4$, 0.71 g sodium citrate•2H2O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM $MgSO_4$) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 4: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μg pRK5-PRO DNA is mixed with about 1 μg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500 μl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μCi/ml ^{35}S-cysteine and 200 μCi/ml ^{35}S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μg/ml bovine insulin and 0.1 μg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell

cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 promoter/enhancer containing vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 promoter/enhancer containing vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+}-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Fugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3 x 10^{-7} cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mL of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3 x 10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2 x 10^6 cells/mL. On day 0, pH is determined. On

day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μl of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 5: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 6: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni^{2+}-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+}-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni^{2+}-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His_{10}-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB

Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 9: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the

aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 10: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of a PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as

limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

What is claimed:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 8 (SEQ ID NO:14), Figure 8 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:144), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID

NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512),

Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580(SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), Figure 610 (SEQ ID NO:610), Figure 612 (SEQ ID NO:612), Figure 614 (SEQ ID NO:614), Figure 616 (SEQ ID NO:616), Figure 618 (SEQ ID NO:618), Figure 620 (SEQ ID NO:620), Figure 622 (SEQ ID NO:622), Figure 624 (SEQ ID NO:624), Figure 626 (SEQ ID NO:626), Figure 628 (SEQ ID NO:628), Figure 630 (SEQ ID NO:630), Figure 632 (SEQ ID NO:632), Figure 634 (SEQ ID NO:634), Figure 636 (SEQ ID NO:636), Figure 638 (SEQ ID NO:638), Figure 640 (SEQ ID NO:640), Figure 642 (SEQ ID NO:642), Figure 644 (SEQ ID NO:644), Figure 646 (SEQ ID NO:646), Figure 648 (SEQ ID NO:648), Figure 650 (SEQ ID NO:650), Figure 652 (SEQ ID NO:652), Figure 654 (SEQ ID NO:654), Figure 656 (SEQ ID NO:656), Figure 658 (SEQ ID NO:658), Figure 660 (SEQ ID NO:660), Figure 662 (SEQ ID NO:662), Figure 664 (SEQ ID NO:664), Figure 666 (SEQ ID NO:666), Figure 668 (SEQ ID NO:668), Figure 670 (SEQ ID NO:670), Figure 672 (SEQ ID NO:672), Figure 674 (SEQ ID NO:674), Figure 676 (SEQ ID NO:676), Figure 678 (SEQ ID NO:678), Figure 680 (SEQ ID NO:680), Figure 682 (SEQ ID NO:682), Figure 684 (SEQ ID NO:684), Figure 686 (SEQ ID NO:686), Figure 688 (SEQ ID NO:688), Figure 690 (SEQ ID NO:690), Figure 692 (SEQ ID NO:692), Figure 694 (SEQ ID NO:694), Figure 696 (SEQ ID NO:696), Figure 698 (SEQ ID NO:698), Figure 700 (SEQ ID NO:700), Figure 702 (SEQ ID NO:702), Figure 704 (SEQ ID NO:704), Figure 706 (SEQ ID NO:706), Figure 708 (SEQ ID NO:708), Figure 710 (SEQ ID NO:710), Figure 712 (SEQ ID NO:712), Figure 714 (SEQ ID NO:714), Figure 716 (SEQ ID NO:716), Figure 718 (SEQ ID NO:718), Figure 720 (SEQ ID NO:720), Figure 722 (SEQ ID NO:722), Figure 724 (SEQ ID NO:724), Figure 726 (SEQ ID NO:726), Figure 728 (SEQ ID NO:728), Figure 730 (SEQ ID NO:730), Figure 732 (SEQ ID NO:732), Figure 734 (SEQ ID NO:734), Figure 736 (SEQ ID NO:736), Figure 740 (SEQ ID NO:740), and Figure 742 (SEQ ID NO:742).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21

(SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figure 289 (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295

(SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303(SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figure 311 (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure 339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figure 349 (SEQ ID NO:349), Figure 351 (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figure 525 (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID

NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), Figure 609 (SEQ ID NO:609), Figure 611 (SEQ ID NO:611), Figure 613 (SEQ ID NO:613), Figure 615 (SEQ ID NO:615), Figure 617 (SEQ ID NO:617), Figure 619 (SEQ ID NO:619), Figure 621 (SEQ ID NO:621), Figure 623 (SEQ ID NO:623), Figure 625 (SEQ ID NO:625), Figure 627 (SEQ ID NO:627), Figure 629 (SEQ ID NO:629), Figure 631 (SEQ ID NO:631), Figure 633 (SEQ ID NO:633), Figure 635 (SEQ ID NO:635), Figure 637 (SEQ ID NO:637), Figure 639 (SEQ ID NO:639), Figure 641 (SEQ ID NO:641), Figure 643 (SEQ ID NO:643), Figure 645 (SEQ ID NO:645), Figure 647 (SEQ ID NO:647), Figure 649 (SEQ ID NO:649), Figure 651 (SEQ ID NO:651), Figure 653 (SEQ ID NO:653), Figure 655 (SEQ ID NO:655), Figure 657 (SEQ ID NO:657), Figure 659 (SEQ ID NO:659), Figure 661 (SEQ ID NO:661), Figure 663 (SEQ ID NO:663), Figure 665 (SEQ ID NO:665), Figure 667 (SEQ ID NO:667), Figure 669 (SEQ ID NO:669), Figure 671 (SEQ ID NO:671), Figure 673 (SEQ ID NO:673), Figure 675 (SEQ ID NO:675), Figure 677 (SEQ ID NO:677), Figure 679 (SEQ ID NO:679), Figure 681 (SEQ ID NO:681), Figure 683 (SEQ ID NO:683), Figure 685 (SEQ ID NO:685), Figure 687 (SEQ ID NO:687), Figure 689 (SEQ ID NO:689), Figure 691 (SEQ ID NO:691), Figure 693 (SEQ ID NO:693), Figure 695 (SEQ ID NO:695), Figure 697 (SEQ ID NO:697), Figure 699 (SEQ ID NO:699), Figure 701 (SEQ ID NO:701), Figure 703 (SEQ ID NO:703), Figure 705 (SEQ ID NO:705), Figure 707 (SEQ ID NO:707), Figure 709 (SEQ ID NO:709), Figure 711 (SEQ ID NO:711), Figure 713 (SEQ ID NO:713), Figure 715 (SEQ ID NO:715), Figure 717 (SEQ ID NO:717), Figure 719 (SEQ ID NO:719), Figure 721 (SEQ ID NO:721), Figure 723 (SEQ ID NO:723), Figure 725 (SEQ ID NO:725), Figure 727 (SEQ ID NO:727), Figure 729 (SEQ ID NO:729), Figure 731 (SEQ ID NO:731), Figure 733 (SEQ ID NO:733), Figure 735 (SEQ ID NO:735), Figure 737 (SEQ ID NO:737), Figure 739 (SEQ ID NO:739), and Figure 741 (SEQ ID NO:741).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63

(SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figure 289 (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303(SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figure 311 (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID

NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure 339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figure 349 (SEQ ID NO:349), Figure 351 (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figure 525 (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597),

Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), Figure 609 (SEQ ID NO:609), Figure 611 (SEQ ID NO:611), Figure 613 (SEQ ID NO:613), Figure 615 (SEQ ID NO:615), Figure 617 (SEQ ID NO:617), Figure 619 (SEQ ID NO:619), Figure 621 (SEQ ID NO:621), Figure 623 (SEQ ID NO:623), Figure 625 (SEQ ID NO:625), Figure 627 (SEQ ID NO:627), Figure 629 (SEQ ID NO:629), Figure 631 (SEQ ID NO:631), Figure 633 (SEQ ID NO:633), Figure 635 (SEQ ID NO:635), Figure 637 (SEQ ID NO:637), Figure 639 (SEQ ID NO:639), Figure 641 (SEQ ID NO:641), Figure 643 (SEQ ID NO:643), Figure 645 (SEQ ID NO:645), Figure 647 (SEQ ID NO:647), Figure 649 (SEQ ID NO:649), Figure 651 (SEQ ID NO:651), Figure 653 (SEQ ID NO:653), Figure 655 (SEQ ID NO:655), Figure 657 (SEQ ID NO:657), Figure 659 (SEQ ID NO:659), Figure 661 (SEQ ID NO:661), Figure 663 (SEQ ID NO:663), Figure 665 (SEQ ID NO:665), Figure 667 (SEQ ID NO:667), Figure 669 (SEQ ID NO:669), Figure 671 (SEQ ID NO:671), Figure 673 (SEQ ID NO:673), Figure 675 (SEQ ID NO:675), Figure 677 (SEQ ID NO:677), Figure 679 (SEQ ID NO:679), Figure 681 (SEQ ID NO:681), Figure 683 (SEQ ID NO:683), Figure 685 (SEQ ID NO:685), Figure 687 (SEQ ID NO:687), Figure 689 (SEQ ID NO:689), Figure 691 (SEQ ID NO:691), Figure 693 (SEQ ID NO:693), Figure 695 (SEQ ID NO:695), Figure 697 (SEQ ID NO:697), Figure 699 (SEQ ID NO:699), Figure 701 (SEQ ID NO:701), Figure 703 (SEQ ID NO:703), Figure 705 (SEQ ID NO:705), Figure 707 (SEQ ID NO:707), Figure 709 (SEQ ID NO:709), Figure 711 (SEQ ID NO:711), Figure 713 (SEQ ID NO:713), Figure 715 (SEQ ID NO:715), Figure 717 (SEQ ID NO:717), Figure 719 (SEQ ID NO:719), Figure 721 (SEQ ID NO:721), Figure 723 (SEQ ID NO:723), Figure 725 (SEQ ID NO:725), Figure 727 (SEQ ID NO:727), Figure 729 (SEQ ID NO:729), Figure 731 (SEQ ID NO:731), Figure 733 (SEQ ID NO:733), Figure 735 (SEQ ID NO:735), Figure 737 (SEQ ID NO:737), Figure 739 (SEQ ID NO:739), and Figure 741 (SEQ ID NO:741).

5. A vector comprising the nucleic acid of Claim 1.

6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

7. A host cell comprising the vector of Claim 5.

8. The host cell of Claim 7, wherein said cell is a CHO cell, an *E.coli* cell or a yeast cell.

9. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

10. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 8 (SEQ ID NO:14), Figure 8 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure

18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:144), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID

NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562),

Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580(SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), Figure 610 (SEQ ID NO:610), Figure 612 (SEQ ID NO:612), Figure 614 (SEQ ID NO:614), Figure 616 (SEQ ID NO:616), Figure 618 (SEQ ID NO:618), Figure 620 (SEQ ID NO:620), Figure 622 (SEQ ID NO:622), Figure 624 (SEQ ID NO:624), Figure 626 (SEQ ID NO:626), Figure 628 (SEQ ID NO:628), Figure 630 (SEQ ID NO:630), Figure 632 (SEQ ID NO:632), Figure 634 (SEQ ID NO:634), Figure 636 (SEQ ID NO:636), Figure 638 (SEQ ID NO:638), Figure 640 (SEQ ID NO:640), Figure 642 (SEQ ID NO:642), Figure 644 (SEQ ID NO:644), Figure 646 (SEQ ID NO:646), Figure 648 (SEQ ID NO:648), Figure 650 (SEQ ID NO:650), Figure 652 (SEQ ID NO:652), Figure 654 (SEQ ID NO:654), Figure 656 (SEQ ID NO:656), Figure 658 (SEQ ID NO:658), Figure 660 (SEQ ID NO:660), Figure 662 (SEQ ID NO:662), Figure 664 (SEQ ID NO:664), Figure 666 (SEQ ID NO:666), Figure 668 (SEQ ID NO:668), Figure 670 (SEQ ID NO:670), Figure 672 (SEQ ID NO:672), Figure 674 (SEQ ID NO:674), Figure 676 (SEQ ID NO:676), Figure 678 (SEQ ID NO:678), Figure 680 (SEQ ID NO:680), Figure 682 (SEQ ID NO:682), Figure 684 (SEQ ID NO:684), Figure 686 (SEQ ID NO:686), Figure 688 (SEQ ID NO:688), Figure 690 (SEQ ID NO:690), Figure 692 (SEQ ID NO:692), Figure 694 (SEQ ID NO:694), Figure 696 (SEQ ID NO:696), Figure 698 (SEQ ID NO:698), Figure 700 (SEQ ID NO:700), Figure 702 (SEQ ID NO:702), Figure 704 (SEQ ID NO:704), Figure 706 (SEQ ID NO:706), Figure 708 (SEQ ID NO:708), Figure 710 (SEQ ID NO:710), Figure 712 (SEQ ID NO:712), Figure 714 (SEQ ID NO:714), Figure 716 (SEQ ID NO:716), Figure 718 (SEQ ID NO:718), Figure 720 (SEQ ID NO:720), Figure 722 (SEQ ID NO:722), Figure 724 (SEQ ID NO:724), Figure 726 (SEQ ID NO:726), Figure 728 (SEQ ID NO:728), Figure 730 (SEQ ID NO:730), Figure 732 (SEQ ID NO:732), Figure 734 (SEQ ID NO:734), Figure 736 (SEQ ID NO:736), Figure 740 (SEQ ID NO:740), or Figure 742 (SEQ ID NO:742).

12. A chimeric molecule comprising a polypeptide according to Claim 10 fused to a heterologous amino acid sequence.

13. The chimeric molecule of Claim 12, wherein said heterologous amino acid sequence is an epitope tag sequence or an Fc region of an immunoglobulin.

14. An antibody which specifically binds to a polypeptide according to Claim 10.

15. The antibody of Claim 14, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

16. A composition of matter comprising (a) a polypeptide of Claim 10, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, in combination with a carrier.

17. The composition of matter of Claim 16, wherein said carrier is a pharmaceutically acceptable carrier.

18. The composition of matter of Claim 16 comprising a therapeutically effective amount of (a), (b), (c) or (d).

19. An article of manufacture, comprising:

a container;

a label on said container; and

a composition of matter comprising (a) a polypeptide of Claim 10, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, contained within said container, wherein label on said container indicates that said composition of matter can be used for treating an immune related disease.

20. A method of treating an immune related disorder in a mammal in need thereof comprising administering to said mammal a therapeutically effective amount of (a) a polypeptide of Claim 10, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide.

21. The method of Claim 20, wherein the immune related disorder is systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barré syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host-disease.

22. A method for determining the presence of a PRO69457 PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081,

PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204,

PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903, or PRO1970 polypeptide in a sample suspected of containing said polypeptide, said method comprising exposing said sample to an anti-PRO69457, anti-PRO69458, anti-PRO52268, anti-PRO69459, anti-PRO62927, anti-PRO59136, anti-PRO37121, anti-PRO69460, anti-PRO60475, anti-PRO34451, anti-PRO38070, anti-PRO23756, anti-PRO10404, anti-PRO69461, anti-PRO70006, anti-PRO69462, anti-PRO2081, anti-PRO70007, anti-PRO69463, anti-PRO62908, anti-PRO69464, anti-PRO52804, anti-PRO60438, anti-PRO69465, anti-PRO37421, anti-PRO37596, anti-PRO36124, anti-PRO69466, anti-PRO60499, anti-PRO69467, anti-PRO61824, anti-PRO69468, anti-PRO21341, anti-PRO38213, anti-PRO69469, anti-PRO37172, anti-PRO35991, anti-PRO36905, anti-PRO69470, anti-PRO36451, anti-PRO69471, anti-PRO37492, anti-PRO70008, anti-PRO69472, anti-PRO69473, anti-PRO36996, anti-PRO22613, anti-PRO69475, anti-PRO61755, anti-PRO70009, anti-PRO69476, anti-PRO4881, anti-PRO12876, anti-PRO70010, anti-PRO37534, anti-PRO21928, anti-PRO69478, anti-PRO69479, anti-PRO69480, anti-PRO69481, anti-PRO69482, anti-PRO69483, anti-PRO38642, anti-PRO69484, anti-PRO66269, anti-PRO1723, anti-PRO22297, anti-PRO61349, anti-PRO69485, anti-PRO69486, anti-PRO69487, anti-PRO36963, anti-PRO23814, anti-PRO57980, anti-PRO20128, anti-PRO4551, anti-PRO69488, anti-PRO39268, anti-PRO69489, anti-PRO69490, anti-PRO69491, anti-PRO69492, anti-PRO37713, anti-PRO58993, anti-PRO69493, anti-PRO69494, anti-PRO69495, anti-PRO70011, anti-PRO62861, anti-PRO36640, anti-PRO36766, anti-PRO69497, anti-PRO69498, anti-PRO69499, anti-PRO69500, anti-PRO69501, anti-PRO70012, anti-PRO69503, anti-PRO69474, anti-PRO69505, anti-PRO69506, anti-PRO69507, anti-PRO51301, anti-PRO69508, anti-PRO69509, anti-PRO69510, anti-PRO69511, anti-PRO51309, anti-PRO50578, anti-PRO69512, anti-PRO69513, anti-PRO69514, anti-PRO10607, anti-PRO61705, anti-PRO49214, anti-PRO39648, anti-PRO69515, anti-PRO38497, anti-PRO29371, anti-PRO70013, anti-PRO69516, anti-PRO69517, anti-PRO69518, anti-PRO70014, anti-PRO69520, anti-PRO69521, anti-PRO69522, anti-PRO69523, anti-PRO60513, anti-PRO2512, anti-PRO69524, anti-PRO12569, anti-PRO69525, anti-PRO69526, anti-PRO69527, anti-PRO69528, anti-PRO69529, anti-PRO12166, anti-PRO2154, anti-PRO69530, anti-PRO51916, anti-PRO52174, anti-PRO69531, anti-PRO69532, anti-PRO69533, anti-PRO69534, anti-PRO54728, anti-PRO70015, anti-PRO69536, anti-PRO69537, anti-PRO37498, anti-PRO22175, anti-PRO69538, anti-PRO37015, anti-PRO12187, anti-PRO69539, anti-PRO69880, anti-PRO69541, anti-PRO69542, anti-PRO69543, anti-PRO70016, anti-PRO69545, anti-PRO50197, anti-PRO69546, anti-PRO69547, anti-PRO69548, anti-PRO69549, anti-PRO69550, anti-PRO69551, anti-PRO69552, anti-PRO37460, anti-PRO42223, anti-PRO69553, anti-PRO69554, anti-PRO69555, anti-PRO61014, anti-PRO59915, anti-PRO37891, anti-PRO69556, anti-PRO12875, anti-PRO70017, anti-PRO70018, anti-PRO4426, anti-PRO69558, anti-PRO69559, anti-PRO37676, anti-PRO69560, anti-PRO69561, anti-PRO69562, anti-PRO63204, anti-PRO70019, anti-PRO69564, anti-PRO62830, anti-PRO69565, anti-PRO69566, anti-PRO69567, anti-PRO49675, anti-PRO69568, anti-PRO2013, anti-PRO69569, anti-PRO69570, anti-PRO69571, anti-PRO36403, anti-PRO4676, anti-PRO37657, anti-PRO62097, anti-PRO38081, anti-PRO69572, anti-

PRO69573, anti-PRO69574, anti-PRO69883, anti-PRO69576, anti-PRO37584, anti-PRO11603, anti-PRO70020, anti-PRO51695, anti-PRO69579, anti-PRO69580, anti-PRO69581, anti-PRO69582, anti-PRO69583, anti-PRO69584, anti-PRO69585, anti-PRO69586, anti-PRO69587, anti-PRO69588, anti-PRO69589, anti-PRO70021, anti-PRO69590, anti-PRO70022, anti-PRO69592, anti-PRO37029, anti-PRO69593, anti-PRO69594,.anti-PRO69595, anti-PRO1207, anti-PRO69596, anti-PRO69597, anti-PRO51139, anti-PRO62545, anti-PRO3615, anti-PRO38036, anti-PRO69598, anti-PRO4701, anti-PRO69599, anti-PRO69600, anti-PRO69601, anti-PRO69887, anti-PRO69603, anti-PRO69604, anti-PRO70023, anti-PRO69606, anti-PRO69607, anti-PRO69608, anti-PRO69609, anti-PRO69610, anti-PRO9902, anti-PRO69611, anti-PRO69612, anti-PRO69613, anti-PRO69614, anti-PRO69615, anti-PRO70024, anti-PRO69616, anti-PRO49619, anti-PRO69617, anti-PRO69618, anti-PRO38040, anti-PRO69619, anti-PRO69620, anti-PRO69621, anti-PRO69622, anti-PRO4401, anti-PRO70025, anti-PRO69625, anti-PRO12025, anti-PRO70026, anti-PRO69627, anti-PRO69628, anti-PRO22637, anti-PRO69629, anti-PRO70027, anti-PRO70028, anti-PRO69632, anti-PRO69634, anti-PRO36857, anti-PRO69893, anti-PRO69635, anti-PRO6180, anti-PRO69637, anti-PRO69638, anti-PRO69639, anti-PRO69640, anti-PRO69641, anti-PRO62766, anti-PRO53782, anti-PRO61472, anti-PRO38179, anti-PRO69642, anti-PRO69643, anti-PRO69644, anti-PRO69645, anti-PRO11608, anti-PRO69646, anti-PRO59825, anti-PRO69647, anti-PRO69648, anti-PRO70029, anti-PRO1213, anti-PRO70030, anti-PRO50195, anti-PRO69651, anti-PRO37538, anti-PRO69652, anti-PRO59210, anti-PRO23374, anti-PRO24844, anti-PRO70031, anti-PRO69653, anti-PRO69654, anti-PRO69655, anti-PRO69656, anti-PRO70032, anti-PRO69659, anti-PRO69660, anti-PRO58054, anti-PRO69661, anti-PRO69662, anti-PRO69898, anti-PRO69664, anti-PRO69665, anti-PRO69666, anti-PRO69667, anti-PRO69669, anti-PRO69671, anti-PRO69672, anti-PRO58204, anti-PRO49419, anti-PRO69673, anti-PRO69674, anti-PRO49810, anti-PRO70033, anti-PRO69676, anti-PRO58076, anti-PRO69677, anti-PRO69678, anti-PRO69679, anti-PRO1718, anti-PRO51161, anti-PRO69680, anti-PRO59281, anti-PRO36102, anti-PRO61799, anti-PRO69681, anti-PRO69682, anti-PRO69901, anti-PRO69684, anti-PRO69685, anti-PRO69686, anti-PRO69687, anti-PRO38469, anti-PRO69688, anti-PRO70034, anti-PRO59354, anti-PRO59189, anti-PRO38197, anti-PRO69902, anti-PRO69690, anti-PRO61569, anti-PRO69903, or anti-PRO1970 antibody and determining binding of said antibody to a component of said sample.

23. A method of diagnosing an immune related disease in a mammal, said method comprising detecting the level of expression of a gene encoding PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551,

PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower level of expression of said gene in the test sample as

compared to the control sample is indicative of the presence of an immune related disease in the mammal from which the test tissue cells were obtained.

24. A method of diagnosing an immune related disease in a mammal, said method comprising (a) contacting an an anti-PRO69457, anti-PRO69458, anti-PRO52268, anti-PRO69459, anti-PRO62927, anti-PRO59136, anti-PRO37121, anti-PRO69460, anti-PRO60475, anti-PRO34451, anti-PRO38070, anti-PRO23756, anti-PRO10404, anti-PRO69461, anti-PRO70006, anti-PRO69462, anti-PRO2081, anti-PRO70007, anti-PRO69463, anti-PRO62908, anti-PRO69464, anti-PRO52804, anti-PRO60438, anti-PRO69465, anti-PRO37421, anti-PRO37596, anti-PRO36124, anti-PRO69466, anti-PRO60499, anti-PRO69467, anti-PRO61824, anti-PRO69468, anti-PRO21341, anti-PRO38213, anti-PRO69469, anti-PRO37172, anti-PRO35991, anti-PRO36905, anti-PRO69470, anti-PRO36451, anti-PRO69471, anti-PRO37492, anti-PRO70008, anti-PRO69472, anti-PRO69473, anti-PRO36996, anti-PRO22613, anti-PRO69475, anti-PRO61755, anti-PRO70009, anti-PRO69476, anti-PRO4881, anti-PRO12876, anti-PRO70010, anti-PRO37534, anti-PRO21928, anti-PRO69478, anti-PRO69479, anti-PRO69480, anti-PRO69481, anti-PRO69482, anti-PRO69483, anti-PRO38642, anti-PRO69484, anti-PRO66269, anti-PRO1723, anti-PRO22297, anti-PRO61349, anti-PRO69485, anti-PRO69486, anti-PRO69487, anti-PRO36963, anti-PRO23814, anti-PRO57980, anti-PRO20128, anti-PRO4551, anti-PRO69488, anti-PRO39268, anti-PRO69489, anti-PRO69490, anti-PRO69491, anti-PRO69492, anti-PRO37713, anti-PRO58993, anti-PRO69493, anti-PRO69494, anti-PRO69495, anti-PRO70011, anti-PRO62861, anti-PRO36640, anti-PRO36766, anti-PRO69497, anti-PRO69498, anti-PRO69499, anti-PRO69500, anti-PRO69501, anti-PRO70012, anti-PRO69503, anti-PRO69474, anti-PRO69505, anti-PRO69506, anti-PRO69507, anti-PRO51301, anti-PRO69508, anti-PRO69509, anti-PRO69510, anti-PRO69511, anti-PRO51309, anti-PRO50578, anti-PRO69512, anti-PRO69513, anti-PRO69514, anti-PRO10607, anti-PRO61705, anti-PRO49214, anti-PRO39648, anti-PRO69515, anti-PRO38497, anti-PRO29371, anti-PRO70013, anti-PRO69516, anti-PRO69517, anti-PRO69518, anti-PRO70014, anti-PRO69520, anti-PRO69521, anti-PRO69522, anti-PRO69523, anti-PRO60513, anti-PRO2512, anti-PRO69524, anti-PRO12569, anti-PRO69525, anti-PRO69526, anti-PRO69527, anti-PRO69528, anti-PRO69529, anti-PRO12166, anti-PRO2154, anti-PRO69530, anti-PRO51916, anti-PRO52174, anti-PRO69531, anti-PRO69532, anti-PRO69533, anti-PRO69534, anti-PRO54728, anti-PRO70015, anti-PRO69536, anti-PRO69537, anti-PRO37498, anti-PRO22175, anti-PRO69538, anti-PRO37015, anti-PRO12187, anti-PRO69539, anti-PRO69880, anti-PRO69541, anti-PRO69542, anti-PRO69543, anti-PRO70016, anti-PRO69545, anti-PRO50197, anti-PRO69546, anti-PRO69547, anti-PRO69548, anti-PRO69549, anti-PRO69550, anti-PRO69551, anti-PRO69552, anti-PRO37460, anti-PRO42223, anti-PRO69553, anti-PRO69554, anti-PRO69555, anti-PRO61014, anti-PRO59915, anti-PRO37891, anti-PRO69556, anti-PRO12875, anti-PRO70017, anti-PRO70018, anti-PRO4426, anti-PRO69558, anti-PRO69559, anti-PRO37676, anti-PRO69560, anti-PRO69561, anti-PRO69562, anti-PRO63204, anti-PRO70019, anti-PRO69564, anti-PRO62830, anti-PRO69565, anti-PRO69566, anti-PRO69567, anti-PRO49675, anti-PRO69568, anti-PRO2013, anti-PRO69569, anti-PRO69570, anti-PRO69571, anti-PRO36403, anti-PRO4676, anti-PRO37657, anti-PRO62097, anti-PRO38081, anti-PRO69572, anti-PRO69573, anti-PRO69574, anti-PRO69883, anti-PRO69576, anti-PRO37584, anti-PRO11603, anti-PRO70020, anti-

PRO51695, anti-PRO69579, anti-PRO69580, anti-PRO69581, anti-PRO69582, anti-PRO69583, anti-PRO69584, anti-PRO69585, anti-PRO69586, anti-PRO69587, anti-PRO69588, anti-PRO69589, anti-PRO70021, anti-PRO69590, anti-PRO70022, anti-PRO69592, anti-PRO37029, anti-PRO69593, anti-PRO69594, anti-PRO69595, anti-PRO1207, anti-PRO69596, anti-PRO69597, anti-PRO51139, anti-PRO62545, anti-PRO3615, anti-PRO38036, anti-PRO69598, anti-PRO4701, anti-PRO69599, anti-PRO69600, anti-PRO69601, anti-PRO69887, anti-PRO69603, anti-PRO69604, anti-PRO70023, anti-PRO69606, anti-PRO69607, anti-PRO69608, anti-PRO69609, anti-PRO69610, anti-PRO9902, anti-PRO69611, anti-PRO69612, anti-PRO69613, anti-PRO69614, anti-PRO69615, anti-PRO70024, anti-PRO69616, anti-PRO49619, anti-PRO69617, anti-PRO69618, anti-PRO38040, anti-PRO69619, anti-PRO69620, anti-PRO69621, anti-PRO69622, anti-PRO4401, anti-PRO70025, anti-PRO69625, anti-PRO12025, anti-PRO70026, anti-PRO69627, anti-PRO69628, anti-PRO22637, anti-PRO69629, anti-PRO70027, anti-PRO70028, anti-PRO69632, anti-PRO69634, anti-PRO36857, anti-PRO69893, anti-PRO69635, anti-PRO6180, anti-PRO69637, anti-PRO69638, anti-PRO69639, anti-PRO69640, anti-PRO69641, anti-PRO62766, anti-PRO53782, anti-PRO61472, anti-PRO38179, anti-PRO69642, anti-PRO69643, anti-PRO69644, anti-PRO69645, anti-PRO11608, anti-PRO69646, anti-PRO59825, anti-PRO69647, anti-PRO69648, anti-PRO70029, anti-PRO1213, anti-PRO70030, anti-PRO50195, anti-PRO69651, anti-PRO37538, anti-PRO69652, anti-PRO59210, anti-PRO23374, anti-PRO24844, anti-PRO70031, anti-PRO69653, anti-PRO69654, anti-PRO69655, anti-PRO69656, anti-PRO70032, anti-PRO69659, anti-PRO69660, anti-PRO58054, anti-PRO69661, anti-PRO69662, anti-PRO69898, anti-PRO69664, anti-PRO69665, anti-PRO69666, anti-PRO69667, anti-PRO69669, anti-PRO69671, anti-PRO69672, anti-PRO58204, anti-PRO49419, anti-PRO69673, anti-PRO69674, anti-PRO49810, anti-PRO70033, anti-PRO69676, anti-PRO58076, anti-PRO69677, anti-PRO69678, anti-PRO69679, anti-PRO1718, anti-PRO51161, anti-PRO69680, anti-PRO59281, anti-PRO36102, anti-PRO61799, anti-PRO69681, anti-PRO69682, anti-PRO69901, anti-PRO69684, anti-PRO69685, anti-PRO69686, anti-PRO69687, anti-PRO38469, anti-PRO69688, anti-PRO70034, anti-PRO59354, anti-PRO59189, anti-PRO38197, anti-PRO69902, anti-PRO69690, anti-PRO61569, anti-PRO69903 or anti-PRO1970, antibody with a test sample of tissue cells obtained from said mammal and (b) detecting the formation of a complex between the antibody and the polypeptide in the test sample, wherein formation of said complex is indicative of the presence of an immune related disease in the mammal from which the test tissue cells were obtained.

25. A method of identifying a compound that inhibits the activity of PRO69457 PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814,

PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide, said method comprising contacting cells which normally respond to said polypeptide with (a) said polypeptide and (b) a candidate compound, and determining the lack responsiveness by said cell to (a).

26. A method of identifying a compound that inhibits the expression of a gene encoding a PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646,

PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide, said method comprising contacting cells which normally express said polypeptide with a candidate compound, and determining the lack of expression said gene.

27. The method of Claim 26, wherein said candidate compound is an antisense nucleic acid.

28. A method of identifying a compound that mimics the activity of a PRO69457 PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573,

PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide, said method comprising contacting cells which normally respond to said polypeptide with a candidate compound, and determining the responsiveness by said cell to said candidate compound.

31. A method of stimulating the immune response in a mammal, said method comprising administering to said mammal an effective amount of a PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515,

PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO6990 or PRO1970 polypeptide antagonist, wherein said immune response is stimulated.

32. A method of diagnosing an inflammatory immune response in a mammal, said method comprising detecting the level of expression of a gene encoding PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172,

PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901,

PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower level of expression of said gene in the test sample as compared to the control sample is indicative of the presence of an inflammatory immune response in the mammal from which the test tissue cells were obtained.

FIGURE 1

GCGTGAAGCGCGGACCTTTCAACAAGGGCTTTATTAATTCTCACGCTGCGGCCCCGGAAAGCG**ATG**GAGGTGGCG
GCTAATTGCTCCCTACGGGTGAAGAGACCTCTGTTGGATCCCCGCTTCGAGGGTTACAAGCTCTCTCTTGAGCCG
CTGCCTTGTTACCAGCTGGAGCTTGACGCAGCTGTGGCAGAGGTAAAACTTCGAGATGATCAATATACACTGGAA
CACATGCATGCTTTTGGAATGTATAATTACCTGCACTGTGATTCATGGTATCAAGACAGTGTCTACTATATTGAT
ACCCTTGGAAGAATTATGAATTTAACAGTAATGCTGGACACTGCCTTAGGAAAACCACGAGAGGTGTTTCGACTT
CCTACAGATTTGACAGCATGTGACAACCGTCTTTGTGCATCTATCCATTTCTCATCTTCTACCTGGGTTACCTTG
TCAGATGGAACTGGAAGATTGTATGTCATTGGAACAGGTGAACGTGGAAATAGCGCTTCTGAAAAATGGGAGATT
ATGTTTAATGAAGAACTTGGGGATCCTTTTATTATAATTCACAGTATCTCACTGCTAAATGCTGAAGAACATTCT
ATAGCTACCCTACTTCTTCGAATAGAGAAAGAGGAATTGGATATGAAAGGAAGTGGTTTCTATGTTTCTCTGGAG
TGGGTCACTATCAGTAAGAAAAATCAAGATAATAAAAAATATGAAATTATTAAGCGTGATATTCTCCGTGGAAAG
TCAGTGCCACATTATGCTGCTATTGAGCCTGATGGAAATGGTCTAATGATTGTATCCTACAAGTCTTTAACATTT
GTTCAGGCTGGTCAAGATCTTGAAGAAAATATGGATGAAGACATATCAGAGAAAATCAAAGAACCTCTGTATTAC
TGGCAACAGACTGAAGATGATTTGACAGTAACCATACGGCTTCCAGAAGACAGTACTAAGGAGGACATTCAAATA
CAGTTTTTGCCTGATCACATCAACATTGTACTGAAGGATCACCAGTTTTTAGAAGGAAAACTCTATTCATCTATT
GATCATGAAAGCAGTACATGGATAATTAAAGAGAGTAATAGCTTGGAGATTTCCTTGATTAAGAAGAATGAAGGA
CTGACCTGGCCAGAGCTAGTAATTGGAGATAAACAAGGGGAACTTATAAGAGATTCAGCCCAGTGTGCTGCAATA
GCTGAACGTTTGATGCATTTGACCTCTGAAGAACTGAATCCAAATCCAGATAAAGAAAAACCACCTTGCAGTGCT
CAAGAGTTAGAAGAATGTGATATTTTCTTTGAAGAGAGCTCCAGTTTATGCAGATTTGATGGCAATACATTAAAA
ACTACTCATGTGGTGAATCTTGGAAGCAACCAGTACCTTTTCTCTGTCATAGTGGATCCTAAAGAAATGCCCTGC
TTCTGTTTGCGCCATGATGTTGATGCCCTACTCTGGCAACCACACTCCAGCAAACAAGATGATATGTGGGAGCAC
ATCGCAACTTTCAATGCTTTAGGCTATGTCCAAGCATCAAAGAGAGACAAAAAATTTTTTGCCTGTGCTCCAAAT
TACTCGTATGCAGCCCTTTGTGAGTGCCTTCGTCGAGTATTCATCTATCGTCAGCCTGCTCCCATGTCCACTGTA
CTTTACAACAGAAAGGAAGGCAGGCAAGTAGGACAGGTTGCTAAGCAGCAAGTAGCAAGCCTAGAAACCAATGAT
CCTATTTTAGGATTTCAGGCAACAAATGAGAGATTATTTGTTCTTACTACCAAAAACCTCTTTTTAATAAAAGTA
AATACAGAGAAT**TAA**TTATTCTAACATATTGGCCTCTTTGTACTGGAAAAGTATTCAGTGGTACCTGGAGGTCTG
GACAGTTATACTGTAACCTCTTAAGTTTTAATGTGCTAAATATATCTTGTATGATTTTTTATTTTTTAATAACAT
TGGAAATATATTCAAGAGATTATGATTCTGTAAAGCTGTGGAATGAAGCTGCAGATTTAGAGAACATTGGCTTCT
GAAAAAAAAAAAGAGTGAAGATAGTACTAGCAAGTATACTTATTTTTTAAAACAGGCTAGAATCTCATGTTTTAT
ATGAAAGATGTACAATTCAGTGTTTAAAAATAAAAATATTTATTGTGT

FIGURE 2

MEVAANCSLRVKRPLLDPRFEGYKLSLEPLPCYQLELDAAVAEVKLRDDQYTLEHMHAFGMYNYLHCDSWYQDSV
YYIDTLGRIMNLTVMLDTALGKPREVFRLPTDLTACDNRLCASIHFSSSTWVTLSDGTGRLYVIGTGERGNSASE
KWEIMFNEELGDPFIIIHSISLLNAEEHSIATLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDISEKIKEPLYYWQQTEDDLTVTIRLPEDSTKE
DIQIQFLPDHINIVLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTWPELVIGDKQGELIRDSAQ
CAAIAERLMHLTSEELNPNPDKEKPPCSAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSVIVDPK
EMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYVQASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAP
MSTVLYNRKEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLIKVNTEN

FIGURE 3

GAATTCCGGTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGACGCGGCACGGA
GACGGCGGCAGCCTGGACTAGGTGGCAGGCCCTGCATC**<u>ATG</u>**GAAACTCTTTCTAATGCAAGTGGTACTTTTGCCA
TACGCCTTTTAAAGATACTGTGTCAAGATAACCCTTCGCACAACGTGTTCTGTTCTCCTGTGAGCATCTCCTCTG
CCCTGGCCATGGTTCTCCTAGGGGCAAAGGGAAACACCGCAACCCAGATGGCCCAGGCACTGTCTTTAAACACAG
AGGAAGACATTCATCGGGCTTTCCAGTCGCTTCTCACTGAAGTGAACAAGGCTGGCACACAGTACCTGCTGAGAA
CGGCCAACAGGCTCTTTGGAGAGAAAACTTGTCAGTTCCTCTCAACGTTTAAGGAATCCTGTCTTCAATTCTACC
ATGCTGAGCTGAAGGAGCTTTCCTTTATCAGAGCTGCAGAAGAGTCCAGGAAACACATCAACACCTGGGTCTCAA
AAAAGACCGAAGGTAAAATTGAAGAGTTGTTGCCGGGTAGCTCAATTGATGCAGAAACCAGGCTGGTTCTTGTCA
ATGCCATCTACTTCAAAGGAAAGTGGAATGAACCGTTTGACGAAACATACACAAGGGAAATGCCCTTTAAAATAA
ACCAGGAGGAGCAAAGGCCAGTGCAGATGATGTATCAGGAGGCCACGTTTAAGCTCGCCCACGTGGGCGAGGTGC
GCGCGCAGCTGCTGGAGCTGCCCTACGCCAGGAAGGAGCTGAGCCTGCTGGTGCTGCTGCCTGACGACGGCGTGG
AGCTCAGCACGGTGGAAAAAAGTCTCACTTTTGAGAAACTCACAGCCTGGACCAAGCCAGACTGTATGAAGAGTA
CTGAGGTTGAAGTTCTCCTTCCAAAATTTAAACTACAAGAGGATTATGACATGGAATCTGTGCTTCGGCATTTGG
GAATTGTTGATGCCTTCCAACAGGGCAAGGCTGACTTGTCGGCAATGTCAGCGGAGAGAGACCTGTGTCTGTCCA
AGTTCGTGCACAAGAGTTTTGTGGAGGTGAATGAAGAAGGCACCGAGGCAGCGGCAGCGTCGAGCTGCTTTGTAG
TTGCAGAGTGCTGCATGGAATCTGGCCCCAGGTTCTGTGCTGACCACCCTTTCCTTTTCTTCATCAGGCACAACA
GAGCCAACAGCATTCTGTTCTGTGGCAGGTTCTCATCGCCA**<u>TAA</u>**AGGGTGCACTTACCGTGCACTCGGCCATTTC
CCTCTTCCTGTGTCCCCAGATCCCCACTACAGCTCCAAGAGGATGGGCCTAGAAAGCCAAGTGCAAAGATGAGGG
CAGATTCCTTACCTGTCTGCCCTCATGATTTGCCAGCATGAATTCATGATGCTCCACACTCGCTTATGCTACTTA
ATCAGAATCTTGAGAAAATAGACCATAATGATTCCCTGTTGTATTAAAATTGCCATCCCCCGAATTCCCATAGGA
TGGCAAGCAAAGTTCTTCTAGAATTCCACATGCAATTCACTCTGGCGACCCTGTGCTTTCCTGACACTGCGAATA
CATTCCTTAACCCGCTGCCTCAGTGGTAATAAATGGTGCTAGCCGGAATTC

FIGURE 4

METLSNASGTFAIRLLKILCQDNPSHNVFCSPVSISSALAMVLLGAKGNTATQMAQALSLNTEEDIHRAFQSLLT
EVNKAGTQYLLRTANRLFGEKTCQFLSTFKESCLQFYHAELKELSFIRAAEESRKHINTWVSKKTEGKIEELLPG
SSIDAETRLVLVNAIYFKGKWNEPFDETYTREMPFKINQEEQRPVQMMYQEATFKLAHVGEVRAQLLELPYARKE
LSLLVLLPDDGVELSTVEKSLTFEKLTAWTKPDCMKSTEVEVLLPKFKLQEDYDMESVLRHLGIVDAFQQGKADL
SAMSAERDLCLSKFVHKSFVEVNEEGTEAAAASSCFVVAECCMESGPRFCADHPFLFFIRHNRANSILFCGRFSS
P

FIGURE 5

GCTAAGCGTCCCAGCCGCATCCTCCCGCAGCGACGGCGGCCCGGGACCGCGGGCTGTGAACCATGAACACCCGCA
ATAGAGTGGTGAACTCCGGGCTCGGCGCCTCCCCTGCCTCCCGCCCGACCCGGGATCCCCAGGACCCTTCTGGGC
GGCAAGGGGAGCTGAGCCCCGTGGAAGACCAGAGAGAGGGTTTGGAGGCAGCCCCTAAGGGCCCTTCGCGGGAGA
GCGTCGTGCACGCGGGCCAGAGGCGCACAAGTGCATACACCTTGATAGCACCAAATATAAACCGGAGAAATGAGA
TACAAAGAATGCGGAGCAGGAGCTGGCCAACCTGGAGAAGTGGAAGGAGCAGAACAGAGCTAAACCGGTTCACCT
GGTGCCCAGACGGCTAGGTGGAAGCCAGTCAGAAACTGAAGTCAGACAGAAACAACAACTCCAGCTGATGCAATC
TAAATACAAGCAAAAGCTAAAAAGAGAAGAATCTGTAAGAATCAAGAAGGAAGCTGAAGAAGCTGAACTCCAAAA
A**ATG**AAGGCAATTCAGAGAGAGAAGAGCAATAAACTGGAGGAGAAAAAAAGACTTCAAGAAAACCTTAGAAGAGA
AGCATTTAGAGAGCATCAGCAATACAAAACCGCTGAGTTCTTGAGCAAACTGAACACAGAATCGCCAGACAGAAG
TGCCTGTCAAAGTGCTGTTTGTGGCCCACAATCCTCAACATGGGCCAGAAGCTGGGCTTACAGAGATTCTCTAAA
GGCAGAAGAAAACAGAAAATTGCAAAAGATGAAGGATGAACAACATCAAAAGAGTGAATTACTGGAACTGAAACG
GCAGCAGCAAGAGCAAGAAAGAGCCAAAATCCACCAGACTGAACACAGGAGGGTAAATAATGCTTTTCTGGACCG
ACTCCAAGGTAAAAGTCAACCAGGTGGCCTCGAGCAATCTGGAGGCTGTTGGAATATGAATAGTGGTAACAGCTG
GGGTATA**TGA**GAAAATATTGACTCCTATCTGGCCTTCATCAACTGACCTCGAAAAGCCTCATGAGATGCTTTTTC
TTAATGTGATTTTGTTCAGCCTCACTGTTTTTACCTTAATTTCAACTGCCCACACACTTGACCGTGCAGTCAGGA
GTGACTGGCTTCTCCTTGTCCTCATTTATGCATGTTTGGAGGAGCTGATTCCTGAACTCATATTTAATCTCTACT
GCCAGGGAAATGCTACATTATTTTTCTAATTGGAAGTATAATTAGAGTGATGTTGGTAGGGTGGAAAAAGAGGGA
GTCACTTGATGCTTTCAGGTTAATCAGAGCTATGGGTGCTACAGGCTTGTCTTTCTAAGTGACATATTCTTATCT
AATTCTCAGATCAGGTTTTGAAAAGCTTTGGGGGTCTTTTTAGATTTTAATCCCTACTTTCTTTATGGTACAAAT
ATGTACAAAAGAAAAAGGTCTTATATTCTTTTACACAAATTTATAAATAAATTTTGAACTCCTTCTGTAT

FIGURE 6

MKAIQREKSNKLEEKKRLQENLRREAFREHQQYKTAEFLSKLNTESPDRSACQSAVCGPQSSTWARSWAYRDSLK
AEENRKLQKMKDEQHQKSELLELKRQQQEQERAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
GI

FIGURE 7

TAGTTATTAAAGTTCCTATGCAGCTCCGCCTCCGTCCGGCCTCATTTCCTCAAAAAATCCCTGCTTTCCCCGCTC
GCCACGCCCTCCTGCTACCCGGCTTTAAAGCTAGTGAGGCACAGCCTGCGGGGAACGTAGCTAGCTGCAAGCAGA
GGCCGGC**ATG**ACCACCGAGCAGCGACGCAGCCTGCAAGCCTTCCAGGATTATATCCGGAAGACCCTGGACCCTAC
CTACATCCTGAGCTACATGGCCCCCTGGTTTAGGGAGGAAGAGGTGCAGTATATTCAGGCTGAGAAAAACAACAA
GGGCCCAATGGAGGCTGCCACACTTTTTCTCAAGTTCCTGTTGGAGCTCCAGGAGGAAGGCTGGTTCCGTGGCTT
TTTGGATGCCCTAGACCATGCAGGTTATTCTGGACTTTATGAAGCCATTGAAAGTTGGGATTTCAAAAAAATTGA
AAAGTTGGAGGAGTATAGATTACTTTTAAAACGTTTACAACCAGAATTTAAAACCAGAATTATCCCAACCGATAT
CATTTCTGATCTGTCTGAATGTTTAATTAATCAGGAATGTGAAGAAATTCTACAGATTTGCTCTACTAAGGGGAT
GATGGCAGGTGCAGAGAAATTGGTGGAATGCCTTCTCAGATCAGACAAGGAAAACTGGCCCAAAACTTTGAAACT
TGCTTTGGAGAAAGAAAGGAACAAGTTCAGTGAACTGTGGATTGTAGAGAAAGGTATAAAAGATGTTGAAACAGA
AGATCTTGAGGATAAGATGGAAACTTCTGACATACAGATTTTCTACCAAGAAGATCCAGAATGCCAGAATCTTAG
TGAGAATTCATGTCCACCTTCAGAAGTGTCTGATACAAACTTGTACAGCCCATTTAAACCAAGAAATTACCAATT
AGAGCTTGCTTTGCCTGCTATGAAAGGAAAAAACACAATAATATGTGCTCCTACAGGTTGTGGAAAAACCTTTGT
TTCACTGCTTATATGTGAACATCATCTTAAAAAATTCCCACAAGGACAAAAGGGGAAAGTTGTCTTTTTTGCGAA
TCAGATCCCAGTGTATGAACAGCAGAAATCTGTATTCTCAAAATACTTTGAAAGACATGGGTATAGAGTTACAGG
CATTTCTGGAGCAACAGCTGAGAATGTCCCAGTGGAACAGATTGTTGAGAACAATGACATCATCATTTTAACTCC
ACAGATTCTTGTGAACAACCTTAAAAAGGGAACGATTCCATCACTATCCATCTTTACTTTGATGATATTTGATGA
ATGCCACAACACTAGTAAACAACACCCGTACAATATGATCATGTTTAATTATCTAGATCAGAAACTTGGAGGATC
TTCAGGCCCACTGCCCCAGGTCATTGGGCTGACTGCCTCGGTTGGTGTTGGGGATGCCAAAAACACAGATGAAGC
CTTGGATTATATCTGCAAGCTGTGTGCTTCTCTTGATGCGTCAGTGATAGCAACAGTCAAACACAATCTGGAGGA
ACTGGAGCAAGTTGTTTATAAGCCCCAGAAGTTTTTCAGGAAAGTGGAATCACGGATTAGCGACAAATTTAAATA
CATCATAGCTCAGCTGATGAGGGACACAGAGAGTCTGGCAAAGAGAATCTGCAAAGACCTCGAAAACTTATCTCA
AATTCAAAATAGGGAATTTGGAACACAGAAATATGAACAATGGATTGTTACAGTTCAGAAAGCATGCATGGTGTT
CCAGATGCCAGACAAAGATGAAGAGAGCAGGATTTGTAAAGCCCTGTTTTTATACACTTCACATTTGCGGAAATA
TAATGATGCCCTCATTATCAGTGAGCATGCACGAATGAAAGATGCTCTGGATTACTTGAAAGACTTCTTCAGCAA
TGTCCGAGCAGCAGGATTCGAAGAGATTGAGCAAGATCTTACTCAGAGATTTGAAGAAAAGCTGCAGGAACTAGA
AAGTGTTTCCAGGGATCCCAGCAATGAGAATCCTAAACTTGAAGACCTCTGCTTCATCTTACAAGAAGAGTACCA
CTTAAACCCAGAGACAATAACAATTCTCTTTGTGAAAACCAGAGCACTTGTGGACGCTTTAAAAAATTGGATTGA
AGGAAATCCTAAACTCAGTTTTCTAAAACCTGGCATATTGACTGGACGTGGCAAAACAAATCAGAACACAGGAAT
GACCCTCCCGGCACAGAAGTGTATATTGGATGCATTCAAAGCCAGTGGAGATCACAATATTCTGATTGCCACCTC
AGTTGCTGATGAAGGCATTGACATTGCACAGTGCAATCTTGTCATCCTTTATGAGTATGTGGGCAATGTCATCAA
AATGATCCAAACCAGAGGCAGAGGAAGAGCAAGAGGTAGCAAGTGCTTCCTTCTGACTAGTAATGCTGGTGTAAT
TGAAAAAGAACAAATAAACATGTACAAAGAAAAAATGATGAATGACTCTATTTTACGCCTTCAGACATGGGACGA
AGCAGTATTTAGGGAAAAGATTCTGCATATACAGACTCATGAAAAATTCATCAGAGATAGTCAAGAAAAACCAAA
ACCTGTCCCTGATAAGGAAAATAAAAAACTGCTCTGCAGAAAGTGCAAAGCCTTGGCATGTTACACAGCTGACGT
AAGAGTGATAGAGGAATGCCATTACACTGTGCTTGGAGATGCTTTTAAGGAATGCTTTGTGAGTAGACCACATCC
CAAGCCAAAGCAGTTTTCAAGTTTTGAAAAAAGAGCAAAGATATTCTGTGCCCGACAGAACTGCAGCCATGACTG
GGGAATCCATGTGAAGTACAAGACATTTGAGATTCCAGTTATAAAAATTGAAAGTTTTGTGGTGGAGGATATTGC
AACTGGAGTTCAGACACTGTACTCGAAGTGGAAGGACTTTCATTTTGAGAAGATACCATTTGATCCAGCAGAAAT
GTCCAAA**TGA**TATCAGGTCCTCAATCTTCAGCTACAGGGAATGAGTAACTTTGAGTGGAGAAGAAACAAACATAG
TGGGTATAATCATGGATCGCTTGTACCCCTGTGAAAATATATTTTTAAAAATAAAAAAAAAAA

FIGURE 8

MTTEQRRSLQAFQDYIRKTLDPTYILSYMAPWFREEEVQYIQAEKNNKGPMEAATLFLKFLLELQEEGWFRGFLD
ALDHAGYSGLYEAIESWDFKKIEKLEEYRLLLKRLQPEFKTRIIPTDIISDLSECLINQECEEILQICSTKGMMA
GAEKLVECLLRSDKENWPKTLKLALEKERNKFSELWIVEKGIKDVETEDLEDKMETSDIQIFYQEDPECQNLSEN
SCPPSEVSDTNLYSPFKPRNYQLELALPAMKGKNTIICAPTGCGKTFVSLLICEHHLKKFPQGQKGKVVFFANQI
PVYEQQKSVFSKYFERHGYRVTGISGATAENVPVEQIVENNDIIILTPQILVNNLKKGTIPSLSIFTLMIFDECH
NTSKQHPYNMIMFNYLDQKLGGSSGPLPQVIGLTASVGVGDAKNTDEALDYICKLCASLDASVIATVKHNLEELE
QVVYKPQKFFRKVESRISDKFKYIIAQLMRDTESLAKRICKDLENLSQIQNREFGTQKYEQWIVTVQKACMVFQM
PDKDEESRICKALFLYTSHLRKYNDALIISEHARMKDALDYLKDFFSNVRAAGFEEIEQDLTQRFEEKLQELESV
SRDPSNENPKLEDLCFILQEEYHLNPETITILFVKTRALVDALKNWIEGNPKLSFLKPGILTGRGKTNQNTGMTL
PAQKCILDAFKASGDHNILIATSVADEGIDIAQCNLVILYEYVGNVIKMIQTRGRGRARGSKCFLLTSNAGVIEK
EQINMYKEKMMNDSILRLQTWDEAVFREKILHIQTHEKFIRDSQEKPKPVPDKENKKLLCRKCKALACYTADVRV
IEECHYTVLGDAFKECFVSRPHPKPKQFSSFEKRAKIFCARQNCSHDWGIHVKYKTFEIPVIKIESFVVEDIATG
VQTLYSKWKDFHFEKIPFDPAEMSK

FIGURE 9

GGAAAAAAGCGACTTGTGGCGGTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAAT**ATG**GACCTCGCGGC
GGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGACGAGGTGGCCGAGAAGTGCCAGAAACTGTT
CCTGGACTTCTTGGAGGAGTTTCAGAGCAGCGATGGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTCG
TCCTGAGAGAAACACATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCA
AGAGGAGTTCTATAGAGTTTACCCTTACCTGTGTCGGGCCTTGAAAACATTCGTCAAAGACCGTAAAGAGATCCC
TCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGACACAAGATTCGAGAGCTCACCTCATCCAG
AATTGGTTTGCTCACTCGCATCAGTGGGCAGGTGGTGCGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAAC
TTTTCTGTGCTTGGACTGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTG
CCGAAATCCAGTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTTGTTGATTTTCAAAA
GGTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATCCCCCGCAGTTTAGAAGTAATTTTAAGGGC
TGAAGCTGTGGAATCAGCTCAAGCTGGTGACAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTC
CAAGCTTAGCACACCAGGAGCACGTGCAGAAACTAATTCCCGTGTCAGTGGTGTTGATGGATATGAGACAGAAGG
CATTCGAGGACTCCGGGCCCTTGGTGTTAGGGACCTTTCTTATAGGCTGGTCTTTCTTGCCTGCTGTGTTGCGCC
AACCAACCCAAGGTTTGGGGGGAAAGAGCTCAGAGATGAGGAACAGACAGCTGAGAGCATTAAGAACCAAATGAC
TGTGAAAGAATGGGAGAAAGTGTTTGAGATGAGTCAAGATAAAAATCTATACCACAATCTTTGTACCAGCCTGTT
CCCTACTATACATGGCAATGATGAAGTAAAACGGGGTGTCCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC
AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTACAGCTAAGAGCCAATT
TCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGTGGTAAAGCGTCCAGTGCTGCTGGCTTAAC
AGCAGCTGTTGTGAGAGATGAAGAATCTCATGAGTTTGTCATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGG
TGTGTGTTGTATTGATGAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTCATGAAGCTATGGAACAGCA
GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCGGACGTCCATTTTGGCAGCAGCAAACCC
AATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATATAAATTTGTCAGCTCCCATCATGTCCCGATT
CGATCTCTTCTTTATCCTTGTGGATGAATGTAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTT
GCATTCAAGAATTGAGGAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAG
ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACATCTCCGCCAGAGAGA
TGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACAGCTTGAGAGCATGATTCGTCTCTCTGAAGC
TATGGCTCGGATGCACTGCTGTGATGAGGTCCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATC
AATCATCCGTGTGGAAACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC
TGGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAATGAAGACATAAATCA
AGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTACTGCCGAATCTCTAACCTTATTGTGCTTCA
CCTCAGAAAGGTGGAAGAAGAAGAGGACGAGTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGA
AATCGAATCAGAGATAGACTCTGAAGAAGAACTTATAAATAAAAAAAGAATCATAGAGAAAGTTATTCATCGACT
CACACACTATGATCATGTTCTAATTGAGCTCACCCAGGCTGGATTGAAAGGCTCCACAGAGGGAAGTGAGAGCTA
TGAAGAAGATCCCTACTTGGTAGTTAACCCTAACTACTTGCTCGAAGAT**TGA**GATAGTGAAAGTAACTGACCAGA
GCTGAGGAACTGTGGCACAGCACCTCGTGGCCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTTTCTGG
AAGTGATGCTTCCAGGATTTGTTTTCAGAAACAAGAATTGAGTTGATGGTCCTATGTGTCACATTCATCACAGGT
TTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCCTGTCCCAGTGAAGTTGGAACCAAATAATGTGT
AGTCTCTATAACCAATACCTTTGTTTTCATGTGTAAGAAAAGGCCCATTACTTTTAAGGTATGTGCTGTCCTATT
GAGCAAATAACTTTTTTTCAATTGCCAGCTACTGCTTTTATTCATCAAAATAAAATAACTTGTTCTG

FIGURE 10

MDLAAAAEPGAGSQHLEVRDEVAEKCQKLFLDFLEEFQSSDGEIKYLQLAEELIRPERNTLVVSFVDLEQFNQQL
STTIQEEFYRVYPYLCRALKTFVKDRKEIPLAKDFYVAFQDLPTRHKIRELTSSRIGLLTRISGQVVRTHPVHPE
LVSGTFLCLDCQTVIRDVEQQFKYTQPNICRNPVCANRRRFLLDTNKSRFVDFQKVRIQETQAELPRGSIPRSLE
VILRAEAVESAQAGDKCDFTGTLIVVPDVSKLSTPGARAETNSRVSGVDGYETEGIRGLRALGVRDLSYRLVFLA
CCVAPTNPRFGGKELRDEEQTAESIKNQMTVKEWEKVFEMSQDKNLYHNLCTSLFPTIHGNDEVKRGVLLMLFGG
VPKTTGEGTSLRGDINVCIVGDPSTAKSQFLKHVEEFSPRAVYTSGKASSAAGLTAAVVRDEESHEFVIEAGALM
LADNGVCCIDEFDKMDVRDQVAIHEAMEQQTISITKAGVKATLNARTSILAAANPISGHYDRSKSLKQNINLSAP
IMSRFDLFFILVDECNEVTDYAIARRIVDLHSRIEESIDRVYSLDDIRRYLLFARQFKPKISKESEDFIVEQYKH
LRQRDGSGVTKSSWRITVRQLESMIRLSEAMARMHCCDEVQPKHVKEAFRLLNKSIIRVETPDVNLDQEEEIQME
VDEGAGGINGHADSPAPVNGINGYNEDINQESAPKASLRLGFSEYCRISNLIVLHLRKVEEEEDESALKRSELVN
WYLKEIESEIDSEEELINKKRIIEKVIHRLTHYDHVLIELTQAGLKGSTEGSESYEEDPYLVVNPNYLLED

FIGURE 11

ATATAACCGCGTGGCCCGCGCGCGCTTCCCTCCCGGCGCAGTCACCGGCGCGGTCTATGGCTGCGACTTCTCT
A**<u>ATG</u>**TCTGCTTTGGCTGCCCGGCTGCTGCAGCCCGCGCACAGCTGCTCCCTTCGCCTTCGCCCTTTCCACCTCGC
GGCAGTTCGAAATGAAGCTGTTGTCATTTCTGGAAGGAAACTGGCCCAGCAGATCAAGCAGGAAGTGCGGCAGGA
GGTAGAAGAGTGGGTGGCCTCAGGCAACAAACGGCCACACCTGAGTGTGATCCTGGTTGGCGAGAATCCTGCAAG
TCACTCCTATGTCCTCAACAAAACCAGGGCAGCTGCAGTTGTGGGAATCAACAGTGAGACAATTATGAAACCAGC
TTCAATTTCAGAGGAAGAATTGTTGAATTTAATCAATAAACTGAATAATGATGATAATGTAGATGGCCTCCTTGT
TCAGTTGCCTCTTCCAGAGCATATTGATGAGAGAAGGATCTGCAATGCTGTTTCTCCAGACAAGGATGTTGATGG
CTTTCATGTAATTAATGTAGGACGAATGTGTTTGGATCAGTATTCCATGTTACCGGCTACTCCATGGGGTGTGTG
GGAAATAATCAAGCGAACTGGCATTCCAACCCTAGGGAAGAATGTGGTTGTGGCTGGAAGGTCAAAAAACGTTGG
AATGCCCATTGCAATGTTACTGCACACAGATGGGGCGCATGAACGTCCCGGAGGTGATGCCACTGTTACAATATC
TCATCGATATACTCCCAAAGAGCAGTTGAAGAAACATACAATTCTTGCAGATATTGTAATATCTGCTGCAGGTAT
TCCAAATCTGATCACAGCAGATATGATCAAGGAAGGAGCAGCAGTCATTGATGTGGGAATAAATAGAGTTCACGA
TCCTGTAACTGCCAAACCCAAGTTGGTTGGAGATGTGGATTTTGAAGGAGTCAGACAAAAAGCTGGGTATATCAC
TCCAGTTCCTGGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATTGCTGCAAAAAAGGT
GCTGAGGCTTGAAGAGCGAGAAGTGCTGAAGTCTAAAGAGCTTGGGGTAGCCACTAAT**<u>TAA</u>**CTACTGTGTCTTCT
GTGTCACAAACAGCACTCCAGGCCAGCTCAAGAAGCAAAGCAGGCCAATAGAAATGCAATATTTTTAATTTATTC
TACTGAAATGGTTTAAAATGATGCCTTGTATTTATTGAAAGCTTAAATGGGTGGGTGTTTCTGCACATACCTCTG
CAGTACCTCACCAGGGAGCATTCCAGTATCATGCAGGGTCCTGTGATCTAGCCAGGAGCAGCCATTAACCTAGTG
ATTAATATGGGAGACATTACCATATGGAGGATGGATGCTTCACTTTGTCAAGCACCTCAGTTACACATTCGCCTT
TTCTAGGATTGCATTTCCCAAGTGCTATTGCAATAACAGTTGATACTCATTTTAGGTACCAGACCTTTTGAGTTC
AACTGATCAAACCAAAGGAAAAGTGTTGCTAGAGAAAATTGGGGAAAAGGTGAAAAAGAAAAAATGGTAGTAATT
GAGCAGAAAAAAATTAATTTATATATGTATTGATTGGCAACCAGATTTATCTAAGTAGAACTGAATTGGCTAGGA
AAAAAGAAAAACTGCATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGTT
TAGGATTATTCCTTGCTATTAGTACTCATTTTATGTATGTTACCCTTCAGTAAGTTCTCCCCATTTTAGTTTTCT
AGGACTGAAAGGATTCTTTTCTACATTATACATGTGTGTTGTCATATTTGGCTTTTGCTATATACTTTAACTTCA
TTGTTAAATTTTTGTATTGTATAGTTTCTTTGGTGTATCTTAAAACCTATTTTTGAAAAACAAACTTGGCTTGAT
AATCATTTGGGCAGCTTGGGTAAGTACGCAACTTACTTTTCCACCAAAGAACTGTCAGCAGCTGCCTGCTTTTCT
GTGATGTATGTATCCTGTTGACTTTTCCAGAAATTTTTTAAGAGTTTGAGTTACTATTGAATTTAATCAGACTTT
CTGATTAAAGGGTTTTCTTTCTTTTTTAATAAAACACATCTGTCTGGTATGGTA

FIGURE 12

MSALAARLLQPAHSCSLRLRPFHLAAVRNEAVVISGRKLAQQIKQEVRQEVEEWVASGNKRPHLSVILVGENPAS
HSYVLNKTRAAAVVGINSETIMKPASISEEELLNLINKLNNDDNVDGLLVQLPLPEHIDERRICNAVSPDKDVDG
FHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGKNVVVAGRSKNVGMPIAMLLHTDGAHERPGGDATVTIS
HRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAAVIDVGINRVHDPVTAKPKLVGDVDFEGVRQKAGYIT
PVPGGVGPMTVAMLMKNTIIAAKKVLRLEEREVLKSKELGVATN

FIGURE 13

GGCAGCTGCACGGCTCCTGGCCCCGGAGCATGCGCGAGAGCCGCCCCGGAGCGCCCCGGAGCCCCCCGCCGTCCC
GCCCGCGGCGTCCCGCGCCCCGCCGCCAGCGCACCCCCGGACGCTATGGCCCACCCCTCCGGCTGGCCCCTTCTG
TAGG**ATG**GTAGCACACAACCAGGTGGCAGCCGACAATGCAGTCTCCACAGCAGCAGAGCCCCGACGGCGGCCAGA
ACCTTCCTCCTCTTCCTCCTCCTCGCCCGCGGCCCCCGCGCGCCCGCGGCCGTGCCCCGCGGTCCCGGCCCCGGC
CCCCGGCGACACGCACTTCCGCACATTCCGTTCGCACGCCGATTACCGGCGCATCACGCGCGCCAGCGCGCTCCT
GGACGCCTGCGGATTCTACTGGGGGCCCCTGAGCGTGCACGGGGCGCACGAGCGGCTGCGCGCCGAGCCCGTGGG
CACCTTCCTGGTGCGCGACAGCCGCCAGCGGAACTGCTTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCCAC
GAGCATCCGCGTGCACTTTCAGGCCGGCCGCTTTCACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGA
GCTGCTGGAGCACTACGTGGCGGCGCCGCGCCGCATGCTGGGGGCCCCGCTGCGCCAGCGCCGCGTGCGGCCGCT
GCAGGAGCTGTGCCGCCAGCGCATCGTGGCCACCGTGGGCCGCGAGAACCTGGCTCGCATCCCCCTCAACCCCGT
CCTCCGCGACTACCTGAGCTCCTTCCCCTTCCAGATT**TGA**CCGGCAGCGCCCGCCGTGCACGCAGCATTAACTGG
GATGCCGTGTTATTTTGTTATTACTTGCCTGGAACCATGTGGGTACCCTCCCCGGCCTGGGTTGGAGGGAGCGGA
TGGGTGTAGGGGCGAGGCGCCTCCCGCCCTCGGCTGGAGACGAGGCCGCAGACCCCTTCTCACCTCTTGAGGGGG
TCCTCCCCCTCCTGGTGCTCCCTCTGGGTCCCCCTGGTTGTTGTAGCAGCTTAACTGTATCTGGAGCCAGGACCT
GAACTCGCACCTCCTACCTCTTCATGTTTACATATACCCAGTATCTTTGCACAAACCAGGGGTTGGGGGAGGGTC
TCTGGCTTTATTTTTCTGCTGTGCAGAATCCTATTTTATATTTTTTAAAGTCAGTTTAGGTAATAAACTTTATTA
TGAAAGTTTTTTTTTT

FIGURE 14

MVAHNQVAADNAVSTAAEPRRRPEPSSSSSSSPAAPARPRPCPAVPAPAPGDTHFRTFRSHADYRRITRASALLD
ACGFYWGPLSVHGAHERLRAEPVGTFLVRDSRQRNCFFALSVKMASGPTSIRVHFQAGRFHLDGSRESFDCLFEL
LEHYVAAPRRMLGAPLRQRRVRPLQELCRQRIVATVGRENLARIPLNPVLRDYLSSFPFQI

FIGURE 15

GGAAACTGAAAGTGAAATAGGGAGCTGGCTACCAGCGTTGAGTTGCCCTGTAAAGCCAAACCCCCTAAAGGTCTC
CACACTGCTGTTTAACGGCACACTTGACA**ATG**GCTTCAGCAGCACGCTTGACAATGATGTGGGAGGAGGTCACAT
GCCCTATCTGCCTGGACCCCTTCGTGGAGCCTGTGAGCATCGAGTGTGGCCACAGCTTCTGCCAGGAATGCATCT
CTCAGGTTGGGAAAGGTGGGGGCAGCGTCTGTCCTGTGTGCCGGCAGCGCTTTCTGCTCAAGAATCTCCGGCCCA
ATCGACAGCTAGCCAACATGGTGAACAACCTTAAAGAAATCAGCCAGGAGGCCAGAGAGGGCACACAGGGGGAAC
GGTGTGCAGTGCATGGAGAGAGACTTCACCTGTTCTGTGAGAAAGATGGGAAGGCCCTTTGCTGGGTATGTGCCC
AGTCTCGGAAACACCGTGACCACGCCATGGTCCCTCTTGAGGAGGCTGCACAGGAGTACCAGGAGAAGCTCCAGG
TGGCATTAGGGGAACTGAGAAGAAAGCAGGAGTTGGCTGAGAAGTTGGAAGTGGAAATTGCAATAAAGAGAGCAG
ACTGGAAGAAAACAGTGGAAACACAGAAATCTAGGATTCACGCAGAGTTTGTGCAGCAAAAAAACTTCCTGGTTG
AAGAAGAACAGAGGCAGCTGCAGGAGCTGGAGAAGGATGAGAGGGAGCAGCTGAGAATCCTGGGGGAGAAAGAGG
CCAAGCTGGCCCAGCAGAGCCAGGCCCTACAGGAGCTCATCTCAGAGCTAGATCGAAGGTGCCACAGCTCAGCAC
TGGAACTGCTGCAGGAGGTGATAATTGTCCTGGAAAGGAGTGAGTCCTGGAACCTGAAGGACCTGGATATTACCT
CTCCAGAACTCAGGAGTGTGTGCCATGTGCCAGGGCTGAAGAAGATGCTGAGGACATGTGCAGTCCACATCACTC
TGGATCCAGACACAGCCAATCCGTGGCTGATACTTTCAGAAGATCGGAGACAAGTGAGGCTTGGAGACACCCAGC
AGAGCATACCTGGAAATGAAGAGAGATTTGATAGTTATCCTATGGTCCTGGGTGCCCAGCACTTTCACTCTGGAA
AACATTACTGGGAGGTAGATGTGACAGGAAAGGAGGCCTGGGACCTGGGTGTCTGCAGAGACTCTGTGCGCAGGA
AGGGGCACTTTTTGCTTAGTTCCAAGAGTGGCTTCTGGACAATTTGGTTGTGGAACAAACAAAAATATGAGGCTG
GCACCTACCCCCAGACTCCCCTCCACCTTCAGGTGCCTCCATGCCAAGTTGGGATTTTCCTGGACTATGAGGCTG
GCATGGTCTCCTTCTACAACATCACTGACCATGGCTCCCTCATCTACTCCTTCTCTGAATGTGCCTTTACAGGAC
CTCTGCGGCCCTTCTTCAGTCCTGGTTTCAATGATGGAGGAAAAAACACAGCCCCTCTAACCCTCTGTCCACTGA
ATATTGGATCACAAGGATCCACTGACTAT**TGA**TGGCTTTCTCTGGACACTGCCACTCTCCCCATTGGCACCGCTT
CTCAGCCACAAACCCTGCCTCTTTTCCCCATGAACTCTGAACCACCTTTGTCTCTGCAGAGGCATCCGGATCCCA
GCAAGCGAGCTTTAGCAGGGAAGTCACTTCACCATCAACATTCCTGCCCCAGATGGCTTTGTGATTCCCTCCAGT
GAAGCAGCCTCCTTATATTTGGCCCAAACTCATCTTGATCAACCAAAAACATGTTTCTGCCTTCTTTATGGGACT
TAAGTTTTTTTTTTCTCCTCTCCATCTCTAGGATGTCGTCTTTGGTGAGATCTCTATTATATCTTGTATGGTTTG
CAAAAGGGCTTCCTAAAAATAAAAAATAAAATTTAAAAAACTGTGAAAAAAAAAAAAAAAAA

FIGURE 16

MASAARLTMMWEEVTCPICLDPFVEPVSIECGHSFCQECISQVGKGGGSVCPVCRQRFLLKNLRPNRQLANMVNN
LKEISQEAREGTQGERCAVHGERLHLFCEKDGKALCWVCAQSRKHRDHAMVPLEEAAQEYQEKLQVALGELRRKQ
ELAEKLEVEIAIKRADWKKTVETQKSRIHAEFVQQKNFLVEEEQRQLQELEKDEREQLRILGEKEAKLAQQSQAL
QELISELDRRCHSSALELLQEVIIVLERSESWNLKDLDITSPELRSVCHVPGLKKMLRTCAVHITLDPDTANPWL
ILSEDRRQVRLGDTQQSIPGNEERFDSYPMVLGAQHFHSGKHYWEVDVTGKEAWDLGVCRDSVRRKGHFLLSSKS
GFWTIWLWNKQKYEAGTYPQTPLHLQVPPCQVGIFLDYEAGMVSFYNITDHGSLIYSFSECAFTGPLRPFFSPGF
NDGGKNTAPLTLCPLNIGSQGSTDY

FIGURE 17

CCTCGGTTCCGCGGCGCACCGGAGGGCAGC**ATG**TCGCGGCGGCGGCACAGCGACGAGAACGACGGTGGGCAGCCT
CACAAAAGGAGAAAGACCTCTGATGCAAATGAAACTGAAGATCATTTGGAATCTTTAATATGTAAAGTAGGAGAA
AAGAGTGCCTGCTCTTTGGAGAGCAACCTAGAAGGCTTGGCTGGTGTTTTGGAAGCTGATCTTCCTAACTACAAG
AGCAAGATCTTAAGGCTTCTTTGTACAGTTGCACGCCTATTACCTGAGAAGCTGACAATTTATACAACATTAGTT
GGACTACTGAATGCCAGGAATTACAATTTTGGTGGAGAATTTGTAGAAGCCATGATTCGTCAACTTAAAGAATCA
TTGAAAGCAAACAATTATAATGAAGCCGTGTATTTGGTCCGTTTTTATCTGATCTTGTGAATTGTCATGTGATT
GCCGCCCCATCAATGGTTGCTATGTTTGAAAATTTTGTAAGCGTAACTCAGGAAGAAGATGTACCTCAGGTGCGA
CGAGATTGGTATGTGTATGCATTTCTGTCATCTTTGCCCTGGGTTGGAAAGGAGTTGTACGAAAAGAAAGATGCA
GAGATGGACCGCATCTTTGCCAACACTGAAAGCTATCTTAAAAGACGCCAAAAGACTCATGTACCCATGTTACAG
GTATGGACTGCTGATAAACCACATCCACAAGAAGAGTATTTAGATTGCCTGTGGGCCCAGATTCAGAAATTGAAA
AAGGATCGCTGGCAGGAACGGCACATCCTAAGACCTTATCTTGCCTTTGACAGCATCCTGTGTGAAGCACTGCAG
CACAATCTGCCTCCTTTTACACCACCTCCTCACACTGAAGATTCAGTGTACCCAATGCCAAGGGTCATCTTCAGA
ATGTTTGATTACACAGATGATCCCGAGGGTCCTGTCATGCCAGGGAGTCATTCAGTGGAAAGATTTGTAATAGAA
GAGAATCTTCACTGCATCATTAAGTCCCACTGGAAGGAAAGGAAGACTTGTGCTGCACAGTTAGTGAGCTATCCA
GGGAAGAACAAGATCCCCTTGAACTACCACATAGTTGAGGTGATCTTTGCAGAGCTGTTTCAACTTCCAGCACCC
CCTCACATTGATGTGATGTACACAACACTCCTCATTGAACTGTGCAAACTTCAACCTGGCTCTCTACCCCAAGTT
CTTGCACAGGCAACTGAAATGCTATACATGCGTTTGGACACAATGAACACTACCTGTGTAGACAGGTTTATTAAT
TGGTTTTCTCATCATCTAAGTAACTTCCAGTTCCGTTGGAGCTGGGAAGATTGGTCAGATTGTCTTAGTCAAGAT
CCTGAAAGTCCCAAACCGAAGTTTGTAAGAGAAGTTCTAGAAAAATGTATGAGGTTGTCTTACCATCAGCGTATA
TTAGATATTGTTCCTCCTACCTTCTCAGCTCTGTGTCCTGCAAACCCAACCTGCATTTACAAGTATGGAGATGAA
AGTAGCAATTCTCTTCCTGGACATTCTGTTGCCCTCTGTTTAGCTGTTGCCTTTAAAAGTAAGGCAACCAATGAT
GAAATCTTCAGCATTCTGAAAGATGTACCAAATCCTAACCAGGATGATGACGACGATGAAGGATTCAGTTTTAAC
CCATTGAAAATAGAAGTCTTTGTACAGACTCTGCTACACTTGGCAGCCAAATCATTCAGCCACTCCTTCAGTGCT
CTTGCAAAGTTTCATGAAGTCTTCAAAACCCTAGCTGAAAGTGATGAAGGAAAGTTACATGTGCTAAGAGTTATG
TTTGAGGTCTGGAGGAACCATCCACAGATGATTGCTGTACTAGTGGATAAGATGATTCGTACACAAATAGTTGAT
TGTGCTGCCGTAGCAAATTGGATCTTCTCTTCAGAACTATCTCGTGACTTTACCAGATTGTTTGTTTGGGAAATT
TTGCACTCTACAATTCGTAAGATGAACAAACATGTCCTGAAGATCCAGAAAGAGCTGGAAGAAGCTAAAGAGAAA
CTTGCTAGGCAACACAAACGGCGAAGTGATGATGACGACAGAAGCAGTGACAGGAAAGACGGGGTTCTTGAGGAA
CAAATAGAACGACTTCAGGAAAAAGTGGAATCTGCTCAGAGTGAACAAAAGAATCTTTTCCTCGTTATATTTCAG
CGGTTTATCATGATCTTGACCGAGCACCTAGTACGATGCGAAACTGATGGGACCAGTGTATTAACACCATGGTAT
AAGAACTGTATAGAGAGGCTGCAGCAGATCTTCCTACAGCATCACCAAATAATCCAGCAGTACATGGTGACCCTG
GAGAACCTTCTCTTCACTGCTGAATTAGACCCTCATATCTTGGCCGTGTTCCAGCAGTTCTGTGCCCTGCAGGCC
TAAGGGTCATTTTTTCCTCATGTCAAGGTTTTTTTGATATCTTAAAATAATTTGTCTTATTTTTTGATGGTTTG
AATGCTTGCTTTCTTGTAGTATCCTTTCACTTCTTAAAGGAAACAAAGGGGAAGAGGACAGTGAATGAACATGGC
ATTACTTTTAATTGCCCTGAAAAGCAAATACTTCCTAACGGCAGTAATGTGACTATGACCATGATATATTATATA
TGTGACAGATACAAATTCTCTGTGATCAGTTTGTTATTTTTTTTCTCCTTAAGGCAACAAAATAATTGGTTTGAG
GTATGTGAAACACTAGAGGTCAACCTTACATAGTATATAGAACTGATGGGTTTACCCAGCTACCCAGTAGCATAA
CTTTTCACAGCTCGGGGATGAATTAACATGGCTGAAATAAAACTAAAAGTATG

FIGURE 18

MSRRRHSDENDGGQPHKRRKTSDANETEDHLESLICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTV
ARLLPEKLTIYTTLVGLLNARNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVAMFE
NFVSVTQEEDVPQVRRDWYVYAFLSSLPWVGKELYEKKDAEMDRIFANTESYLKRRQKTHVPMLQVWTADKPHPQ
EEYLDCLWAQIQKLKKDRWQERHILRPYLAFDSILCEALQHNLPPFTPPPHTEDSVYPMPRVIFRMFDYTDDPEG
PVMPGSHSVERFVIEENLHCIIKSHWKERKTCAAQLVSYPGKNKIPLNYHIVEVIFAELFQLPAPPHIDVMYTTL
LIELCKLQPGSLPQVLAQATEMLYMRLDTMNTTCVDRFINWFSHHLSNFQFRWSWEDWSDCLSQDPESPKPKFVR
EVLEKCMRLSYHQRILDIVPPTFSALCPANPTCIYKYGDESSNSLPGHSVALCLAVAFKSKATNDEIFSILKDVP
NPNQDDDDDEGFSFNPLKIEVFVQTLLHLAAKSFSHSFSALAKFHEVFKTLAESDEGKLHVLRVMFEVWRNHPQM
IAVLVDKMIRTQIVDCAAVANWIFSSELSRDFTRLFVWEILHSTIRKMNKHVLKIQKELEEAKEKLARQHKRRSD
DDDRSSDRKDGVLEEQIERLQEKVESAQSEQKNLFLVIFQRFIMILTEHLVRCETDGTSVLTPWYKNCIERLQQI
FLQHHQIIQQYMVTLENLLFTAELDPHILAVFQQFCALQA

FIGURE 19

CACACCCTGACAAGCTGCCAGGCAGGTTCTCTTCCTCTCACATACTGACCCACGGCTCCACCCTCTCTCCCCTGG
AAAGGACACC**<u>ATG</u>**AGCACTGAAAGCATGATCCGGGACGTGGAGCTGGCCGAGGAGGCGCTCCCCAAGAAGACAGG
GGGGCCCCAGGGCTCCAGGCGGTGCTTGTTCCTCAGCCTCTTCTCCTTCCTGATCGTGGCAGGCGCCACCACGCT
CTTCTGCCTGCTGCACTTTGGAGTGATCGGCCCCCAGAGGGAAGAGTCCCCCAGGGACCTCTCTCTAATCAGCCC
TCTGGCCCAGGCAGTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCTCA
AGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAA
CCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTC
CACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGC
CATCAAGAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTGGG
AGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGA
GTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG**<u>TGA</u>**GGAGGACGAACATCCAACCTTCCCAAACGCCTCCCCTG
CCCCAATCCCTTTATTACCCCCTCCTTCAGACACCCTCAACCTCTTCTGGCTCAAAAAGAGAATTGGGGGCTTAG
GGTCGGAACCCAAGCTTAGAACTTTAAGCAACAAGACCACCACTTCGAAACCTGGGATTCAGGAATGTGTGGCCT
GCACAGTGAAGTGCTGGCAACCACTAAGAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGAT
CCCTGACATCTGGAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGCAGGACTTGAGAAGACCTCA
CCTAGAAATTGACACAAGTGGACCTTAGGCCTTCCTCTCTCCAGATGTTTCCAGACTTCCTTGAGACACGGAGCC
CAGCCCTCCCCATGGAGCCAGCTCCCTCTATTTATGTTTGCACTTGTGATTATTTATTATTTATTTATTATTTAT
TTATTTACAGATGAATGTATTTATTTGGGAGACCGGGGTATCCTGGGGGACCCAATGTAGGAGCTGCCTTGGCTC
AGACATGTTTTCCGTGAAAACGGAGGCTGAACAATAGGCTGTTCCCATGTAGCCCCCTGGCCTCTGTGCCTTCTT
TTGATTATGTTTTTTAAAATATTATCTGATTAAGTTGTCTAAACAATGCTGATTTGGTGACCAACTGTCACTCAT
TGCTGAGGCCTCTGCTCCCCAGGGAGTTGTGTCTGTAATCGGCCTACTATTCAGTGGCGAGAAATAAAGGTTGCT
TAGGAAAGAA

FIGURE 20

MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQREESPRDLSLISPLAQ
AVRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHV
LLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQ
VYFGIIAL

FIGURE 21

GGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCCGAAGGAC
TGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCGGAGCCCACAGAGCAGGGCACCG
GC**ATG**GCCAAAGCCGCGGCGATCGGCATCGACCTGGGCACCACCTACTCCTGCGTGGGGGTGTTCCAACACGGCA
AGGTGGAGATCATCGCCAACGACCAGGGCAACCGCACCACCCCCAGCTACGTGGCCTTCACGGACACCGAGCGGC
TCATCGGGGATGCGGCCAAGAACCAGGTGGCGCTGAACCCGCAGAACACCGTGTTTGACGCGAAGCGGCTGATCG
GCCGCAAGTTCGGCGACCCGGTGGTGCAGTCGGACATGAAGCACTGGCCTTTCCAGGTGATCAACGACGGAGACA
AGCCCAAGGTGCAGGTGAGCTACAAGGGGGAGACCAAGGCATTCTACCCCGAGGAGATCTCGTCCATGGTGCTGA
CCAAGATGAAGGAGATCGCCGAGGCGTACCTGGGCTACCCGGTGACCAACGCGGTGATCACCGTGCCGGCCTACT
TCAACGACTCGCAGCGCCAGGCCACCAAGGATGCGGGTGTGATCGCGGGGCTCAACGTGCTGCGGATCATCAACG
AGCCCACGGCCGCCGCCATCGCCTACGGCCTGGACAGAACGGGCAAGGGGGAGCGCAACGTGCTCATCTTTGACC
TGGGCGGGGGCACCTTCGACGTGTCCATCCTGACGATCGACGACGGCATCTTCGAGGTGAAGGCCACGGCCGGGG
ACACCCACCTGGGTGGGGAGGACTTTGACAACAGGCTGGTGAACCACTTCGTGGAGGAGTTCAAGAGAAAACACA
AGAAGGACATCAGCCAGAACAAGCGAGCCGTGAGGCGGCTGCGCACCGCCTGCGAGAGGGCCAAGAGGACCCTGT
CGTCCAGCACCCAGGCCAGCCTGGAGATCGACTCCCTGTTTGAGGGCATCGACTTCTACACGTCCATCACCAGGG
CGAGGTTCGAGGAGCTGTGCTCCGACCTGTTCCGAAGCACCCTGGAGCCCGTGGAGAAGGCTCTGCGCGACGCCA
AGCTGGACAAGGCCCAGATTCACGACCTGGTCCTGGTCGGGGGCTCCACCCGCATCCCCAAGGTGCAGAAGCTGC
TGCAGGACTTCTTCAACGGGCGCGACCTGAACAAGAGCATCAACCCCGACGAGGCTGTGGCCTACGGGGCGGCGG
TGCAGGCGGCCATCCTGATGGGGGACAAGTCCGAGAACGTGCAGGACCTGCTGCTGCTGGACGTGGCTCCCCTGT
CGCTGGGGCTGGAGACGGCCGGAGGCGTGATGACTGCCCTGATCAAGCGCAACTCCACCATCCCCACCAAGCAGA
CGCAGATCTTCACCACCTACTCCGACAACCAACCCGGGGTGCTGATCCAGGTGTACGAGGGCGAGAGGGCCATGA
CGAAAGACAACAATCTGTTGGGGCGCTTCGAGCTGAGCGGCATCCCTCCGGCCCCCAGGGGCGTGCCCCAGATCG
AGGTGACCTTCGACATCGATGCCAACGGCATCCTGAACGTCACGGCCACGGACAAGAGCACCGGCAAGGCCAGCA
AGATCACCATCACCAACGACAAGGGCCGCCTGAGCAAGGAGGAGATCGAGCGCATGGTGCAGGAGGCGGAGAAGT
ACAAAGCGGAGGACGAGGTGCAGCGCGAGAGGGTGTCAGCCAAGAACGCCCTGGAGTCCTACGCCTTCAACATGA
AGAGCGCCGTGGAGGATGAGGGGCTCAAGGGCAAGATCAGCGAGGCGGACAAGAAGAAGGTTCTGGACAAGTGTC
AAGAGGTCATCTCGTGGCTGGACGCCAACACCTTGGCCGAGAAGGACGAGTTTGAGCACAAGAGGAAGGAGCTGG
AGCAGGTGTGTAACCCCATCATCAGCGGACTGTACCAGGGTGCCGGTGGTCCCGGGCCTGGGGGCTTCGGGGCTC
AGGGTCCCAAGGGAGGGTCTGGGTCAGGCCCTACCATTGAGGAGGTGGAT**TAG**GGGCCTTTGTTCTTTAGTATGT
TTGTCTTTGAGGTGGACTGTTGGGACTCAAGGACTTTGCTGCTGTTTTCCTATGTCATTTCTGCTTCAGCTCTTT
GCTGCTTCACTTCTTTGTAAAGTTAAGTTGTAACCTGATGGTAATTAGCTGGCTTCATTATTTTTGTAGTACAAC
CGATATGTTCATTAGAATTCTTTGCATTTAATGTTGATACTGTAAGGGTGTTTCGTTCCCTTTAAATGAATCAAC
ACTGCCACCTTCTGTACGAGTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTGGCGAAAACACTACAAAGGC
TGGGAATGTATGTTTTTATAATTTGTTTATTTAAATATGAAAAATAAAATGTTAAACTTT

FIGURE 22

MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKRLIG
RKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYF
NDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGD
THLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAV
QAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMT
KDNNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKASKITITNDKGRLSKEEIERMVQEAEKY
KAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD

FIGURE 23

GTTCGGTGGCCCATAGGGGAAGATGGCGGCTGCTCCTTTGGAGGAGCGGGATTGAGAGGATCGGGGTGGGGAGAC
CAAACAAGAGAGACATTTCTGGCTCTGAAGGCGAACGCTTCGCTGGCCATTTAGGAGCTCTGCTCAAAGCCAGAC
GTATCCTAGAAGGAAAACATCACC**ATG**GCTACAGAAATTGGTTCTCCTCCTCGTTTTTCCATATGCCAAGGTTC
CAGCACCAGGCACCTCGACAGCTGTTTTATAAGCGACCTGATTTTGCACAACAGCAAGCAATGCAACAGCTTACT
TTTGATGGAAAACGAATGAGAAAAGCTGTGAACCGAAAAACCATAGACTACAATCCATCTGTAATTAAGTATTTG
GAGAACAGAATATGGCAAAGAGACCAGAGAGATATGCGGGCAATTCAGCCTGATGCAGGTTATTACAATGATCTG
GTCCCACCTATAGGAATGTTGAATAATCCTATGAATGCAGTAACAACAAAATTTGTTCGGACATCAACAAATAAA
GTAAAGTGTCCTGTATTTGTTGTTAGGTGGACTCCAGAAGGAAGACGCTTGGTCACTGGAGCTTCTAGTGGGGAG
TTTACCCTGTGGAATGGACTCACTTTCAATTTTGAAACAATATTACAGGCTCACGACAGCCCAGTGAGGGCCATG
ACGTGGTCACATAATGACATGTGGATGTTGACAGCAGACCACGGAGGATATGTGAAATATTGGCAGTCGAACATG
AACAACGTCAAGATGTTCCAGGCACATAAGGAGGCGATTAGAGAGGCCAGGTTTATACACAATATACCATTTTCT
GTAGTCCCTATTGTCATGGTTAAATTATTCTCTAAGTGTATTCTGGGTGCAGAGATGCATGGGCTCTGTCAGTTT
CTGGGAAACTTTCTGCACCCTATAAACACAATATTTTTCTTTGTTTTCACACATTCACCATTTTGCTGGCACCTT
TCTGAAGTAGTGTTGTCCCGGTATCAGCCTTTGCAATATGTTAGAGATGTACTGTCTGCCGCATTTTGCACTGGT
TTTCTCTTTTCATTTATGATTAATAATGTGTATACGTTATTCCTTTTTATTATCTACTGTGTAAGACAAGAATAT
TTCATTCCAAATAAAGAATTCAGTCTT**TAA**TTATGCAACTGAATAAAATCTAAAGCCTACAGAAAACAACTTCAG
AATTCACACAAAGTGGAAAAAGGCTTAAGTGAAGACCTGGTTGGCTTGGTTATGCCACGACTTCCAAAGGAAAGT
ATAGGACTAAAACCCTCACAGATAACTGGATGTGGCAAACATTAACGGAGTAATGAATGGGTTCTTCAAGCTTTG
CAGCTGTAAGCAGATCATTGTCAAGAAGACTCTAGGACTTTTCTTCTGATTCACTGTTGATAACATCACTTATGC
AAATGTATACAATAAGTGGAGTTTAAAATATTTTCAGTGAGTTGTATATTTTTACACATCAGTGAGGTATGTATA
GTAAAACTGGGGGAAAAAGTTCCAAATACAAGCCTGAAGAATTGCTGCAGCCTCAGAATAAAGCTAAGCAGCATT
CTTTAAGGTTGTGCCACCCATGTGTGGGAGGAGGTTGACATCTTTATGGAAACATCATCCACTGTAGTCATTTGT
TCATACTTTCAGAATCTTAACAGAAATTGTTGGATGAACATGCTTCTGCTTTGTAGATTTTGCCTTAGTGTCATG
CCCATACATTGAGTTTACACAGCTGGTCCTTCATAGGATTCCAAAGTTCAAGGGAGTTTTTAGAGTTAGTTGAGA
AACTTGATGATCTTTCACTGCTGGGAAAAACTGACTCCTTCTTGCAGCAGATTCTTTGGCTTTACACACAAGTCT
GAATGTCCTTATTTTAAAGTTTTCCTCAAAGGTGCAACATTCATGGAATAGCTTGCCAGGAAGATGTGAAACTTT
TCTACAGACCTTTGAAATGGATGAGAAACATTGTATGTAGGGATGTTTAGCAATCAGTCTTTTAATAGACAGCCC
ACATTGTTTCAGCTTATTTCATGAAGTGTCTGAGGCAGAAGCTGATGATAATTTTGGGAGCAGTATTCGTGTGTG
ATTTAAAAGACTGCAGGAATACTGCAAAAATAGAATCCATTTATTTCACCACTTAAGGCAGCTTCATGTGATTT
CCTCGTATCATAGAAAATAGAGAAGGAACATGGATAGCATTAGCACTAATAATACACACTTGAAGTTCTCAGAAT
ACTGATGATTGAAAACTCAAACAACTGCTCTGTTGAAGTCTTCTTTTGATGAGATGCCTATGTTAGCTGACGACA
TTCACTTTAAGGGCTTCTTCACTGGATTCTTCCCTCTCCTGTTTATAATGCAGCACAGTGTTTTTATTTTTCCCT
GTCTGAGAAGCACAGATTATCTGTTAAATGCTGACTTCTTTCCCCTGCTGTGTGTCTTCATGTAACAGTTTCTCA
CCCACGGATAATAAATTTGCTACATGCTCTG

FIGURE 24

MATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQQLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRD
QRDMRAIQPDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRWTPEGRRLVTGASSGEFTLWNGLT
FNFETILQAHDSPVRAMTWSHNDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIPFSVVPIVMVK
LFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFTHSPFCWHLSEVVLSRYQPLQYVRDVLSAAFCTGFLFSFMIN
NVYTLFLFIIYCVRQEYFIPNKEFSL

FIGURE 25

CGGTGCCTGGTGCGGGAGCTACGGGGCCCAGGGATTGTGTTTAAAGTAGTGCTTCTACCAAC**ATG**TCCCGTGGTT
CCAGCGCCGGTTTTGACCGCCACATTACCATTTTTTCACCCGAGGGTCGGCTCTACCAAGTAGAATATGCTTTTA
AGGCTATTAACCAGGGTGGCCTTACATCAGTAGCTGTCAGAGGGAAAGACTGTGCAGTAATTGTCACACAGAAGA
AAGTACCTGACAAATTATTGGATTCCAGCACAGTGACTCACTTATTCAAGATAACTGAAAACATTGGTTGTGTGA
TGACCGGAATGACAGCTGACAGCAGATCCCAGGTACAGAGGGCACGCTATGAGGCAGCTAACTGGAAATACAAGT
ATGGCTATGAGATTCCTGTGGACATGCTGTGTAAAAGAATTGCCGATATTTCTCAGGTCTACACACAGAATGCTG
AAATGAGGCCTCTTGGTTGTTGTATGATTTTAATTGGTATAGATGAAGAGCAAGGCCCTCAGGTATATAAGTGTG
ATCCTGCAGGTTACTACTGTGGGTTTAAAGCCACTGCAGCGGGAGTTAAACAAACTGAGTCAACCAGCTTCCTTG
AAAAAAAAGTGAAGAAGAAATTTGATTGGACATTTGAACAGACAGTGGAAACTGCAATTACATGCCTGTCTACTG
TTCTATCAATTGATTTCAAACCTTCAGAAATAGAAGTTGGAGTAGTGACAGTTGAAAATCCTAAATTCAGGATTC
TTACAGAAGCAGAGATTGATGCTCACCTTGTTGCTCTAGCAGAGAGAGAC**TAA**ACATTGTCGTTAGTTTACCAGA
TCCGTGATGCCACTTACCTGTGTGTTTGGTAACAACAAACAAACATCATGGAGGTCCCTGGATTGAAAAAGGAGC
CTCTCCCACTCCTCCTACCACCGAAGTGGTTAGGACTCTATATAAATAAAAACAAGGCTTTTGGAAAAAAAAAAA
AAAA

FIGURE 26

MSRGSSAGFDRHITIFSPEGRLYQVEYAFKAINQGGLTSVAVRGKDCAVIVTQKKVPDKLLDSSTVTHLFKITEN
IGCVMTGMTADSRSQVQRARYEAANWKYKYGYEIPVDMLCKRIADISQVYTQNAEMRPLGCCMILIGIDEEQGPQ
VYKCDPAGYYCGFKATAAGVKQTESTSFLEKKVKKKFDWTFEQTVETAITCLSTVLSIDFKPSEIEVGVVTVENP
KFRILTEAEIDAHLVALAERD

FIGURE 27

CAGGGGCGTGCAGCCCGCTTGCCAATCAGAGCGCGGCTGAGCGGCCCCGCAGCCAACCCCCGAGGAGCGGCCGGC
TGGCGTCCGCCGCGCCCAGGAGTTGGGG**ATG**TCCTACAAACCCATCGCCCCTGCTCCCAGCAGCACCCCTGGCTC
CAGCACCCCTGGGCCGGGCACCCCGGTCCCTACAGGAAGCGTCCCGTCGCCGTCGGGCTCAGTGCCAGGAGCCGG
CGCTCCTTTCAGACCGCTGTTTAACGACTTTGGACCGCCTTCCATGGGCTACGTGCAGGCGATGAAGCCACCCGG
CGCCCAGGGCTCCCAGAGCACCTACACGGACCTGCTGTCAGTCATAGAGGAGATGGGCAAAGAGATCCGGCCTAC
CTATGCTGGCAGCAAGAGCGCCATGGAGCGCCTGAAGAGAGGTATCATCCATGCCCGGGCCCTAGTCAGAGAGTG
CCTGGCAGAGACAGAGCGGAACGCCCGCACG**TAA**CAGGAAGCGCCTCGGCCTCAGCGTCTGGACCTATCCGGCCA
CTGCAGAGCACCCGCTTCTCCCTGGCCTTCATCCCGAGTTGCACTAACCATCCTGGGCTTCCTGTCCTGTGTCCC
TTGGTGGGTCCCCTCCAGGAACCAAGGAGTGGCCCTCCAGGTGGCAGCACTAAGGACACCCCCCCACAACAAGAG
TTAGCAGCGAGGTCCCCATGAGTCCCACCCATGACCTGCCGACAGTGTTGCCCACCGGAACTTTTGTGGCCCCTA
CCGCTCAGCCCTTCCCAGCACTTCTCCCACTTTGTCCCGAGCCTCCTTCTCGCCCAGCAGGGGCACAGGCCTGGC
ACCTCCCTGCCTTGTGTCCTGAGCCATAGTGACTCTTTTATCTGTGTGTCTTTTGCTAAATATGCCCTTTTTATA
TTAATAAAAGATGATTTGGAGTTGTGCTCTC

FIGURE 28

MSYKPIAPAPSSTPGSSTPGPGTPVPTGSVPSPSGSVPGAGAPFRPLFNDFGPPSMGYVQAMKPPGAQGSQSTYT
DLLSVIEEMGKEIRPTYAGSKSAMERLKRGIIHARALVRECLAETERNART

FIGURE 29

GCGCCTTTGTCCTACGGCGGGCAGGTGGGCCGACGCGGAGGCGGCAGCGGCGGGCCTGAGGCGAAGGAGCGGCCG
GGAGCCCGCCGCGCTGGTAGCGATATTAATAAGGCAGCGGAAAGAAGAAATATGAATACGGCTCCATCAAGACCC
AGCCCCACACGAAGGGATCCATATGGCTTTGGAGACAGTCGAGATTCAAGGCGTGATCGATCCCCAATTCGAGGA
AGTCCAAGGAGAGAGCCCAGGGATGGCAGAAATGGCCGGGATGCCCGGGACAGCAGAGACATTCGAGACCCCCGA
GACTTGCGGGACCACAGACATAGTAGAGATTTGCGGGATCACAGAGACAGCAGGAGTGTGCGCGACGTTCGGGAC
GTGAGGGATCTTAGAGACTTTCGTGATCTAAGAGACTCTAGGGATTTTCGAGATCAGCGAGACCCCATGTACGAC
AGATACAGAGACATGAGAGACTCCCGAGATCCTATGTACAGGAGAGAAGGCTCTTATGACCGATACCTACGAATG
GATGACTATTGCAGGAGAAAGGATGACTCTTATTTTGACCGTTACAGAGATAGCTTTGATGGACGGGGCCCTCCA
GGCCCAGAAAGTCAGTCTCGTGCAAAAGAGCGTTTGAAACGTGAGGAACGGCGTAGAGAAGAGCTTTATCGTCAA
TATTTTGAGGAAATCCAGAGACGCTTTGATGCCGAAAGGCCCGTTGATTGTTCTGTGATTGTGGTCAACAAACAG
ACAAAAGACTATGCTGAGTCTGTGGGGCGGAAGGTGCGAGACCTGGGCATGGTAGTGGACTTGATCTTCCTTAAC
ACAGAAGTGTCACTGTCACAAGCCTTGGAGGATGTTAGCAGGGGAGGTTCTCCTTTTGCTATTGTCATCACCCAG
CAACACCAGATTCACCGCTCCTGCACAGTCAACATCATGTTTGGAACCCCGCAAGAGCATCGCAACATGCCCCAA
GCAGATGCCATGGTGCTGGTGGCCAGAAATTATGAGCGTTACAAGAATGAGTGCCGGGAGAAGGAACGTGAGGAG
ATTGCCAGACAGGCAGCCAAGATGGCCGATGAAGCCATCCTGCAGGAAAGAGAGAGAGGAGGCCCTGAGGAGGGA
GTGCGTGGGGGCCACCCTCCAGCCATCCAGAGCCTCATCAACCTGCTGGCAGACAACAGGTACCTCACTGCTGAA
GAGACTGACAAGATCATCAACTACCTGCGAGAGCGGAAGGAGCGGCTGATGAGGAGCAGCACCGACTCTCTGCCT
GGCCCGATTTCCCGCCAACCACTCGGGGCGACCTCGGGTGCCTCGCTGAAGACACAGCCAAGCTCCCAACCGCTC
CAGAGCGGCCAAGTGCTCCCCTCTGCTACACCCACTCCATCTGCACCCCCCACCTCCCAGCAAGAGCTTCAGGCC
AAAATCCTCAGCCTCTTCAATAGTGGCACAGTGACGGCCAATAGCAGCTCTGCATCCCCCTCGGTTGCTGCCGGA
AACACCCCAAACCAGAATTTTTCCACAGCAGCAAACAGCCAGCCTCAACAAAGATCACAGGCTTCTGGCAATCAG
CCTCCAAGCATTTTGGGACAGGGAGGATCTGCTCAGAACATGGGCCCCAGACCTGGGGCTCCTTCCCAAGGGCTT
TTTGGCCAGCCTTCCAGTCGCCTGGCACCTGCTAGCAACATGACTAGCCAGAGGCCTGTGTCTTCCACAGGTATC
AACTTTGACAATCCAAGTGTACAGAAGGCTCTGGATACCCTGATCCAGAGTGGCCCTGCTCTCTCCCACCTGGTT
AGCCAGACCACAGCACAGATGGGGCAGCCACAGGCCCCCATGGGATCTTACCAGAGGCATTACTGAAGCTAAATC
TTTCAACTCTCCCCAGTCCCCTCTCCCCTGGCCTCCTCCCACTTACTTGTTCTAAATAGAGCTGTTTGAGATGTT
CTCTGCGCTCCCAGGCCGGCATCGAGTGTCATCAATTTCTACCACCTGCTCTCTCTTCTGCCCAAGGCTGTGTTG
CTTATTCCTTACAAAGTTTATACTGCATTTGGGGCTGTATCTTTTTTTGTTTTGTTTTTTTTTTTTCCTCTTTG
GAACTCTTGTGTTGTTAATAAAATGAAATGATTACTTTTTAATTAAAATGTCGAC

FIGURE 30

APLSYGGQVGRRGGGSGGPEAKERPGARRAGSDINKAAERRNMNTAPSRPSPTRRDPYGFGDSRDSRRDRSPIRG
SPRREPRDGRNGRDARDSRDIRDPRDLRDHRHSRDLRDHRDSRSVRDVRDVRDLRDFRDLRDSRDFRDQRDPMYD
RYRDMRDSRDPMYRREGSYDRYLRMDDYCRRKDDSYFDRYRDSFDGRGPPGPESQSRAKERLKREERRREELYRQ
YFEEIQRRFDAERPVDCSVIVVNKQTKDYAESVGRKVRDLGMVVDLIFLNTEVSLSQALEDVSRGGSPFAIVITQ
QHQIHRSCTVNIMFGTPQEHRNMPQADAMVLVARNYERYKNECREKEREEIARQAAKMADEAILQERERGGPEEG
VRGGHPPAIQSLINLLADNRYLTAEETDKIINYLRERKERLMRSSTDSLPGPISRQPLGATSGASLKTQPSSQPL
QSGQVLPSATPTPSAPPTSQQELQAKILSLFNSGTVTANSSSASPSVAAGNTPNQNFSTAANSQPQQRSQASGNQ
PPSILGQGGSAQNMGPRPGAPSQGLFGQPSSRLAPASNMTSQRPVSSTGINFDNPSVQKALDTLIQSGPALSHLV
SQTTAQMGQPQAPMGSYQRHY

FIGURE 31

AACAATAGGAAACGTCAAAATTGGGATAGTCGGCAGTTCTGGCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGG
GTCGTAGTGCTGTTTCTGGTATTCTCATCGCGGTCACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTC
TCCATGGCCTGGGCACCAGTTCCCGGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCCAGAGGCCAATTCG
TCGCGGCGGCGGTGGAGATCGCAGGTCGCTCAGGCTTGCAG**ATG**GGTCAAGGGTTGTGGAGAGTGGTCAGAAACC
AGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCAGAGAGCAGAGCAGGAGAATGGCTGCGAGCA
ACATTTCTAACACCAATCATCGTAAACAAGTCCAAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAAT
CGAAAGAACAGGAAGGATTCATTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGTCCTACCTGA
ATGCAACTGACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACTTCTCTGGCAAGGGTTGT
GCAAATCCACTTGGGGTCACTGGTCCATATACAATAAGAACCCACCTTTAGGATTTTCTTTTAGAAAAGTGTATA
TGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCCAGATGAGGGAGTGAACTACTTTATGTCCAAGGGTA
TCCTGGATGATTCGCCAAAGGAAATAGCAAAGTTTATCTTCTGTACAAGAACACTAAATTGGAAAAAACTGAGAA
TCTATCTTGATGAAAGGAGAGATGTCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAA
ATGCACTGAGAGAATTTTTTCGTCATATCCATGCCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTGATGCTGTCTATG
TACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATGTGAAGAATAAAATGTCAAAAAGGG
AATTTATTCGAAATACCCGTCGCGCTGCTCAAAATATTAGTGAAGATTTTGTAGGGCATCTTTATGACAATATCT
ACCTTATTGGCCATGTGGCTGCA**TAA**AAAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCC
AAGGACTTAGCAGATATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGC
AACCTTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCCTTGGGGAACTAAATAATTTTGCAGAATTTTTCCT
AATTTTGTTTATCACGTTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTTAACGAATGATAAACTGACATT
ATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGAAAAACTTTATCCATTTCCATTCTTTATACAAAT
ACCATGTAATGTGTACATATTTAACTAAAGAGATTTATAGTCATAATTATTTTATTGTAAAGATTTTAACTAAAG
TTTTTCCTTTTCTCTCAAACTGAGTTCTGAAATTTATTTGATTCTGATCTGAAACTATTGTCTTCGTAAAAGTTA
GATCTGACTTCAGACAGAAACCAATACCAGCTTCCTTTTCCTTTAAACTTTGAAGAGTGTTGATTTGTTACTATA
TTACTATGCAAAACTGGCAGTTATTTTTATAATATAAATTTATAATTTGATTTTTTATTTTAAAAACTGGGTTAA
TCAAGTCTCGGTAAGTCCTTTAAACCATTTAGGATTTTTAAAACATCAAAATTTATGATTTACATTCATAGGAAT
AAAATAAAATATTATTAGAACTCTGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 32

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMAASNISNTNHRKQVQGGIDIYHLLKARKSKEQEGFINLEMLP
PELSFTILSYLNATDLCLASCVWQDLANDELLWQGLCKSTWGHWSIYNKNPPLGFSFRKVYMQLDEGSLTFNANP
DEGVNYFMSKGILDDSPKEIAKFIFCTRTLNWKKLRIYLDERRDVLDDLVTLHNFRNQFLPNALREFFRHIHAPE
ERGEYLETLITKFSHRFCACNPDLMRELGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNIS
EDFVGHLYDNIYLIGHVAA

FIGURE 33

AGCAGCTCCAACCAGGGCAGCCTTCCTGAGAAG**ATG**CAACCAATCCTGCTTCTGCTGGCCTTCCTCCTGCTGCCC
AGGGCAGATGCAGGGGAGATCATCGGGGGACATGAGGCCAAGCCCCACTCCCGCCCCTACATGGCTTATCTTATG
ATCTGGGATCAGAAGTCTCTGAAGAGGTGCGGTGGCTTCCTGATACAAGACGACTTCGTGCTGACAGCTGCTCAC
TGTTGGGGAAGCTCCATAAATGTCACCTTGGGGGCCCACAATATCAAAGAACAGGAGCCGACCCAGCAGTTTATC
CCTGTGAAAAGACCCATCCCCCATCCAGCCTATAATCCTAAGAACTTCTCCAACGACATCATGCTACTGCAGCTG
GAGAGAAAGGCCAAGCGGACCAGAGCTGTGCAGCCCCTCAGGCTACCTAGCAACAAGGCCCAGGTGAAGCCAGGG
CAGACATGCAGTGTGGCCGGCTGGGGGCAGACGGCCCCCCTGGGAAAACACTCACACACACTACAAGAGGTGAAG
ATGACAGTGCAGGAAGATCGAAAGTGCGAATCTGACTTACGCCATTATTACGACAGTACCATTGAGTTGTGCGTG
GGGGACCCAGAGATTAAAAAGACTTCCTTTAAGGGGGACTCTGGAGGCCCTCTTGTGTGTAACAAGGTGGCCCAG
GGCATTGTCTCCTATGGACGAAACAATGGCATGCCTCCACGAGCCTGCACCAAAGTCTCAAGCTTTGTACACTGG
ATAAAGAAAACCATGAAACGCTAC**TAA**CTACAGGAAGCAAACTAAGCCCCCGCTGTAATGAAACACCTTCTCTGG
AGCCAAGTCCAGATTTACACTGGGAGAGGTGCCAGCAACTGAATAAATACCTCTCCCAGTGTAAATCTGGAGCCA
AGTCCAGATTTACACTGGGAGAGGTGCCAGCAACTGAATAAATACCTCTTAGCTGAGTGG

FIGURE 34

MQPILLLLAFLLLPRADAGEIIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIQDDFVLTAAHCWGSSINVTLG
AHNIKEQEPTQQFIPVKRPIPHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCSVAGWGQT
APLGKHSHTLQEVKMTVQEDRKCESDLRHYYDSTIELCVGDPEIKKTSFKGDSGGPLVCNKVAQGIVSYGRNNGM
PPRACTKVSSFVHWIKKTMKRY

FIGURE 35A

ATTTCCATCAACCATGATGAAAGTCTGCTGCCTGAGTCCTTAGAGAGCATGATGTATGGTAAGAAGGTGCTCAGC
CAAGAACCAAGCTCTTTTCAGGAGAGCCCAAGTACCAATACTGAATCTAGAAAAGATGTTATTACCATCTCAATA
AGCAAAGATGGGAACTGCCAGTCTGGTGGCCCTGAGGCAGAAATAGCTTCTGGCCCTACTTTTATGGGTAGCTTA
GAAGCAGGAGGAGTAGCTCAAGCAAACATCAAAAATGGAAAACATTTGTTGATGTCTATTTCAAAGGAAGGGGAG
CTCTGCTGCAGTGAGGCAGGACAGAGACCTGAAAACATTGGCCAGCTGGAAGCCAAGTGTTTAGCTTCCCCTTCC
TTGAATCCAGGAAATGAAAGTGGGTTTGTAGATATGTGCAGTCTTAGTGTCTGTGACTCCAAAAGAAACCTGTCA
TCAGATCAGCAATTAATTGATTTATTGGAAAACAAAAGCTTAGAAAGTAAATTGATTTTGAGTCAGAACCACAGT
GATGAGGAGGAAGAAGAGGAGGAAAACGAGGAGGAAAACTTAGCCATGGCAGTAGGCATGGGGGAAAGGCCAGAG
GTATTGCATCTCACGGAGCCCACTACTAACATCTCAAGGGAAAAGAACCAAGGCTTCCAAGATGAAACCAAGAAA
GGAAGCTTAGAGGTGGCAAACCAGACTCCTGGGCTACAGAGGGCTTTCCCCGCTCCAGCAGCCTGTCAGTGCCAC
TGCAAACACATGGAGAGGTGGATGCATGGCCTCGAGAATGATGAATTTGAAATCGAGAAACCCAAGGCTTATATC
CCAGATCTGTTCAAAAGTAAAACCAATACTATCGCCATGGAGGGTGAACCCACTGCTATTCCATCACAGCCGTTT
AAAGTGAAGCATGAGCTTTTAAAAGAACCTTGGAAAGAAAGTGCAGAGGGGCAAAACGTTTTCCCCACATATCCT
CTTGAAGGAAGTGAGCTCAAATCAGAAGACATGGATTTTGAGAATAAAGATGATTATGATAGAGACGGAAACTGC
CATAGTCAAGATTATCCAGGGAAGTACTCTGAAGAGGAGAGCAAGAGCTCAACATCGGGCATCACAGGAGACATT
GGGGATGAGCTACAGGAGGCTCGAGCTCCCACTATTGCTCAGCTGCTACAGGAGAAAACTCTCTATTCCTTCTCT
GAGTGGCCAAAGGACCGCGTGATAATTAACCGCCTAGATAATATCTGCCACGTGGTGTTAAAGGGGAAGTGGCCC
TCTAGCCAGCAGTATGAGCCCTCAGGCACACTGCCCACCCCGGTATTAACCAGCAGTGCTGGTTCTCGAACCAGC
CTCTCAGAGCCGGAAGCAGCAGAACACAGCTTCAGCAACGGCGCAGCATTGGCGGCCCAGATCCACAAGGAGAGC
TTCTTAGCTCCAGTATTCACAAAGGATGAACAAAAGCACAGGCGTCCCTATGAGTTTGAGGTGGAGAGGGATGCA
AAGGCTCGGGGCCTGGAGCAGTTCTCTGCCACCCACGGGCACACCCCTATCATCCTCAATGGCTGGCATGGGGAG
TCAGCTATGGACCTCTCCTGCTCATCAGAGGGGTCCCCAGGAGCCACATCCCCTTTCCCAGTGAGCGCCAGCACC
CCTAAGATTGGGGCTATCAGTTCACTTCAGGGAGCCCTTGGCATGGACTTGTCTGGGATTCTGCAAGCTGGCCTG
ATCCATCCTGTGACTGGACAGATTGTCAATGGAAGCCTCAGAAGAGATGATGCAGCCACGAGGAGGCGGAGAGGG
AGGCGGAAACATGTTGAAGGAGGGATGGACCTCATCTTTTTGAAGGAGCAGACACTTCAGGCGGGAATCTTGGAA
GTCCATGAAGACCCAGGGCAGGCCACCTTGAGCACCACACACCCTGAGGGGCCAGGGCCTGCCACCTCGGCTCCT
GAGCCAGCTACGGCAGCCAGCAGCCAAGCCGAGAAATCCATTCCCAGCAAGAGTCTGCTTGACTGGCTAAGGCAG
CAGGCTGACTACTCCTTAGAAGTTCCTGGCTTTGGGGCAAATTTTTCAGACAAACCAAAGCAGAGGAGGCCACGC
TGTAAAGAACCTGGAAAATTAGATGTCAGCTCCCTGAGCGGGGAAGAGAGAGTTCCTGCCATCCCCAAGGAGCCA
GGACTGAGGGGGTTTCTTCCAGAAAACAAGTTCAATCACACTCTGGCTGAGCCTATTCTTCGAGATACGGGCCCC
CGCAGGAGGGGGAGGCGGCCTCGGAGCGAACTCCTGAAGGCTCCTTCCATTGTGGCAGACTCTCCCTCTGGAATG
GGGCCACTGTTCATGAATGGACTGATTGCTGGGATGGACCTGGTAGGACTTCAGAACATGAGAAATATGCCAGGC
ATCCCCCTCACCGGGCTGGTGGGGTTTCCAGCTGGCTTTGCCACGATGCCAACAGGTGAAGAGGTCAAAAGTACC
CTGAGCATGCTGCCCATGATGCTGCCAGGCATGGCTGCTGTGCCCCAGATGTTTGGTGTTGGGGGACTCCTCAGT
CCACCCATGGCAACCACCTGCACTTCCACTGCTCCGGCGTCTCTATCAAGCACAACGAAAAGTGGTACGGCAGTG
ACTGAAAAGACTGCGGAAGACAAGCCGAGTAGCCATGATGTGAAAACAGACACTTTAGCTGAGGACAAGCCTGGT
CCAGGTCCATTTTCTGATCAGTCTGAACCTGCAATAACTACTAGTAGTCCTGTGGCTTTTAACCCATTTCTCATC
CCAGGAGTATCTCCTGGACTCATTTACCCATCCATGTTCCTCTCCCCTGGTATGGGCATGGCTCTGCCAGCCATG
CAGCAGGCCAGACACTCGGAAATAGTAGGTCTGGAGAGCCAGAAGAGGAAGAAGAAGAAGACAAAGGGGGACAAC
CCCAACTCCCACCCAGAGCCTGCTCCCAGCTGTGAAAGGGAGCCCAGCGGTGATGAGAACTGTGCCGAACCCAGT
GCCCCTTTGCCCGCAGAGAGAGAACATGGGGCACAGGCTGGGGAGGGGGCACTCAAAGACTCCAACAACGACACC
AATTAGAACTTTTTTCATTTAAGAAATTATTGTGACTTGTAAGTTTCTTATCCCATAAAGGTTTGTTACTTCCCT
CACTTCACCTCCATAAGAACCTGTGTTTCCATAAGTAAGATTACGTACCTGATTTCCTGTCTGAGAACTATGGTA
ACAGATGTTAATAGTTGCAGGGTCTCACCACTTCATTAGATAAGTGTTGTCTACCTAGTCTAGGAGGCACAGAAT
TCTCATTCTGTTATCCAGTTCATTCCAGCAATCATAGTTAATACAGTACTTGGTGACACGCCCTACCCCCTTCTC
TTCCAAGTTTCCCACTCACTTGAGGAGGAAAAATGGCAAAAGAAAGCTGTCTAGGGTTTTACCATTGAAGGGTGG
AAGAACAGAGACAAAGAGGAGCTCTTTTTCTGTGAGCTGGGTTGCACAGGAAGAATGTCACAGGGAACCAAAAAG
CACAGAAAAAGGAAGTGCTGGTGCATATTTTTGAGTTAAAATATTTCCCTATTTTATCATGATTACTAAGTGAGT

FIGURE 35B

AGTATAGACAGAAGTATATAACTAATGGTTGAAAATACATATATTCATTTCTTTATAAAAAACAAAAACCTTACC
GGTAGTAATATAATTTCCCCCTTGGTGGTTTTTCAGACACCTGCAGCAAGAAGAAATACTGACTGACTAGGCATT
ATTTTCTATACATCCCTCTCACCAGTGAAAAGATTCCTCTTGCTGCGAGAAAGCTTTACCCACCATGAGTTATTG
CTGTCGACGGGGGTGGGGCAAGGACCCGCGCTCCGTAGAGCTACACGCTGCTTCACAAGCACACGGCCAGCGCTC
TGCTCTCACCTGGTTCGCTTACAGATTTCTCTAGCCATTAATTTGCCTCTCTGTGTTTAAAGAGCACCAGGACCG
AATGGATTTTCACTTCAGGCTTTCCTTCACCAAGAATAAGGTTCTTTCTGGAGCCTGCAAGAAGACAGTTGCCCA
ACACTTTGACACTTGCTAGTAGGTCCTTTGATCAAGAGTGTCTGAGGCTGTCAAATGTGTGCCACCCTTTATAAT
ACAGCTATGAAAAGTTACTTCTCCATTAATTTCTCCATTCTGTTTATATCTTACAGTTGGACCCAAATTCCAAAT
TATCAGTTAATCGAAACTACATTGCAAGTCAACATTATTTTCTCTTCTTCCTCAGCTTCTCCATGTTTAGGAACT
GAGAAAGAACCTGCCTAAGCAGCACTTCCCCATGTCCTTTCACCTTCATGTTAACGTCCCTTCTGATGGTCTCAC
TCTTCACAGGTAGTTCACACTCTGAGACTTGAAGTAAGCTCATGGTTCAGTACTCTGGGGGCGCAGGGCTGCGCA
GGACCCTTGGAAATGTTGCAAGTGTTACTAGTACCAGTTTCACTTTTTGTTGTCACAATTTACTGTATTTTTTAC
TTTTTCTGTTACAGTTTTGCTAATTTATCAGAAGGTCCAAAAGTCTGACATAACTATTTCATTTTGCATTATTTA
TTTATGATGCTTTTTTCATTGTCTTTTATACATTTGGGATTATAAATTATGTAAATGTTAAAATGAGCATCTCAA
AGAAGTCTGTTAAATCATGACTGAAAAAAATCAATCAGATGTATCTTCAAAAAGTGGAGTCCCAGTTTTATGAAT
CAGAGATATAAACCAGAAATTCTATAACTGATCATAGAAGAAGAATCCAGTAATTGAACAAATCCTATTTAATGA
CATCCTTGTAGCATAGATGGTCTATAATGCTGACCACAGATTTCTTAGAAATGCTGCTCTCTCTATTTAACTAAC
ATTTTGTTCAGTTTTGCCTCCAGTGGAAGCAGAAAGGGTTTTTTCAGCTGTTAAATCCTAAAAATCAATATAATT
TATTTATGTAAGAAAAATAACTCAATCAATATATTTTTGAACCTTTTAAGTACTAATTTTCTTTTTATCACGTAG
AAAAAAAAATGTATTTGCCCTAAATCCTTAAAATACAAATGCTATAAAAATTCCTGTATCTTGAAAGCCTTACTG
CAAATGAGTATTATAGACATCCC

FIGURE 36

ISINHDESLLPESLESMMYGKKVLSQEPSSFQESPSTNTESRKDVITISISKDGNCQSGGPEAEIASGPTFMGSL
EAGGVAQANIKNGKHLLMSISKEGELCCSEAGQRPENIGQLEAKCLASPSLNPGNESGFVDMCSLSVCDSKRNLS
SDQQLIDLLENKSLESKLILSQNHSDEEEEEEENEEENLAMAVGMGERPEVLHLTEPTTNISREKNQGFQDETKK
GSLEVANQTPGLQRAFPAPAACQCHCKHMERWMHGLENDEFEIEKPKAYIPDLFKSKTNTIAMEGEPTAIPSQPF
KVKHELLKEPWKESAEGQNVFPTYPLEGSELKSEDMDFENKDDYDRDGNCHSQDYPGKYSEEESKSSTSGITGDI
GDELQEARAPTIAQLLQEKTLYSFSEWPKDRVIINRLDNICHVVLKGKWPSSQQYEPSGTLPTPVLTSSAGSRTS
LSEPEAAEHSFSNGAALAAQIHKESFLAPVFTKDEQKHRRPYEFEVERDAKARGLEQFSATHGHTPIILNGWHGE
SAMDLSCSSEGSPGATSPFPVSASTPKIGAISSLQGALGMDLSGILQAGLIHPVTGQIVNGSLRRDDAATRRRRG
RRKHVEGGMDLIFLKEQTLQAGILEVHEDPGQATLSTTHPEGPGPATSAPEPATAASSQAEKSIPSKSLLDWLRQ
QADYSLEVPGFGANFSDKPKQRRPRCKEPGKLDVSSLSGEERVPAIPKEPGLRGFLPENKFNHTLAEPILRDTGP
RRRGRRPRSELLKAPSIVADSPSGMGPLFMNGLIAGMDLVGLQNMRNMPGIPLTGLVGFPAGFATMPTGEEVKST
LSMLPMMLPGMAAVPQMFGVGGLLSPPMATTCTSTAPASLSSTTKSGTAVTEKTAEDKPSSHDVKTDTLAEDKPG
PGPFSDQSEPAITTSSPVAFNPFLIPGVSPGLIYPSMFLSPGMGMALPAMQQARHSEIVGLESQKRKKKKTKGDN
PNSHPEPAPSCEREPSGDENCAEPSAPLPAEREHGAQAGEGALKDSNNDTN

FIGURE 37

TAGCTAGGCAGGAAGTCGGCGCGGGCGGCGCGGACAGTATCTGTGGGTACCCGGAGCACGGAGATCTCGCCGGCT
TTACGTTCACCTCGGTGTCTGCAGCACCCTCCGCTTCCTCTCCTAGGCGACGAGACCCAGTGGCTAGAAGTTCAC
C**ATG**TCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCACTGTTGAGGTTGATCTCTT
CACCTCAAAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGCCCTAGAGCTCCG
GGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGGCTGTTGAGCACATCAATAAAACTATTGCGCC
TGCCCTGGTTAGCAAGAAACTGAACGTCACAGAACAAGAGAAGATTGACAAACTGATGATCGAGATGGATGGAAC
AGAAAATAAATCTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCCTTGCCGTCTGCAAAGCTGGTGCCGTTGA
GAAGGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAACTCTGAAGTCATCCTGCCAGTCCCGGCGTT
CAATGTCATCAATGGCGGTTCTCATGCTGGCAACAAGCTGGCCATGCAGGAGTTCATGATCCTCCCAGTCGGTGC
AGCAAACTTCAGGGAAGCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATA
TGGGAAAGATGCCACCAATGTGGGGGATGAAGGCGGGTTTGCTCCCAACATCCTGGAGAATAAAGAAGGCCTGGA
GCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTGGTCATCGGCATGGACGTAGCGGCCTCCGA
GTTCTTCAGGTCTGGGAAGTATGACCTGGACTTCAAGTCTCCCGATGACCCCAGCAGGTACATCTCGCCTGACCA
GCTGGCTGACCTGTACAAGTCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGA
CTGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTCACAGTGACCAACCC
AAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGT
GACCGAGTCTCTTCAGGCGTGCAAGCTGGCCCAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCGGGGGA
GACTGAAGATACCTTCATCGCTGACCTGGTTGTGGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCCTTGCCG
ATCTGAGCGCTTGGCCAAGTACAACCAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAGGCTAAGTTTGCCGG
CAGGAACTTCAGAAACCCCTTGGCCAAG**TAA**GCTGTGGGCAGGCAAGCCCTTCGGTCACCTGTTGGCTACACAGA
CCCCTCCCCTCGTGTCAGCTCAGGCAGCTCGAGGCCCCCGACCAACACTTGCAGGGGTCCCTGCTAGTTAGCGCC
CCACCGCCGTGGAGTTCGTACCGCTTCCTTAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAGCT
CTAGCTTTGCAGTCGTGTAATTGGCCCAAGTCATTGTTTTTCTCGCCTCACTTTCCACCAAGTGTCTAGAGTCAT
GTGAGCCTCGTGTCATCTCCGGGGTGGCCACAGGCTAGATCCCCGGTGGTTTTGTGCTCAAAATAAAAAGCCTCA
GTGACCCATGAG

FIGURE 38

MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTGIYEALELRDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLNVTEQEKIDKLMIEMDGTENKSKFGANAILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVPAF
NVINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEKYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDQLADLYKSFIKDYPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGVMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEELGSKAKFAGRNFRNPLAK

FIGURE 39

GCCTGAGTGAGTCTCTGGCGTCCCAAATTGCCTGTTTTCTCGCAGGCTCTATTCCGTTCGCTGGTTCGCCACCT
CAGGGGAACG**<u>ATG</u>**GCCATGGAGTCCACAGCCACTGCCGCCGTCGCCGCGGACGTGGTTTCTGCCGACAAAATTGA
AGATGTCCCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGTGAAGCTAAGAAACTATT
GGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTCCAGGAAGCAGCTAGTCT
TTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTTCTATGGGAAATCACTTCTGGA
GTTGGCAAGAATGGAGAATGGTGTGTTGGGAAACGCCTTGGAAGGTGTGCATGTGGAAGAGGAAGAAGGAGAAAA
AACAGAAGATGAATCTCTGGTAGAAAATAATGATAACATAGATGAGGAAGCAAGGGAAGAGTTGAGAGAACAGGT
TTATGACGCCATGGGAGAAAAAGAAGAAGCCAAAAAAACAGAAGACAAGTCTTTGGCAAAGCCTGAAACTGATAA
AGAACAGGACAGTGAAATGGAGAAGGGTGGAAGAGAAGATATGGATATAAGTAAATCTGCAGAGGAGCCACAGGA
AAAAGTTGACTTGACTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGAGCAGCACCAGAAGGACC
GAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAAGAAAAATCAGTTTCTGG
AACTGATGTCCAAGAAGAGTGCAGAGAAAAAGGAGGTCAGGAGAAGCAGGGAGAGGTAATTGTGAGCATAGAGGA
GAAGCCAAAAGAAGTTTCAGAAGAGCAGCCTGTGGTGACTCTAGAAAAGCAGGGCACTGCAGTGGAGGTAGAAGC
AGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGGACGAGCCAGAGGAGAAGGTAGTTACCTCTGA
AAACGAGGCAGGAAAGGCGGTTCTTGAACAACTGGTAGGTCAAGAAGTACCACCTGCTGAAGAGTCACCAGAGGT
GCAAACAGAGGCTGCAGAGGCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAGCCTGGGCAGGAGGCTCC
AGTTCTCCCTAAGGATGGTGCAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCTATTGAACCACAGACTTC
TATAGAAAGACTGACAGAAACAAAAGATGGCTCAGGACTAGAGGAGAAGGTCAGGGCAAAGCTGGTTCCTAGTCA
GGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACCAAGGTAGCCCAGGGAGC
TACTGAGAAATCACCTGAAGACAAAGTTCAGATAGCTGCTAATGAAGAGACACAAGAGAGAGAAGAACAGATGAA
AGAGGGTGAAGAAACTGAAGGCTCGGAAGAGGATGATAAAGAAAATGATAAGACTGAAGAAATGCCAAATGATTC
AGTCCTTGAAAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAGCTTGCCTGGGATATGCT
GGATTTAGCAAAGATCATTTTTAAAAGGCAAGAAACAAAAGAAGCACAGCTTTATGCTGCCCAGGCACATCTTAA
ACTCGGAGAAGTTAGTGTTGAATCTGAAAACTATGTGCAAGCTGTGGAGGAGTTCCAGTCCTGCCTTAACCTGCA
GGAACAGTACCTGGAAGCCCACGACCGTCTGCTTGCAGAGACCCACTACCAGCTGGGCTTGGCTTATGGGTACAA
CTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAACAGAATGGCTGTACTAAA
CGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGAATACAAGAAAGAAATTGAGGAACTAAAGGAACTGCTACCCGA
AATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCTGAACTGGCTCTGAAAGCTAC
TCTGGTGGAGAGTTCTACTTCAGGTTTCACTCCTGGTGGAGGAGGCTCTTCAGTCTCCATGATTGCCAGTAGAAA
GCCAACAGACGGTGCTTCCTCATCAAATTGTGTGACTGATATTTCCCACCTTGTCAGAAAGAAGAGGAAACCAGA
GGAAGAGAGTCCCCGGAAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTGAACGGAGGCAGTGGGGATGC
TGTCCCGAGTGGAAATGAAGTTTCGGAAAACATGGAGGAGGAGGCTGAGAATCAGCTGAAACGCGGAGCAGCAGT
GGAGGGGACACTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGT**<u>TAA</u>**GAGGGGGCACAGCCTCCTCCCAAGGG
AAAGTGTTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATTCTTTTTGTATAACTTCAATAAAGATTGTAAG
CAAAAAAAAAA

FIGURE 40

MAMESTATAAVAADVVSADKIEDVPAPSTSADKVESLDVDSEAKKLLGLGQKHLVMGDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLELARMENGVLGNALEGVHVEEEEGEKTEDESLVENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEEPQEKVDLTLDWLTETSEEAKGGAAPEGPNEA
EVTSGKPEQEVPDAEEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKEVSEEQPVVTLEKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAEESPEVQTEAAEASAVEAGSEVSEKPGQEAPVLP
KDGAVNGPSVVGDQTPIEPQTSIERLTETKDGSGLEEKVRAKLVPSQEETKLSVEESEAAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPNDSVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFKRQETKEAQLYAAQAHLKLGEVSVESENYVQAVEEFQSCLNLQEQYLEAHDRLLAETHYQLGLAYGYNSQY
DEAVAQFSKSIEVIENRMAVLNEQVKEAEGSSEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLVE
SSTSGFTPGGGGSSVSMIASRKPTDGASSSNCVTDISHLVRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVPS
GNEVSENMEEEAENQLKRGAAVEGTLEAGATVESTAC

FIGURE 41

TTTCTTCGCGGCTGCTCAAG**<u>ATG</u>**AACCGACTCTTCGGGAAAGCGAAACCCAAGGCTCCGCCGCCCAGCCTGACTG
ACTGCATTGGCACGGTGGACAGTAGAGCAGAATCCATTGACAAGAAGATTTCTCGATTGGATGCTGAGCTAGTGA
AGTATAAGGATCAGATCAAGAAGATGAGAGAGGGTCCTGCAAAGAATATGGTCAAGCAGAAAGCCTTGCGAGTTT
TAAAGCAAAAGAGGATGTATGAGCAGCAGCGGGACAATCTTGCCCAACAGTCATTCAACATGGAACAAGCCAATT
ATACCATCCAGTCTTTGAAGGACACCAAGACCACGGTTGATGCTATGAAACTGGGAGTAAAGGAAATGAAGAAGG
CATACAAGCAAGTGAAGATCGACCAGATTGAGGATTTACAAGACCAGCTAGAGGATATGATGGAAGATGCAAATG
AAATCCAAGAAGCACTGAGTCGCAGTTATGGCACCCCAGAACTGGATGAAGATGATTTAGAAGCAGAGTTGGATG
CACTAGGTGATGAGCTTCTGGCTGATGAAGACAGTTCTTATTTGGATGAGGCAGCATCTGCACCTGCAATTCCAG
AAGGTGTTCCCACTGATACAAAAAACAAGGATGGAGTTCTGGTGGATGAATTTGGATTGCCACAGATCCCTGCTT
CA**<u>TAG</u>**ATTTGCATCATTCAAGCATATCTTGTAAAACAAACACATATTATGGGACTAGGAAATATTTATCTTTCCA
AATTTGCCATAACAGATTTAGGTTTCTTTCCTTTCTTTGAAGGAAAGTTTAATTACATTGCTCTTTTATTTTTTC
CATTAAGAGACTCATTGCTTGGGAAATGCTTTCTTCGTACTAAAATTTGATTCCTTTTTTTCTTATGAAAAACGA
ACTCAGTTTAAAAGTATTTTTAGCTCGTATGACTTGTTTTCATTCATTAATAATAATTTGAAATAAAACTAAGGA
AATGGAATCTTAAAAGTCTATGACAGTGTAACTCTACAGTCCTCAAAATGACCCTGTAAATTTGGATAAGACCAA
AGATGAGATTATTGGGGCTGGTCATATTATGATTCAGAATCCATTTCTATTGTGGGTATTATAGGGTTGGGTTAA
AGGTGATGGCCCTTTTTGATGGGTTTTGTTGTGTCTTGTGAACAAGTCGTTACTGTGTCCATTATTGGAATG

FIGURE 42

MNRLFGKAKPKAPPPSLTDCIGTVDSRAESIDKKISRLDAELVKYKDQIKKMREGPAKNMVKQKALRVLKQKRMY
EQQRDNLAQQSFNMEQANYTIQSLKDTKTTVDAMKLGVKEMKKAYKQVKIDQIEDLQDQLEDMMEDANEIQEALS
RSYGTPELDEDDLEAELDALGDELLADEDSSYLDEAASAPAIPEGVPTDTKNKDGVLVDEFGLPQIPAS

FIGURE 43

GGAATCAGAGGGAGCATTCACTGAGTGCTTATTGGTTCTACGCACTGTTAGGTGTTCCTTTGTGTCTTACCTCAT
CCACCTCTCGCATCCCCCCTTGGAACAAGATAGCATCATTACCCTACATCTCTTGAAGGTTCAGGTCCCTGGGCT
GCAAGGAGATAAGAGGCTCCCTCACACAGCCTCTGGAGGGCTAAATGAGATCCTACAGCAATGCCCTGGTGGGGC
TTCTCTCTCCCTCTTATGTCACTTGTCACACCTGCTC**TAG**GTAATCATTTTCCTCCAGATGAGAGGTGTAGGAAA
GGACCTGATGCCAGCAAGGAAAAAGGAATTGGTAACATGCTCTTTGTTTACCTAAAATCTGTCCCCACAACAAGA
ATGTAACTTCCTTCGAGGCAGAAATTCAATTTTCTTCTCCCAGCCCACCTACAAAGGCCCACTCAAGAGCAAGTT
CTGTGTAAAGGTGCTTAACTAATACAGGTTCTTTGACAAAATGATAAAACATTTGTAACCTGAAAAAAA

FIGURE 44

ESEGAFTECLLVLRTVRCSFVSYLIHLSHPPLEQDSIITLHLLKVQVPGLQGDKRLPHTASGGLNEILQQCPGGA
SLSLLCHLSHLL

FIGURE 45

CGGCACGAGGCGACTTTGGTGGAGGTAGTTCTTTGGCAGCGGGC**ATG**GCGGGTACCGTGGTGCTGGACGATGTGG
AGCTGCGGGAGGCTCAGAGAGATTACCTGGACTTCCTGGACGACGAGGAAGACCAGGGAATTTATCAGAGCAAAG
TTCGGGAGCTGATCAGTGACAACCAATACCGGCTGATTGTCAATGTGAATGACCTGCGCAGGAAAAACGAGAAGA
GGGCTAACCGGCTTCTGAACAATGCCTTTGAGGAGCTGGTTGCCTTCCAGCGGGCCTTAAAGGATTTTGTGGCCT
CCATTGATGCTACCTATGCCAAGCAGTATGAGGAGTTCTACGTAGGACTGGAAGGCAGCTTTGGCTCCAAGCACG
TCTCCCCGCGGACTCTTACCTCCTGCTTCCTCAGCTGTGTGGTCTGTGTGGAGGGCATTGTCACTAAATGTTCTC
TAGTTCGTCCCAAAGTCGTCCGCAGTGTCCACTACTGTCCTGCTACTAAGAAGACCATAGAGCGACGTTATTCTG
ATCTCACCACCCTGGTGGCCTTTCCCTCCAGCTCTGTCTATCCTACCAAGGATGAGGAGAACAATCCCCTTGAGA
CAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACCATCCAGGAGATGCCGGAGAAGGCCCCAGCCG
GCCAGCTCCCCCGCTCTGTGGACGTCATTCTGGATGATGACTTGGTGGATAAAGCGAAGCCTGGTGACCGGGTTC
AGGTGGTGGGAACCTACCGTTGCCTTCCTGGAAAGAAGGGAGGCTACACCTCTGGGACCTTCAGGACTGTCCTGA
TTGCCTGTAATGTTAAGCAGATGAGCAAGGATGCTCAGCCCTCTTTCTCTGCTGAGGATATAGCCAAGATCAAGA
AGTTCAGTAAAACCCGATCCAAGGATATCTTTGACCAGCTGGCCAAGTCATTGGCCCCAAGTATCCATGGGCATG
ACTATGTCAAGAAAGCAATCCTCTGCTTGCTCTTGGGAGGGGTGGAACGAGACCTAGAAAATGGCAGCCACATCC
GTGGGGACATCAATATTCTTCTAATAGGAGACCCATCCGTTGCCAAGTCTCAGCTTCTGCGGTATGTGCTTTGCA
CTGCACCCCGAGCTATCCCCACCACTGGCCGGGGCTCCTCTGGAGTGGGTCTGACGGCTGCTGTCACCACAGACC
AGGAAACAGGAGAGCGCCGTCTGGAAGCAGGGGCCATGGTCCTGGCTGACCGAGGCGTGGTTTGCATTGATGAAT
TTGACAAAATGTCTGACATGGATCGCACAGCCATCCATGAAGTGATGGAGCAGGGTCGAGTGACCATTGCCAAGG
CTGGCATCCATGCTCGGCTGAATGCCCGCTGCAGTGTTTTGGCAGCTGCCAACCCTGTCTACGGCAGGTATGACC
AGTATAAGACTCCAATGGAGAACATTGGGCTACAGGACTCACTGCTGTCACGATTTGACTTGCTCTTCATCATGC
TGGATCAGATGGATCCTGAGCAGGATCGGGAGATCTCAGACCATGTCCTTCGGATGCACCGTTACAGAGCACCTG
GGGAGCAGGATGGCGATGCTATGCCCTTGGGTAGTGCTGTGGATATCCTGGCCACAGATGATCCCAACTTTAGCC
AGGAAGATCAGCAGGACACCCAGATTTATGAGAAGCATGACAACCTTCTACATGGGACCAAGAAGAAAAAGGAGA
AGATGGTGAGTGCAGCATTCATGAAGAAGTACATCCATGTGGCCAAAATCATCAAGCCTGTCCTGACACAGGAGT
CGGCCACCTACATTGCAGAAGAGTATTCACGCCTGCGCAGCCAGGATAGCATGAGCTCAGACACCGCCAGGACAT
CTCCAGTTACAGCCCGAACACTGGAAACTCTGATTCGACTGGCCACAGCCCATGCGAAGGCCCGCATGAGCAAGA
CTGTGGACCTGCAGGATGCAGAGGAAGCTGTGGAGTTGGTCCAGTATGCTTACTTTAAGAAGGTTCTGGAGAAGG
AGAAGAAACGTAAGAAGCGAAGTGAGGATGAATCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGG
AGCAGAAGAGGAAGAGAAGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTCATACGACCCCTATGACTTCA
GTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGGCAGACTCACAGGAGACCAAGGAATCCCAGA
AAGTGGAGTTGAGTGAATCCAGGTTGAAGGCATTCAAGGTGGCCCTCTTGGATGTGTTCCGGGAAGCTCATGCGC
AGTCAATCGGCATGAATCGCCTCACAGAATCCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCC
AGGCTGCTCTGAGCAAGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCCTCATC**TGA**GGAG
GCCTCGTCTCTGAACTTGGGTTGTGCCGAGAGAGTTTGTTCTGTGTTTCCCACCCTCTCCCTGACCCAAGTCTTT
GCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGGCGAGGAATGTTGGTGATGAAGCTGAGTTCAGGACTCG
GTGGACCCTTTGGGAATGGGTCATGAAAGCTGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGAC
TATTGCATCTTCATTGCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCCAATTGTAAATAAC
ATATGACTTCTGAGTACTTTTGGGGGCACAACTGTTTTCTGTTTGCTGTTTTTTTGTTTTGTTTTTTTTCTCCAG
AGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGAGAGAAGCTCTGAGGCACGTCATGCAGGTCA
AGAAAGCTTTCTTTGCAGTAGCACCAGTTAAGGTGAATATGTATTGTATCACAAAACAAACCCAATATCCAGATG
AATATCCGAGATGTTGAATAAACTTAGCCATTTCGTACAAAAAAAGGGGGGCCCGGTAAAC

FIGURE 46

MAGTVVLDDVELREAQRDYLDFLDDEEDQGIYQSKVRELISDNQYRLIVNVNDLRRKNEKRANRLLNNAFEELVA
FQRALKDFVASIDATYAKQYEEFYVGLEGSFGSKHVSPRTLTSCFLSCVVCVEGIVTKCSLVRPKVVRSVHYCPA
TKKTIERRYSDLTTLVAFPSSSVYPTKDEENNPLETEYGLSVYKDHQTITIQEMPEKAPAGQLPRSVDVILDDDL
VDKAKPGDRVQVVGTYRCLPGKKGGYTSGTFRTVLIACNVKQMSKDAQPSFSAEDIAKIKKFSKTRSKDIFDQLA
KSLAPSIHGHDYVKKAILCLLLGGVERDLENGSHIRGDINILLIGDPSVAKSQLLRYVLCTAPRAIPTTGRGSSG
VGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDEFDKMSDMDRTAIHEVMEQGRVTIAKAGIHARLNARCSVLA
AANPVYGRYDQYKTPMENIGLQDSLLSRFDLLFIMLDQMDPEQDREISDHVLRMHRYRAPGEQDGDAMPLGSAVD
ILATDDPNFSQEDQQDTQIYEKHDNLLHGTKKKKEKMVSAAFMKKYIHVAKIIKPVLTQESATYIAEEYSRLRSQ
DSMSSDTARTSPVTARTLETLIRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKRSEDESETE
DEEEKSQEDQEQKRKRRKTRQPDAKDGDSYDPYDFSDTEEEMPQVHTPKTADSQETKESQKVELSESRLKAFKVA
LLDVFREAHAQSIGMNRLTESINRDSEEPFSSVEIQAALSKMQDDNQVMVSEGIIFLI

FIGURE 47

AATGCCACCTGCTTGAAGGCTATATGTGACAAGTCACTAGAGGTTCACCTGCAGGTTGACGCCATGTACACAAAT
GTCAAAGTAACTAATATTTGCTCTGATGGGACACTCTACTGCCAGGTGCCTTGTAAGGGTCTGAACAAGCTCAGT
GACCTTCTACGTAAGATAGAGGACTACTTCCATTGCAAGCACATGACCTCTGAGTGCTTTGTTTCATTACCCTTC
TGTGGGAAAATCTGCCTCTTCCATTGCAAAGGAAAATGGTTACGAGTAGAGATCACAAATGTTCACAGCAGCCGG
GCTCTTGATGTTCAGTTCCTGGACTCTGGCACTGTGACATCTGTAAAAGTGTCAGAGCTCAGGGAAATTCCACCT
CGGTTTCTACAAGAAATGATTGCAATACCACCTCAGGCCATTAAGTGCTGTTTAGCAGATCTTCCACAATCTATT
GGCATGTGGACACCAGATGCAGTGCTGTGGTTAAGAGATTCTGTTTTGAATTGCTCGGACTGTAGCATTAAGGTT
ACAAAAGTGGATGAAACCAGAGGGATCGCACATGTTTATTTATTTACCCCTAAGAACTTCCCTGACCCTCATCGC
AGTATTAATCGCCAGATTACAAATGCAGACTTGTGGAAGCATCAGAAGGATGTGTTTTTGAGTGCCATATCCAGT
GGAGCTGACTCTCCCAACAGCAAAAATGGCAACATGCCCATGTCGGGCAACACTGGAGAGAATTTCAGAAAGAAC
CTCACAGATGTCATCAAAAAGTCCATGGTGGACCATACGAGCGCTTTCTCCACAGAGGAACTGCCACCTCCTGTC
CACTTATCAAAGCCAGGGGAACACATGGATGTGTATGTGCCTGTGGCCTGTCACCCAGGCTACTTCGTCATCCAG
CCTTGGCAGGAGATACATAAGTTGGAAGTTCTGATGGAAGAGATGATTCTATATTACAGCGTGTCTGAAGAGCGC
CACATAGCAGTGGAGAAAGACCAAGTGTATGCTGCAAAAGTGGAAAATAAGTGGCACAGGGTGCTTTTAAAAGGA
ATCCTGACCAATGGACTGGTATCTGTGTATGAGCTGGATTATGGCAAACACGAATTAGTCAACATAAGAAAAGTA
CAGCCCCTAGTGGACATGTTCCGAAAGCTGCCCTTCCAAGCAGTCACAGCTCAACTTGCAGGAGTGAAGTGCAAC
CAGTGGTCTGAGGAGGCTTCTATGGTGTTTCGAAATCATGTGGAGAAGAAACCTCTGGTGGCACTGGTGCAGACA
GTCATTGAAAATGCTAACCCTTGGGACCGGAAAGTAGTGGTCTACTTAGTGGACACATCGTTGCCAGACACCGAT
ACCTGGATTCATGATTTTATGTCAGAGTATCTGATAGAGCTTTCAAAAGTTAAT**TAA**TGACTGCCTCTGAAACCT
TGACAACTAATTCAGATTTTTTAGCAATAACAAAATGTAGTAGGCTTAAAAAAAATCTTAACTCTGCTACATGGC
TCTGACTGCTGTGGGGGATTGAAAAGAATATGCTTATGTTTGATGAAAGATATTTAACAAGTTTTGTTTTAACAG
AGTTGACTTTTCAAAGAAAATTGTACTTGAATTATTACTATAATATTAGAATAAAAATGTTTATC

FIGURE 48

NATCLKAICDKSLEVHLQVDAMYTNVKVTNICSDGTLYCQVPCKGLNKLSDLLRKIEDYFHCKHMTSECFVSLPF
CGKICLFHCKGKWLRVEITNVHSSRALDVQFLDSGTVTSVKVSELREIPPRFLQEMIAIPPQAIKCCLADLPQSI
GMWTPDAVLWLRDSVLNCSDCSIKVTKVDETRGIAHVYLFTPKNFPDPHRSINRQITNADLWKHQKDVFLSAISS
GADSPNSKNGNMPMSGNTGENFRKNLTDVIKKSMVDHTSAFSTEELPPPVHLSKPGEHMDVYVPVACHPGYFVIQ
PWQEIHKLEVLMEEMILYYSVSEERHIAVEKDQVYAAKVENKWHRVLLKGILTNGLVSVYELDYGKHELVNIRKV
QPLVDMFRKLPFQAVTAQLAGVKCNQWSEEASMVFRNHVEKKPLVALVQTVIENANPWDRKVVVYLVDTSLPDTD
TWIHDFMSEYLIELSKVN

FIGURE 49

GCGGAAGGAACCGCCGGGGGCC**ATG**GACGGAGCAGTGATGGAAGGGCCGCTTTTTTTGCAGAGTCAGCGCTTTGG
GACCAAGAGGTGGAGGAAGACCTGGGCCGTGCTCTACCCGGCCAGTCCCCACGGCGTAGCGCGGCTCGAGTTCTT
TGACCATAAGGGGTCGAGCTCTGGGGGTGGCCGAGGGAGCTCGCGCCGCCTGGACTGCAAAGTGATCCGTCTGGC
TGAGTGTGTGAGTGTGGCCCCCGTCACCGTGGAGACCCCCCCTGAGCCCGGCGCCACTGCCTTCCGCCTGGACAC
TGCTCAGCGCTCGCACCTGCTGGCGGCCGACGCGCCGTCCAGTGCAGCCTGGGTGCAGACGCTGTGCCGAAACGC
CTTTCCGAAAGGCAGCTGGACTCTGGCGCCTACCGATAACCCACCTAAGCTTTCTGCCCTGGAGATGCTGGAGAA
CTCCTTGTACAGCCCTACCTGGGAAGGATCCCAATTCTGGGTAACGGTGCAGAGGACTGAGGCCGCCGAGCGCTG
TGGCCTGCATGGCTCCTACGTGCTGAGGGTGGAGGCTGAAAGGCTGACTCTCCTGACCGTGGGGGCCCAGAGTCA
GATACTGGAGCCACTCCTGTCCTGGCCCTACACTCTGTTGCGTCGCTATGGCCGGGACAAGGTCATGTTCTCTTT
CGAGGCCGGCCGCCGCTGCCCCTCAGGCCCTGGAACCTTCACCTTCCAGACGGCACAGGGAAATGACATCTTCCA
GGCAGTTGAGACTGCCATCCACCGGCAGAAGGCCCAGGGAAAGGCCGGACAGGGGCACGATGTTCTCAGAGCTGA
CTCCCATGAAGGGGAGGTGGCAGAGGGGAAGTTGCCTTCCCCACCTGGCCCCCAAGAGCTCCTCGACAGTCCCCC
AGCCCTGTATGCTGAGCCCTTAGACTCCCTGCGCATTGCTCCATGCCCTTCCCAGGACTCCCTATACTCAGACCC
CTTGGACAGCACGTCTGCTCAGGCAGGAGAGGGAGTACAACGGAAGAAACCTCTCTATTGGGACTTGTATGAGCA
TGCGCAGCAGCAGTTGCTGAAGGCCAAGCTGACAGACCCCAAAGAGGATCCCATCTATGATGAACCTGAGGGCCT
GGCCCCAGTCCCTCCCCAGGGCCTTTATGATCTGCCTCGGGAGCCCAAGGATGCATGGTGGTGCCAAGCTCGGGT
GAAGGAGGAGGGCTATGAGCTCCCCTACAACCCTGCCACTGATGACTACGCTGTGCCACCCCCTCGGAGCACAAA
GCCCCTCCTTGCTCCCAAGCCCCAGGGCCCAGCCTTCCCTGAACCTGGTACTGCAACTGGCAGTGGCATCAAAAG
CCACAACTCAGCCCTGTACAGCCAGGTCCAGAAGAGCGGGGCCTCAGGGAGCTGGGACTGTGGGCTCTCTAGAGT
AGGGACTGACAAGACTGGGGTCAAGTCAGAGGGCTCTACC**TGA**GAAGGACGGCAAGGCTGAGGTGGCTAAGGGGG
ACCATGGGGAGGTGGCACTAGGGATCAAAGAAGATGGTTAGAACCAGCAGAAGCCAGAGGGTGGGAGGGGCCATG
CTGTGTGAGACCAGGGGACCAGAGGGATGGGAGAGTCAAGGGAAGGACAATCCCAGGAAGTCCTAAGAAGTGGGG
CAGATGGCAGGGCTGAGGATGGGCTCTGCATCCCCCAAAGCCATCCCTTCCCTACTTCCCCAAATGAAGGGACGG
CTGTGGGACCAGGTCTGTGGAAAGTGGTGCATGGTCAGAATGGGTGCAGTTTGAGGGGCCTGTGTGGAGGCCTCA
GGGAGATGTTGGACTGTGCCTGGATCCTTACTCCTGCATTGTTCTTTGCCAGAGACCTATTTAAAAATTTTAAAA
TTCTCATTAAAGTCAAAAAAAAAAAAAAAAAAA

FIGURE 50

MDGAVMEGPLFLQSQRFGTKRWRKTWAVLYPASPHGVARLEFFDHKGSSSGGGRGSSRRLDCKVIRLAECVSVAP
VTVETPPEPGATAFRLDTAQRSHLLAADAPSSAAWVQTLCRNAFPKGSWTLAPTDNPPKLSALEMLENSLYSPTW
EGSQFWVTVQRTEAAERCGLHGSYVLRVEAERLTLLTVGAQSQILEPLLSWPYTLLRRYGRDKVMFSFEAGRRCP
SGPGTFTFQTAQGNDIFQAVETAIHRQKAQGKAGQGHDVLRADSHEGEVAEGKLPSPPGPQELLDSPPALYAEPL
DSLRIAPCPSQDSLYSDPLDSTSAQAGEGVQRKKPLYWDLYEHAQQQLLKAKLTDPKEDPIYDEPEGLAPVPPQG
LYDLPREPKDAWWCQARVKEEGYELPYNPATDDYAVPPPRSTKPLLAPKPQGPAFPEPGTATGSGIKSHNSALYS
QVQKSGASGSWDCGLSRVGTDKTGVKSEGST

FIGURE 51

AGTAAAAGTCCACAGTTACCGTGAGAGAAAAAAAGAGGAGAAAGCAGTGCAGCCAAACTCGGAAGAAAAGAGAGG
AGGAAAAGGACTCGACTTTCACA[illegible]TGGAACAACCTTCTTTCCAGTGCTAAGGCTCTCTGATCTGGGAACAACAC
CTGGAC**<u>ATG</u>**GCTCCAGAGATCAACTTGCCGGGCCCAATGAGCCTCATTGATAACACTAAAGGGCAGCTGGTGGTG
AATCCAGAAGCTCTGAAGATCCTATCTGCAATTACGCAGCCTGTGGTGGTGGTGGCGATTGTGGGCCTCTATCGC
ACAGGCAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAAAAACGGCTTCTCTCTAGGCTCCACAGTGAAGTCT
CACACCAAGGGAATCTGGATGTGGTGTGTGCCTCATCCCAAGAAGCCAGAACACACCCTAGTTCTGCTCGACACT
GAGGGCCTGGGAGATATAGAGAAGGGTGACAATGAGAATGACTCCTGGATCTTTGCCTTGGCCATCCTCCTGAGC
AGCACCTTCGTGTACAATAGCATGGGAACCATCAACCAGCAGGCCATGGACCAACTTCACTATGTGACAGAGCTG
ACAGATCGAATCAAGGCAAACTCCTCACCTGGTAACAATTCTGTAGACGACTCAGCTGACTTTGTGAGCTTTTTT
CCAGCATTTGTGTGGACTCTCAGAGATTTCACCCTGGAACTGGAAGTAGATGGAGAACCCATCACTGCTGATGAC
TACTTGGAGCTTTCGCTAAAGCTAAGAAAAGGTACTGATAAGAAAAGTAAAAGCTTTAATGATCCTCGGTTGTGC
ATCCGAAAGTTCTTCCCCAAGAGGAAGTGCTTCGTCTTCGATTGGCCCGCTCCTAAGAAGTACCTTGCTCACCTA
GAGCAGCTAAAGGAGGAAGAGCTGAACCCTGATTTCATAGAACAAGTTGCAGAATTTTGTTCCTACATCCTCAGC
CATTCCAATGTCAAGACTCTTTCAGGTGGCATTGCAGTCAATGGGCCTCGTCTAGAGAGCCTGGTGCTGACCTAC
GTCAATGCCATCAGCAGTGGGGATCTACCCTGCATGGAGAACGCAGTCCTGGCCTTGGCCCAGATAGAGAACTCA
GCCGCAGTGGAAAAGGCTATTGCCCACTATGAACAGCAGATGGGCCAGAAGGTGCAGCTGCCCACGGAAACCCTC
CAGGAGCTGCTGGACCTGCACAGGGACAGTGAGAGAGAGGCCATTGAAGTCTTCATGAAGAACTCTTTCAAGGAT
GTGGACCAAATGTTCCAGAGGAAATTAGGGGCCCAGTTGGAAGCAAGGCGAGATGACTTTTGTAAGCAGAATTCC
AAAGCATCATCAGATTGTTGCATGGCTTTACTTCAGGATATATTTGGCCCTTTAGAAGAAGATGTCAAGCAGGGA
ACATTTTCTAAACCAGGAGGTTACCGTCTCTTTACTCAGAAGCTGCAGGAGCTGAAGAATAAGTACTACCAGGTG
CCAAGGAAGGGGATACAGGCCAAAGAGGTGCTGAAAAAATATTTGGAGTCCAAGGAGGATGTGGCTGATGCACTT
CTACAGACTGATCAGTCACTCTCAGAAAAGGAAAAAGCGATTGAAGTGGAACGTATAAAGGCTGAATCTGCAGAA
GCTGCAAAGAAAATGTTGGAGGAAATACAAAAGAAGAATGAGGAGATGATGGAACAGAAAGAGAAGAGTTATCAG
GAACATGTGAAACAATTGACTGAGAAGATGGAGAGGGACAGGGCCCAGTTAATGGCAGAGCAAGAGAAGACCCTC
GCTCTTAAACTTCAGGAACAGGAACGCCTTCTCAAGGAGGGATTCGAGAATGAGAGCAAGAGACTTCAAAAAGAC
ATATGGGATATCCAGATGAGAAGCAAATCATTGGAGCCAATATGTAACATACTC**<u>TAA</u>**AGTCCAAGGAGCAAAAT
TTGCCTGTCCAGCTCCCTCTCCCCAAGAAACAACATGAATGAGCAACTTCAGAGTGTCAAACAACTGCCATTAAA
CTTAACTCAAAATCATGATGCATGCATTTTTGTTGAACCATAAAGTTTGCAAAGTAAAGGTTAAGTATGAGGTCA
ATGTTTT

FIGURE 52

MAPEINLPGPMSLIDNTKGQLVVNPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKKNGFSLGSTVKSHT
KGIWMWCVPHPKKPEHTLVLLDTEGLGDIEKGDNENDSWIFALAILLSSTFVYNSMGTINQQAMDQLHYVTELTD
RIKANSSPGNNSVDDSADFVSFFPAFVWTLRDFTLELEVDGEPITADDYLELSLKLRKGTDKKSKSFNDPRLCIR
KFFPKRKCFVFDWPAPKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLESLVLTYVN
AISSGDLPCMENAVLALAQIENSAAVEKAIAHYEQQMGQKVQLPTETLQELLDLHRDSEREAIEVFMKNSFKDVD
QMFQRKLGAQLEARRDDFCKQNSKASSDCCMALLQDIFGPLEEDVKQGTFSKPGGYRLFTQKLQELKNKYYQVPR
KGIQAKEVLKKYLESKEDVADALLQTDQSLSEKEKAIEVERIKAESAEAAKKMLEEIQKKNEEMMEQKEKSYQEH
VKQLTEKMERDRAQLMAEQEKTLALKLQEQERLLKEGFENESKRLQKDIWDIQMRSKSLEPICNIL

FIGURE 53

GCCCCGCCGCCGGCAGTGGACCGCTGTGCGAACCCTGAACCCTACGGTCCCGACCCGCGGGCGAGGCCGGGTA
CCTGGGCTGGGATCCGGAGCAAGCGGGCGAGGGCAGCGCCCTAAGCAGGCCCGGAGCG**ATG**GCAGCCTTGATGAC
CCCGGGAACCGGGGCCCCACCCGCGCCTGGTGACTTCTCCGGGGAAGGGAGCCAGGGACTTCCCGACCCTTCGCC
AGAGCCCAAGCAGCTCCCGGAGCTGATCCGCATGAAGCGAGACGGAGGCCGCCTGAGCGAAGCGGACATCAGGGG
CTTCGTGGCCGCTGTGGTGAATGGGAGCGCGCAGGGCGCACAGATCGGGGCCATGCTGATGGCCATCCGACTTCG
GGGCATGGATCTGGAGGAGACCTCGGTGCTGACCCAGGCCCTGGCTCAGTCGGGACAGCAGCTGGAGTGGCCAGA
GGCCTGGCGCCAGCAGCTTGTGGACAAGCATTCCACAGGGGGTGTGGGTGACAAGGTCAGCCTGGTCCTCGCACC
TGCCCTGGCGGCATGTGGCTGCAAGGTGCCAATGATCAGCGGACGTGGTCTGGGGCACACAGGAGGCACCTTGGA
TAAGCTGGAGTCTATTCCTGGATTCAATGTCATCCAGAGCCCAGAGCAGATGCAAGTGCTGCTGGACCAGGCGGG
CTGCTGTATCGTGGGTCAGAGTGAGCAGCTGGTTCCTGCGGACGGAATCCTATATGCAGCCAGAGATGTGACAGC
CACCGTGGACAGCCTGCCACTCATCACAGCCTCCATTCTCAGTAAGAAACTCGTGGAGGGGCTGTCCGCTCTGGT
GGTGGACGTTAAGTTCGGAGGGGCCGCCGTCTTCCCCAACCAGGAGCAGGCCCGGGAGCTGGCAAAGACGCTGGT
TGGCGTGGGAGCCAGCCTAGGGCTTCGGGTCGCGGCAGCGCTGACCGCCATGGACAAGCCCCTGGGTCGCTGCGT
GGGCCACGCCCTGGAGGTGGAGGAGGCGCTGCTCTGCATGGACGGCGCAGGCCCGCCAGACTTAAGGGACCTGGT
CACCACGCTCGGGGGCGCCCTGCTCTGGCTCAGCGGACACGCGGGGACTCAGGCTCAGGGCGCTGCCCGGGTGGC
CGCGGCGCTGGACGACGGCTCGGCCCTTGGCCGCTTCGAGCGGATGCTGGCGGCGCAGGGCGTGGATCCCGGTCT
GGCCCGAGCCCTGTGCTCGGGAAGTCCCGCAGAACGCCGGCAGCTGCTGCCTCGCGCCCGGGAGCAGGAGGAGCT
GCTGGCGCCCGCAGATGGCACCGTGGAGCTGGTCCGGGCGCTGCCGCTGGCGCTGGTGCTGCACGAGCTCGGGGC
CGGGCGCAGCCGCGCTGGGGAGCCGCTCCGCCTGGGGGTGGGCGCAGAGCTGCTGGTCGACGTGGGTCAGAGGCT
GCGCCGTGGGACCCCCTGGCTCCGCGTGCACCGGGACGGCCCCGCGCTCAGCGGCCCGCAGAGCCGCGCCCTGCA
GGAGGCGCTCGTACTCTCCGACCGCGCGCCATTCGCCGCCCCCTCGCCCTTCGCAGAGCTCGTTCTGCCGCCGCA
GCAA**TAA**AGCTCCTTTGCCGCGAAA

FIGURE 54

MAALMTPGTGAPPAPGDFSGEGSQGLPDPSPEPKQLPELIRMKRDGGRLSEADIRGFVAAVVNGSAQGAQIGAML
MAIRLRGMDLEETSVLTQALAQSGQQLEWPEAWRQQLVDKHSTGGVGDKVSLVLAPALAACGCKVPMISGRGLGH
TGGTLDKLESIPGFNVIQSPEQMQVLLDQAGCCIVGQSEQLVPADGILYAARDVTATVDSLPLITASILSKKLVE
GLSALVVDVKFGGAAVFPNQEQARELAKTLVGVGASLGLRVAAALTAMDKPLGRCVGHALEVEEALLCMDGAGPP
DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAAQGVDPGLARALCSGSPAERRQLLPRA
REQEELLAPADGTVELVRALPLALVLHELGAGRSRAGEPLRLGVGAELLVDVGQRLRRGTPWLRVHRDGPALSGP
QSRALQEALVLSDRAPFAAPSPFAELVLPPQQ

FIGURE 55

AAGATGGCGGCGCGGGGCCGCGCCCGCGCTCCCAGGCTCTCCTCCCCCAGCCTTCCTCCGGCTGGCAGCACGACT
CGCGTAGCCGTGCGCCGATTGCCTCTCGGCCTGGGCA**ATG**GTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGGAGGTTGCAGAGGA
AAGTGGTCGCTTATGGTCAGAGGAGCTCCTGCATGACCCGATGGGCCGGGACAGGGCAGCAGAAGAGGCCAATGC
GGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTGTGATTCCTGGGGAAGCTGAGGACAAGGT
GAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCTGGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCT
TTTCTCTCTGGATGGCGCTGGAGCACACTTCCCTGACAGAGAGGAGGAGTATTACACAGAGCCAGAAGTGGCGGA
ATCTGACGCAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAGGAGAG
AAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCTTATGGATTTTCTGAACCC
AAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGTGCCGCTTTTCTGCCAGTTTGGCCCCTCACTT
TAACTCTCTGCCCCGGGCATTTCCAGCTCTTCACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTAC
CAGGTTTGGCACCGTAGCTGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAC
AGATCGAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAATGTGGTGGT
AACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGACTGGTTGCTTGTATTTTCCTT
ATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAACTGAGAGTATTCGGTGGCTAATTCCAGGACAAGA
GCAGGAACATGTGGAG**TAG**TGATGGTCTGAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAG
TGCTACAGTTTCATACATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTG
AACAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGCAAAAATATTCA
AAAAAAAAAAAAAAAAAA

FIGURE 56

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEELLHDPMGRDRAAEEANAVLGLDTQGDHMV
MLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRCNVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNT
ESLKSPKVNCEERNITGLENFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHF
LALDASQHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETLKIFIFNQTGIEAKKNVVVTQADQIGPLPST
LIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

FIGURE 57

CCGTGGACATCTCAGGTCTTCAGGGTCTTCCATCTGGAACTATATAAAGTTCAGAAAAC**ATG**TCTCGAAGATATG
ACTCCAGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCTATTGGACATG
CAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTTTTGCTTGCAGCAGAGAGACGCAACATCCACAAGCTTC
TTGATGAAGTCTTTTTTTCTGAAAAAATTTATAAACTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATAACTT
CTGATGCTAATGTTCTGACTAATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATAC
CTTGTGAGCAGTTGGTTACAGCACTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAACGTCCCTTTG
GTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTCTATCAGAGTGACCCTAGTGGAAATT
ACGGGGGATGGAAGGCCACATGCATTGGAAATAATAGCGCTGCAGCTGTGTCAATGTTGAAACAAGACTATAAAG
AAGGAGAAATGACCTTGAAGTCAGCACTTGCTTTAGCTATCAAAGTACTAAATAAGACCATGGATGTTAGTAAAC
TCTCTGCTGAAAAAGTGGAAATTGCAACACTAACAAGAGAGAATGGAAAGACAGTAATCAGAGTTCTCAAACAAA
AAGAAGTGGAGCAGTTGATCAAAAAACATGAGGAAGAAGAAGCCAAAGCTGAGCGTGAGAAGAAAGAAAAAGAAC
AGAAAGAAAAGGATAAA**TAG**AATCAGAGATTTTATTACTCATTTGGGGCACCATTTCAGTGTAAAAGCAGTCCTA
CTCTTCCACACTAGGAAGGCTTTACTTTTTTTAACTGGTGCAGTGGGAAAATAGGACATTACATACTGAATTGGG
TCCTTGTCATTTCTGTCCAATTGAATACTTTATTGTAACGATGATGGTTACCCTTCATGGACGTCTTAATCTTCC
ACACACATCCCCTTTTTTTGGAATAAAA

FIGURE 58

MSRRYDSRTTIFSPEGRLYQVEYAMEAIGHAGTCLGILANDGVLLAAERRNIHKLLDEVFFSEKIYKLNEDMACS
VAGITSDANVLTNELRLIAQRYLLQYQEPIPCEQLVTALCDIKQAYTQFGGKRPFGVSLLYIGWDKHYGFQLYQS
DPSGNYGGWKATCIGNNSAAAVSMLKQDYKEGEMTLKSALALAIKVLNKTMDVSKLSAEKVEIATLTRENGKTVI
RVLKQKEVEQLIKKHEEEEAKAEREKKEKEQKEKDK

FIGURE 59

CTGAAGAACAAATCAGCCTGGTCACCAGCTTTTCGGAACAGCAGAGACACAGAGGGCAGTC**ATG**AGTGAGGTCAC
CAAGAATTCCCTGGAGAAAATCCTTCCACAGCTGAAATGCCATTTCACCTGGAACTTATTCAAGGAAGACAGTGT
CTCAAGGGATCTAGAAGATAGAGTGTGTAACCAGATTGAATTTTTAAACACTGAGTTCAAAGCTACAATGTACAA
CTTGTTGGCCTACATAAAACACCTAGATGGTAACAACGAGGCAGCCCTGGAATGCTTACGGCAAGCTGAAGAGTT
AATCCAGCAAGAACATGCTGACCAAGCAGAAATCAGAAGTCTAGTCACTTGGGGAAACTACGCCTGGGTCTACTA
TCACTTGGGCAGACTCTCAGATGCTCAGATTTATGTAGATAAGGTGAAACAAACCTGCAAGAAATTTTCAAATCC
ATACAGTATTGAGTATTCTGAACTTGACTGTGAGGAAGGGTGGACACAACTGAAGTGTGGAAGAAATGAAAGGGC
GAAGGTGTGTTTTGAGAAGGCTCTGGAAGAAAAGCCCAACAACCCAGAATTCTCCTCTGGACTGGCAATTGCGAT
GTACCATCTGGATAATCACCCAGAGAAACAGTTCTCTACTGATGTTTTGAAGCAGGCCATTGAGCTGAGTCCTGA
TAACCAATACGTCAAGGTTCTCTTGGGCCTGAAACTGCAGAAGATGAATAAAGAAGCTGAAGGAGAGCAGTTTGT
TGAAGAAGCCTTGGAAAAGTCTCCTTGCCAAACAGATGTCCTCCGCAGTGCAGCCAAATTTTACAGAAGAAAAGG
TGACCTAGACAAAGCTATTGAACTGTTTCAACGGGTGTTGGAATCCACACCAAACAATGGCTACCTCTATCACCA
GATTGGGTGCTGCTACAAGGCAAAAGTAAGACAAATGCAGAATACAGGAGAATCTGAAGCTAGTGGAAATAAAGA
GATGATTGAAGCACTAAAGCAATATGCTATGGACTATTCGAATAAAGCTCTTGAGAAGGGACTGAATCCTCTGAA
TGCATACTCCGATCTCGCTGAGTTCCTGGAGACGGAATGTTATCAGACACCATTCAATAAGGAAGTCCCTGATGC
TGAAAAGCAACAACAATCCCATCAGCGCTACTGCAACCTTCAGAAATATAATGGGAAGTCTGAAGACACTGCTGT
GCAACATGGTTTAGAGGGTTTGTCCATAAGCAAAAAATCAACTGACAAGGAAGAGATCAAAGACCAACCACAGAA
TGTATCTGAAAATCTGCTTCCACAAAATGCACCAAATTATTGGTATCTTCAAGGATTAATTCATAAGCAGAATGG
AGATCTGCTGCAAGCCAAATGTTATGAGAAGGAACTGGGCCGCCTGCTAAGGGATGCCCCTTCAGGCATAGGCAG
TATTTTCCTGTCAGCATCTGAGCTTGAGGATGGTAGTGAGGAAATGGGCCAGGGCGCAGTCAGCTCCAGTCCCAG
AGAGCTCCTCTCTAACTCAGAGCAACTGAAC**TGA**GACAGAGGAGGAAAACAGAGCATCAGAAGCCTGCAGTGGTG
GTTGTGACGGGTAGGAGGATAGGAAGACAGGGGGCCCAACCTGGGATTGCTGAGCAGGGAAGCTTTGCATGTTGC
TCTAAGGTACATTTTTAAAGAGTTGTTTTTTGGCCGGGCGCAGTGCTCATGCCTGTAATCCCAGAACTTTGGGAG
GCCGAGGTGGGCGGATCACGAGGTCTGGAGTTTGAGACCATCCTGGCTAACACAGTGAAATCCCGTCTCTACTAA
AAATACAAAAAATTAGCCAGGCGTGGTGGCTGGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAAT
GGCGTGAACCTGGAAGGAAGAGGTTGCAGAGAGCCAAGATTGCG

FIGURE 60

MSEVTKNSLEKILPQLKCHFTWNLFKEDSVSRDLEDRVCNQIEFLNTEFKATMYNLLAYIKHLDGNNEAALECLR
QAEELIQQEHADQAEIRSLVTWGNYAWVYYHLGRLSDAQIYVDKVKQTCKKFSNPYSIEYSELDCEEGWTQLKCG
RNERAKVCFEKALEEKPNNPEFSSGLAIAMYHLDNHPEKQFSTDVLKQAIELSPDNQYVKVLLGLKLQKMNKEAE
GEQFVEEALEKSPCQTDVLRSAAKFYRRKGDLDKAIELFQRVLESTPNNGYLYHQIGCCYKAKVRQMQNTGESEA
SGNKEMIEALKQYAMDYSNKALEKGLNPLNAYSDLAEFLETECYQTPFNKEVPDAEKQQQSHQRYCNLQKYNGKS
EDTAVQHGLEGLSISKKSTDKEEIKDQPQNVSENLLPQNAPNYWYLQGLIHKQNGDLLQAKCYEKELGRLLRDAP
SGIGSIFLSASELEDGSEEMGQGAVSSSPRELLSNSEQLN

FIGURE 61

CGGGATGCGGCGCGCCGCGCGTTGAACCTCCTTGGCCTGGGCGAAGCTGTGTGGACCAAGCAAGTCAGGAGTGTG
GCC**ATG**TTTTCTGAGCAGGCTGCCCAGAGGGCCCACACTCTACTGTCCCCACCATCAGCCAACAATGCCACCTTT
GCCCGGGTGCCAGTGGCAACCTACACCAACTCCTCACAACCCTTCCGGCTAGGAGAGCGCAGCTTTAGCCGGCAG
TATGCCCACATTTATGCCACCCGCCTCATCCAAATGAGACCCTTCCTGGAGAACCGGGCCCAGCAGCACTGGGGC
AGTGGAGTGGGAGTGAAGAAGCTGTGTGAACTGCAGCCTGAGGAGAAGTGCTGTGTGGTGGGCACTCTGTTCAAG
GCCATGCCGCTGCAGCCCTCCATCCTGCGGGAGGTCAGCGAGGAGCACAACCTGCTCCCCCAGCCTCCTCGGAGT
AAATACATACACCCAGATGACGAGCTGGTCTTGGAAGATGAACTGCAGCGTATCAAACTAAAAGGCACCATTGAC
GTGTCAAAGCTGGTTACGGGGACTGTCCTGGCTGTGTTTGGCTCCGTGAGAGACGACGGGAAGTTTCTGGTGGAG
GACTATTGCTTTGCTGACCTTGCTCCCCAGAAGCCCGCACCCCCACTTGACACAGATAGGTTTGTGCTACTGGTG
TCCGGCCTGGGCCTGGGTGGCGGTGGAGGCGAGAGCCTGCTGGGCACCCAGCTGCTGGTGGATGTGGTGACGGGG
CAGCTTGGGGACGAAGGGGAGCAGTGCAGCGCCGCCCACGTCTCCCGGGTTATCCTCGCTGGCAACCTCCTCAGC
CACAGCACCCAGAGCAGGGATTCTATCAATAAGGCCAAATACCTCACCAAGAAAACCCAGGCAGCCAGCGTGGAG
GCTGTTAAGATGCTGGATGAGATCCTCCTGCAGCTGAGCGCCTCAGTGCCCGTGGACGTGATGCCAGGCGAGTTT
GATCCCACCAATTACACGCTCCCCCAGCAGCCCCTCCACCCCTGCATGTTCCCGCTGGCCACTGCCTACTCCACG
CTCCAGCTGGTCACCAACCCCTACCAGGCCACCATTGATGGAGTCAGATTTTTGGGGACATCAGGACAGAACGTG
AGTGACATTTTCCGATACAGCAGCATGGAGGATCACTTGGAGATCCTGGAGTGGACCCTGCGGGTCCGTCACATC
AGCCCCACAGCCCCGGACACTCTAGGTTGTTACCCCTTCTACAAAACTGACCCGTTCATCTTCCCAGAGTGCCCG
CATGTCTACTTTTGTGGCAACACCCCCAGCTTTGGCTCCAAAATCATCCGAGGTCCTGAGGACCAGACAGTGCTG
TTGGTGACTGTCCCTGACTTCAGTGCCACGCAGACCGCCTGCCTTGTGAACCTGCGCAGCCTGGCCTGCCAGCCC
ATCAGCTTCTCGGGCTTCGGGGCAGAGGACGATGACCTGGGAGGCCTGGGGCTGGGCCCC**TGA**CTCAAAAAAGTG
GTTTTGACCAGAGAGGCCCAGATGGAGGCTGTTCATTCCCTGCAGTGTCGGCATTGTAAATAAAGCCTGGCACTT
GCTGATGCG

FIGURE 62

MFSEQAAQRAHTLLSPPSANNATFARVPVATYTNSSQPFRLGERSFSRQYAHIYATRLIQMRPFLENRAQQHWGS
GVGVKKLCELQPEEKCCVVGTLFKAMPLQPSILREVSEEHNLLPQPPRSKYIHPDDELVLEDELQRIKLKGTIDV
SKLVTGTVLAVFGSVRDDGKFLVEDYCFADLAPQKPAPPLDTDRFVLLVSGLGLGGGGGESLLGTQLLVDVVTGQ
LGDEGEQCSAAHVSRVILAGNLLSHSTQSRDSINKAKYLTKKTQAASVEAVKMLDEILLQLSASVPVDVMPGEFD
PTNYTLPQQPLHPCMFPLATAYSTLQLVTNPYQATIDGVRFLGTSGQNVSDIFRYSSMEDHLEILEWTLRVRHIS
PTAPDTLGCYPFYKTDPFIFPECPHVYFCGNTPSFGSKIIRGPEDQTVLLVTVPDFSATQTACLVNLRSLACQPI
SFSGFGAEDDDLGGLGLGP

FIGURE 63

CGGGCGTCCGCGGTGGCTGCAGTCCCGTCGGTCTCCCTGCTGTCCGGCGCGAGCTCTTCGAGTCTTGCTTGGGAT
GTTTCAGCAGCCCCTGAGAAGGAAGAGGAGGAAGCTGAGGGCCCGCTGAGGGCGCAGGACCTGAGGGAGTCCTAC
ATCCAGCTCGTCCAGGGTGTGCAGGAGTGGCAGGATGGTTGC**ATG**TACCAGGGGGAGTTTGGGTTGAACATGAAG
CTTGGATATGGCAAATTCTCTTGGCCCACAGGCGAGTCATACCATGGGCAGTTTTACCGGGACCACTGCCATGGC
CTGGGTACCTACATGTGGCCAGATGGCTCCAGTTTCACGGGCACATTTTACCTCAGCCACCGAGAAGGCTACGGC
ACCATGTACATGAAGACACGGCTTTTCCAGGGGCTATACAAAGCGGACCAGCGGTTTGGGCCAGGTGTCGAGACC
TACCCCGATGGCAGCCAGGACGTGGGGCTGTGGTTCCGAGAGCAGCTCATCAAGCTGTGCACCCAGATCCCCAGT
GGCTTCTCCCTCCTCAGATACCCTGAGTTCTCCAGCTTCATCACCCACAGCCCTGCCAGGATCAGCCTCTCAGAA
GAGGAGAAAACGGAGTGGGGACTGCAGGAGGGACAGGATCCCTTTTTCTATGACTATAAGCGGTTTCTTCTGAAT
GACAACCTAACGCTGCCTCCAGAAATGTATGTCTACTCGACCAACAGTGACCACCTGCCCATGACAAGCTCTTTC
CGCAAAGAGCTGGACGCCCGCATCTTCCTCAATGAAATTCCTCCGTTCGTTGAGGATGGAGAACCATGGTTCATA
ATCAATGAGACCCCTTTGTTGGTCAAAATCCAGAAGCAAACTTACAAGTTCAGGAACAAGCCAGCTCACACCAGC
TGGAACATGGGCGCCATCCTGGAGGGGAAGCGCAGTGGCTTTGCACCCTGTGGGCCCAAAGAGCAACTTTCCATG
GAGATGATCCTAAAGGCTGAGGAAGGGAACCACGAATGGATTTGTAGGATCCTGAAGGACAACTTTGCTAGTGCT
GACGTGGCGGACGCAAAGGGCTACACTGTGCTTGCTGCGGCTGCTACTCACTGCCACAACGACATTGTCAACCTT
CTCCTGGACTGTGGGGCCGACGTGAACAAGTGCTCAGATGAGGGTCTCACGGCACTCAGCATGTGTTTCCTCCTC
CACTACCCCGCCCAGTCCTTCAAGCCCAATGTTGCTGAACGGACCATACCTGAGCCCCAGGAACCTCCAAAATTC
CCAGTTGTTCCAATCCTTTCATCATCATTTATGGACACAAACCTGGAGTCTCTGTACTATGAGGTGAACGTGCCT
TCCCAGGGTAGCTATGAGCTGAGGCCACCGCCAGCACCACTGCTCCTGCCACGCGTCTCAGGCAGCCACGAGGGC
GGCCACTTCCAGGACACCGGGCAGTGTGGGGGGTCCATGGACCACAGGAGCAGCTCTCTGAAGGGGGACTCCCCG
TTGGTGAAGGGCAGCCTTGGCCATGTGGAAAGCGGGCTTGAGGACGTGTTGGGAAACACAGACCGGGGCAGTCTG
TGCAGTGCTGAGACGAAATTTGAGTCCAACGTGTGTGTGTGCGACTTCTCCATCGAGCTCTCGCAGGCCATGCTG
GAGAGAAGCGCCCAGTCCCACAGCTTGCTGAAGATGGCCTCGCCCTCACCGTGCACCAGCAGCTTCGACAAAGGG
ACCATGCGGAGGATGGCGCTGTCCATGATCGAGCGGAGGAAGCGCTGGCGGACCATCAAGCTGCTGCTGCGCCGG
GGCGCGGACCCCAACCTGTGCTGCGTGCCCATGCAGGTCCTGTTCCTTGCTGTGAAGGCCGGGGACGTGGATGGG
GTGAGGCTGCTGCTGGAGCACGGGGCGAGGACCGACATCTGCTTTCCGCCGCAGCTGAGCACCCTGACACCACTC
CACATCGCTGCCGCCCTTCCTGGGGAGGAGGGGGTACAGATTGTGGAGCTGCTGTTGCATGCCATCACCGATGTG
GACGCCAAGGCATCCGACGAGGACGACACTTACAAGCCCGGCAAGCTGGACCTGCTGCCCTCAAGTCTGAAGCTC
AGCAATGAGCCAGGCCCTCCCCAAGCCTACTACAGCACGGACACAGCCCTCCCGGAGGAGGGGGGCAGGACGGCT
CTGCACATGGCCTGCGAGCGGGAGGATGACAACAAGTGTGCCAGGGACATAGTCCGGCTCCTTCTATCCCACGGA
GCAAATCCTAACCTGCTGTGGAGTGGCCACTCCCCGCTCTCCCTGTCCATTGCCAGTGGGAATGAGCTGGTTGTG
AAGGAGCTCCTGACCCAGGGAGCTGACCCCAACCTGCCCCTGACCAAAGGCTTGGGCAGTGCCCTGTGTGTTGCC
TGTGACCTGACCTACGAGCACCAGAGGAACATGGACAGCAAGCTGGCCCTGATTGACCGACTCATCAGTCACGGG
GCCGACATCCTGAAGCCTGTAATGCTCAGGCAGGGAGAAAAGGAGGCAGTGGGCACAGCCGTGGACTATGGCTAC
TTCAGATTCTTCCAGGACCGGAGGATTGCCCGCTGCCCCTTCCACACGCTGATGCCAGCAGAGCGCGAGACGTTC
CTGGCGCGGAAGCGGCTCCTGGAGTACATGGGCTTGCAGCTACGGCAGGCTGTCTTTGCCAAGGAGAGCCAGTGG
GACCCCACGTGGCTGTACCTGTGCAAGAGAGCGGAGCTGATCCCCAGCCACAGGATGAAGAAGAAGGGCCCCCAGC
CTGCCCAGGGGCCTGGATGTGAAGGAGCAGGGGCAAATTCCCTTCTTCAAGTTCTGCTACCAGTGTGGCCGCTCC
ATCGGGGTCCGCCTCTTGCCCTGCCCTCGCTGCTACGGGATCCTGACCTGCAGCAAGTACTGCAAGACCAAGGCC
TGGACCGAGTTCCACAAGAAGGACTGCGGGGACCTGGTGGCCATCGTGACACAACTGGAGCAAGTTTCCAGGAGG
AGAGAAGAATTCCAG**TGA**AGCAGCAGCTGCACGTCCGAGGCTTGGGGAGGACCCAGGACTGTGTGGGTTTCTTAC
CTGCCTGAGCCACCTCAGGGAATCTTCCAGCCTAATGCAGGCATTTCTGCACCTTTGGGGTCATGCTTTGTAGCA
GTGTCTCCCTTGCGACCTCGCAATAAATTGGCCCCACGGGGTGATTTTGACAGTCAAAAAAAAAA

FIGURE 64

MYQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGYGTMYMKTRLFQGLYK
ADQRFGPGVETYPDGSQDVGLWFREQLIKLCTQIPSGFSLLRYPEFSSFITHSPARISLSEEEKTEWGLQEGQDP
FFYDYKRFLLNDNLTLPPEMYVYSTNSDHLPMTSSFRKELDARIFLNEIPPFVEDGEPWFIINETPLLVKIQKQT
YKFRNKPAHTSWNMGAILEGKRSGFAPCGPKEQLSMEMILKAEEGNHEWICRILKDNFASADVADAKGYTVLAAA
ATHCHNDIVNLLLDCGADVNKCSDEGLTALSMCFLLHYPAQSFKPNVAERTIPEPQEPPKFPVVPILSSSFMDTN
LESLYYEVNVPSQGSYELRPPPAPLLLPRVSGSHEGGHFQDTGQCGGSMDHRSSSLKGDSPLVKGSLGHVESGLE
DVLGNTDRGSLCSAETKFESNVCVCDFSIELSQAMLERSAQSHSLLKMASPSPCTSSFDKGTMRRMALSMIERRK
RWRTIKLLLRRGADPNLCCVPMQVLFLAVKAGDVDGVRLLLEHGARTDICFPPQLSTLTPLHIAAALPGEEGVQI
VELLLHAITDVDAKASDEDDTYKPGKLDLLPSSLKLSNEPGPPQAYYSTDTALPEEGGRTALHMACEREDDNKCA
RDIVRLLLSHGANPNLLWSGHSPLSLSIASGNELVVKELLTQGADPNLPLTKGLGSALCVACDLTYEHQRNMDSK
LALIDRLISHGADILKPVMLRQGEKEAVGTAVDYGYFRFFQDRRIARCPFHTLMPAERETFLARKRLLEYMGLQL
RQAVFAKESQWDPTWLYLCKRAELIPSHRMKKKGPSLPRGLDVKEQGQIPFFKFCYQCGRSIGVRLLPCPRCYGI
LTCSKYCKTKAWTEFHKKDCGDLVAIVTQLEQVSRRREEFQ

FIGURE 65

GGAGCCCATGATTTCCTGGAAGAGCCCTAGAGCTTTGCTTTTTCTCTCCTGCAGCACTTAACCGAAACCAGTTTT
GCAATCAATTCCTGTTCAAAGGCSACCCTACTCTTCCTATCCGTCTTTCTCCAGCCCAGACACTCACAGCCCCCT
GCCAGACCAGGGGACCTCGGAGAGGCAAGGACAGAGGTTCAGGATCTTCCTCTCCCTCGGGACCCAAGGSCACAA
AGGAGAGCTCCGTGGAGAGAAGAAAATCATTTGACTCCTGGGGACACAGATTTGCTGCCACAGAGGCTG**ATG**GAC
AACCAGGCGGAGAGAGAAAGTGAGGCTGGTGTTGGTTTGCAAAGGGATGAGGATGACGCTCCTCTGTGTGAAGAC
GTGGAGCTACAAGACGGAGATCTGTCCCCCGAAGAAAAAATATTTTTGAGAGAATTTCCCAGATTGAAAGAAGAT
CTGAAAGGGAACATTGACAAGCTCCGTGCCCTCGCAGACGATATTGACAAAACCCACAAGAAATTCACCAAGGCT
AACATGGTGGCCACCTCTACTGCTGTCATCTCTGGAGTGATGAGCCTCCTGGGTTTAGCCCTTGCCCCAGCAACA
GGAGGAGGAAGCCTGCTGCTCTCCACCGCTGGTCAAGGTTTGGCAACAGCAGCTGGGGTCACCAGCATCGTGAGT
GGTACGTTGGAACGCTCCAAAAATAAAGAAGCCCAAGCACGGGCGGAAGACATACTGCCCACCTACGACCAAGAG
GACAGGGAGGATGAGGAAGAGAAGGCAGACTATGTCACAGCTGCTGGAAAGATTATCTATAATCTTAGAAACACC
TTGAAGTATGCCAAGAAAAACGTCCGTGCATTTTGGAAACTCAGAGCCAACCCACGCTTGGCCAATGCTACCAAG
CGTCTTCTGACCACTGGCCAAGTCTCCTCCCGGAGCCGCGTGCAGGTGCAAAAGGCCTTTGCGGGAACAACACTG
GCGATGACCAAAAATGCTCGCGTGCTGGGAGGTGTGATGTCCGCCTTCTCCCTTGGCTATGACTTGGCCACTCTC
TCAAAGGAATGGAAGCACCTGAAGGAAGGAGCAAGGACAAAGTTTGCGGAAGAGTTGAGAGCCAAGGCCTTGGAG
CTGGAGAGGAAACTCACAGAACTCACCCAGCTCTACAAGAGCTTGCAGCAGAAAGTGAGGTCAAGGGCCAGAGGG
GTGGGGAAGGATTTAACTGGGACCTGCGAAACCGAGGCTTACTGGAAGGAGTTAAGGGAGCATGTGTGGATGTGG
CTGTGGCTGTGTGTGTGTGTCTGTGTGTCTGTGTGTATGTACAGTTTACA**TGA**ATGTTCCTCAGGACATGGCATACA
ATGGCCTTGGAGGTCCAAATAATATCAAGTACATCTTGGAGATGAGGGTGCCTGTCCTGGACAGACCTCGGCATG
CCTTCTGTTTCTCCTTCAATGCTCCTTAAGGCCTATGTGCTGGGAAAAGGGTCTTCCCTGTTTGTTTGTTTGTTT
GTTTGTTTGTTTGTTTTGAGACTCCAGTCTGGGTGTCAGAATGAGACCCCATCTCAAAAAAAAAAAAAAAAAAAA
AAAAGAAGAAGAATACAGTCATGTATCTCTTGGTGACAGGGACGCATTCTGATAAATGTGTCATTAGGCAATTGC
ATTGTAGTGTGATTATCACAGATTGTACTTATACAAAACTTAGATGGCATAGCCTACTGCATACCTAGGCTATAT
GGGAGAGCCTATTGCTCCCAGGCTACGCACCTGTACAGCATGTGACTACTGAATACTATAGGCAATTGCAGCACA
ATGGGAAATATTTGTGTATCTAAACATATGTAAACAGAGAAAAAGGAAAGTAAAAATATGGCATAAAAGATAAGA
ATTGGCTCTCCTGTACAGGGCACTTACTACGAATGGAGCTTGCAGGGCTGAGAGTTGCTCCAGATGAGTCAGTGA
GTGGTGAATGAATGTGAAGGCCTAGGGCATTACTGTATACTACTGTAGGCTTTATAAACACAGCACACTTAGGGT
ACACAAAATGCATATTAAAACATTTTCTTCCTTCAGTATATTAGGCAATAGGAATTTTTCAAGTCCACTATAAAT
CTTATCAAACCATGGTTGTATATGCAGTTGACCGAAACATTGTTATTGGACACATAACTATAGTTGAAAGAATAA
GCAAAAAGTCTATCTAGGTGTGCTGTCTTGAGCAACTTTTAATTATTCTCCTGTCCTGCAATATGAGTTAATCTT
CTCTGATCGATGTAGATTCCAGGAAGGGGTGTCCAGGACAATTACCTTCCTTCTGGAGAAACTTCCCTTAATCAA
ATAAGAGAACTTCAAAGAAAATCCCTCCCTGTGCTTTGGAAGGGAAGGGAGGTGGGCAGCAGTGGGTCAGAGATA
GACCTTTGTTCTCTTATTTCTGAGGCCCTTCAGTCTCCTTTATTCAAAGCACTCAGCATGCCAAAGCACCCTATT
TTAGGGTATCTTTTTCTGAGCCCTAAACACTGTGTTGGGGATGTCAACTGTGACAGGAAAATATCTTGGGGCCCC
AGAATCACTAAGGAAAACTCAAGCTTAGGGAAACTTCTTAGGGCAAACCCACCTCCCACTCTATTCAAAGTTATC
TCTCTGCTCACTGAGATAGATACATATCTGATTGCCTCCTTTGGAAAGGCTAATCAGAAACTCAAAAGAATGCAA
CTGTTTGTGTCTCACCTATCTGTGACCTGGAAGCTCCCTCCCCACTGAACCAATGTTCTTCTTACATATATTGAT
TAATGTCTTATGTCTCCCTAAAATGTATAAAACCAAGGTATGCCCCAACCATCTTGGCCACATGTCATCAGGACT
TCCTGAGTCTGTGTCACAGTGTGTCCTCAACCTTGGCAAAATAAACTTTCTAAATTAACTGAGACAAAAAAAAAA
AAAAA

FIGURE 66

MDNQAERESEAGVGLQRDEDDAPLCEDVELQDGDLSPEEKIFLREFPRLKEDLKGNIDKLRALADDIDKTHKKFT
KANMVATSTAVISGVMSLLGLALAPATGGGSLLLSTAGQGLATAAGVTSIVSGTLERSKNKEAQARAEDILPTYD
QEDREDEEEKADYVTAAGKIIYNLRNTLKYAKKNVRAFWKLRANPRLANATKRLLTTGQVSSRSRVQVQKAFAGT
TLAMTKNARVLGGVMSAFSLGYDLATLSKEWKHLKEGARTKFAEELRAKALELERKLTELTQLYKSLQQKVRSRA
RGVGKDLTGTCETEAYWKELREHVWMWLWLCVCLCVCVYVQFT

FIGURE 67A

TGCAGAGAACAGAGAAAGGACATCTGCGAGGAAAGTTCCCTGATGGCTGTCAACAAAGTGCCACGTCTCTATGGC
TGTGTACGCTGAGCACACGATTTTATCGCGCCTATCATATCTTGGTGCATAAACGCACCTCACCTCGGTCAACCC
TTGCTCCGTCTTATGAGACAGGCTTTATTATCCGCATTTTATATGAGGGGAATCTGACGGTGGAGAGAGAATTAT
CTTGCTCAAGGCGACACAGCAGAGCCCACAGGTGGCAGAATCCCACCCGAGCCCGCTTCGACCCGCGGGGTGGAA
ACCACGGGCGCCCGCCCGGCTGCGCTTCCAGAGCTGAACTGAGAAGCGAGTCCTCTCCGCCCTGCGGCCACCGCC
CAGCCCCGACCCCCGCCCCGGCCCGATCCTCACTCGCCGCCAGCTCCCCGCGCCCACCCCGGAGTTGGTGGCGCA
GAGGCGGGAGGCGGAGGCGGGAGGGCGGGCGCTGGCACCGGGAACGCCCGAGCGCCGGCAGAGAGCGCGGAGAGC
GCGACACGTGCGGCCCAGAGCACCGGGGCCACCCGGTCCCCGCAGGCCCGGGACCGCGCCCGCTGGCAGGCGACA
CGTGGAAGAATACGGAGTTCTATACCAGAGTTGATTGTTG**ATG**GCACATACTTTTAGAGGATGCTCATTGGCATT
TATGTTTATAATCACGTGGCTGTTGATTAAAGCAAAAATAGATGCGTGCAAGAGAGGCGATGTGACTGTGAAGCC
TTCCCATGTAATTTTACTTGGATCCACTGTCAATATTACATGCTCTTTGAAGCCCAGACAAGGCTGCTTTCACTA
TTCCAGACGTAACAAGTTAATCCTGTACAAGTTTGACAGAAGAATCAATTTTCACCATGGCCACTCCCTCAATTC
TCAAGTCACAGGTCTTCCCCTTGGTACAACCTTGTTTGTCTGCAAACTGGCCTGTATCAATAGTGATGAAATTCA
AATATGTGGAGCAGAGATCTTCGTTGGTGTTGCTCCAGAACAGCCTCAAAATTTATCCTGCATACAGAAGGGAGA
ACAGGGGACTGTGGCCTGCACCTGGGAAAGAGGACGAGACACCCACTTATACACTGAGTATACTCTACAGCTAAG
TGGACCAAAAAATTTAACCTGGCAGAAGCAATGTAAAGACATTTATTGTGACTATTTGGACTTTGGAATCAACCT
CACCCCTGAATCACCTGAATCCAATTTCACAGCCAAGGTTACTGCTGTCAATAGTCTTGGAAGCTCCTCTTCACT
TCCATCCACATTCACATTCTTGGACATAGTGAGGCCTCTTCCTCCGTGGGACATTAGAATCAAATTTCAAAAGGC
TTCCGTGAGCAGATGTACCCTTTATTGGAGAGATGAGGGACTGGTACTGCTTAATCGACTCAGATATCGGCCCAG
TAACAGCAGGCTCTGGAATATGGTTAATGTTACAAAGGCCAAAGGAAGACATGATTTGCTGGATCTGAAACCATT
TACAGAATATGAATTTCAGATTTCCTCTAAGCTACATCTTTATAAGGGAAGTTGGAGTGATTGGAGTGAATCATT
GAGAGCACAAACACCAGAAGAAGAGCCTACTGGGATGTTAGATGTCTGGTACATGAAACGGCACATTGACTACAG
TAGACAACAGATTTCTCTTTTCTGGAAGAATCTGAGTGTCTCAGAGGCAAGAGGAAAAATTCTCCACTATCAGGT
GACCTTGCAGGAGCTGACAGGAGGGAAAGCCATGACACAGAACATCACAGGACACACCTCCTGGACCACAGTCAT
TCCTAGAACCGGAAATTGGGCTGTGGCTGTGTCTGCAGCAAATTCAAAAGGCAGTTCTCTGCCCACTCGTATTAA
CATAATGAACCTGTGTGAGGCAGGGTTGCTGGCTCCTCGCCAGGTCTCTGCAAACTCAGAGGGCATGGACAACAT
TCTGGTGACTTGGCAGCCTCCCAGGAAAGATCCCTCTGCTGTTCAGGAGTACGTGGTGGAATGGAGAGAGCTCCA
TCCAGGGGGTGACACACAGGTCCCTCTAAACTGGCTACGGAGTCGACCCTACAATGTGTCTGCTCTGATTTCAGA
GAACATAAAATCCTACATCTGTTATGAAATCCGTGTGTATGCACTCTCAGGGGATCAAGGAGGATGCAGCTCCAT
CCTGGGTAACTCTAAGCACAAAGCACCACTGAGTGGCCCCCACATTAATGCCATCACAGAGGAAAAGGGGAGCAT
TTTAATTTCATGGAACAGCATTCCAGTCCAGGAGCAAATGGGCTGCCTCCTCCATTATAGGATATACTGGAAGGA
ACGGGACTCCAACTCCCAGCCTCAGCTCTGTGAAATTCCCTACAGAGTCTCCCAAAATTCACATCCAATAAACAG
CCTGCAGCCCCGAGTGACATATGTCCTGTGGATGACAGCTCTGACAGCTGCTGGTGAAAGTTCCCACGGAAATGA
GAGGGAATTTTGTCTGCAAGGTAAAGCCAATTGGATGGCGTTTGTGGCACCAAGCATTTGCATTGCTATCATCAT
GGTGGGCATTTTCTCAACGCATTACTTCCAGCAAAAGGTGTTTGTTCTCCTAGCAGCCCTCAGACCTCAGTGGTG
TAGCAGAGAAATTCCAGATCCAGCAAATAGCACTTGCGCTAAGAAATATCCCATTGCAGAGGAGAAGACACAGCT
GCCCTTGGACAGGCTCCTGATAGACTGGCCCACGCCTGAAGATCCTGAACCGCTGGTCATCAGTGAAGTCCTTCA
TCAAGTGACCCCAGTTTTCAGACATCCCCCCTGCTCCAACTGGCCACAAAGGGAAAAAGGAATCCAAGGTCATCA
GGCCTCTGAGAAAGACATGATGCACAGTGCCTCAAGCCCACCACCTCCAAGAGCTCTCCAAGCTGAGAGCAGACA
ACTGGTGGATCTGTACAAGGTGCTGGAGAGCAGGGGCTCCGACCCAAAGCCAGAAAACCCAGCCTGTCCCTGGAC
GGTGCTCCCAGCAGGTGACCTTCCCACCCATGATGGCTACTTACCCTCCAACATAGATGACCTCCCCTCACATGA
GGCACCTCTCGCTGACTCTCTGGAAGAACTGGAGCCTCAGCACATCTCCCTTTCTGTTTTCCCCTCAAGTTCTCT
TCACCCACTCACCTTCTCCTGTGGTGATAAGCTGACTCTGGATCAGTTAAAGATGAGGTGTGACTCCCTCATGCT
C**TGA**GTGGTGAGGCTTCAAGCCTTAAAGTCAGTGTGCCCTCAACCAGCACAGCCTGCCCCAATTCCCCCAGCCCC
TGCTCCAGCAGCTGTCATCTCTGGGTGCCACCATCGGTCTGGCTGCAGCTAGAGGACAGGCAAGCCAGCTCTGGG
GGAGTCTTAGGAACTGGGAGTTGGTCTTCACTCAGATGCCTCATCTTGCCTTTCCCAGGGCCTTAAAATTACATC
CTTCACTGTGTGGACCTAGAGACTCCAACTTGAATTCCTAGTAACTTTCTTGGTATGCTGGCCAGAAAGGGAAAT
GAGGAGGAGAGTAGAAACCACAGCTCTTAGTAGTAATGGCATACAGTCTAGAGGACCATTCATGCAATGACTATT

FIGURE 67B

TCTAAAGCACCTGCTACACAGCAGGCTGTACACAGCAGATCAGTACTGTTCAACAGAACTTCCTGAGATGATGGA
AATGTTCTACCTCTGCACTCACTGTCCAGTACATTAGACACTAGGCACATTGGCTGTTAATCACTTGGAATGTGT
TTAGCTTGACTGAGGAATTAAATTTTGATTGTAAATTTAAATCGCCACACATGGCTAGTGGCTACTGTATTGGAG
TGCACAGCTCTAGATGGCTCCTAGATTATTGAGAGCCTCCAAAACAAATCAACCTAGTTCTATAGATGAAGACAT
AAAAGACACTGGTAAACACCAATGTAAAAGGGCCCCCAAGGTGGTCATGACTGGTCTCATTTGCAGAAGTCTAAG
AATGTACCTTTTTCTGGCCGGGCGTGGTAGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGA

FIGURE 68

MAHTFRGCSLAFMFIITWLLIKAKIDACKRGDVTVKPSHVILLGSTVNITCSLKPRQGCFHYSRRNKLILYKFDR
RINFHHGHSLNSQVTGLPLGTTLFVCKLACINSDEIQICGAEIFVGVAPEQPQNLSCIQKGEQGTVACTWERGRD
THLYTEYTLQLSGPKNLTWQKQCKDIYCDYLDFGINLTPESPESNFTAKVTAVNSLGSSSSLPSTFTFLDIVRPL
PPWDIRIKFQKASVSRCTLYWRDEGLVLLNRLRYRPSNSRLWNMVNVTKAKGRHDLLDLKPFTEYEFQISSKLHL
YKGSWSDWSESLRAQTPEEEPTGMLDVWYMKRHIDYSRQQISLFWKNLSVSEARGKILHYQVTLQELTGGKAMTQ
NITGHTSWTTVIPRTGNWAVAVSAANSKGSSLPTRINIMNLCEAGLLAPRQVSANSEGMDNILVTWQPPRKDPSA
VQEYVVEWRELHPGGDTQVPLNWLRSRPYNVSALISENIKSYICYEIRVYALSGDQGGCSSILGNSKHKAPLSGP
HINAITEEKGSILISWNSIPVQEQMGCLLHYRIYWKERDSNSQPQLCEIPYRVSQNSHPINSLQPRVTYVLWMTA
LTAAGESSHGNEREFCLQGKANWMAFVAPSICIAIIMVGIFSTHYFQQKVFVLLAALRPQWCSREIPDPANSTCA
KKYPIAEEKTQLPLDRLLIDWPTPEDPEPLVISEVLHQVTPVFRHPPCSNWPQREKGIQGHQASEKDMMHSASSP
PPPRALQAESRQLVDLYKVLESRGSDPKPENPACPWTVLPAGDLPTHDGYLPSNIDDLPSHEAPLADSLEELEPQ
HISLSVFPSSSLHPLTFSCGDKLTLDQLKMRCDSLML

FIGURE 69

AAGACTGTAGGAGCATCTGGTGGGAGGTGGTGGAGGGAGAACTGTGGGTTTGGAAGCTGCGCCCTCCCCCCAGCC
ATGCGTTGGAACAGGAACAGTTACATGGAGAACAACCTTACCTTGTCCGACACCCTCAGATCTTTGTCCCAGGCC
AAGAATCTTTTAATGACAGGATCCTCTGTGATTAGAGAGCAGATGTCAGTG**TGA**GAAGCAGGACAGGGTTTCCGT
GGGAGCAGCAGGGCAGGGAGGAGAAGTGTGCCTCCCGGGGGGAAGTCTCAGGATTGTGGCCGCGGGTGAGGTGGA
TGGGAGAGGGGAGAATGACTTTCACTGGGCAAGGGAGAGAGGCTCCTGCTCTGAGACTCCCCTGAGAAGAGGCCG
AAGGAGGCCCTGGGTGTGAGAATCTACAGGATGTAGAGCTGGGAATCAGCCAGGACCCCCTCCAGCAGACACGGA
GGGACCACTGCAGAGTCATAAAGGAATTCCCATCATTTCCTCATGAGACAGTCACATCAGGGTGTGACCATGGCC
TTGGTATCCCCCACTATGGATGGAGACACTTAGGTTTAGAAAAGTCAGTAAGAGACATTAAGTTTCAGAGGGCAC
AGCTGAAACCACTTTCTTTGTTTATTGATTTTGTTTTTCTTTATTTGATTTTTATTTT

FIGURE 70

KTVGASGGRWWRENCGFGSCALPPAMRWNRNSYMENNLTLSDTLRSLSQAKNLLMTGSSVIREQMSV

FIGURE 71

ATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAATTTTCCTCATGAAGGATTACATGGGC
CGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAAACTAAATCTGGTTGCCCCA
GATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTAC
AAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGAT
CCTTCAAATAACTTCAGGGAAGAACCAGTGAAGAAATCCATTCAGGAATCAGAAGCTTTTTTGCCTCAGAGCATA
CCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATTGGCAATGAGACA
GAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAATTCTTGCATCTCAGTATGCATGGTATA
TCCCAGATTCTTGGCCAATTTGCCTGTATGCCCGAGCACCGAGACTACGACAGCTTTGTGTGTGTCCTGGTGAGC
CGAGGAGGCTCCCAGAGTGTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATG
TTCATGGGAGATTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTATTCAGAACTATGTGGTGTCAGAC
GGCCAGCTGGAGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATGAAGAATGTGGAATTCAAGGCTCAGAAG
CGAGGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAG
CAGTCTCACAGCTCACCGTCCCTGTACCTGCAGTGCCTCTCCCAGAAACTGAGACAAGAAAGGGGGACAATTCCC
GGAAGTGGAATTACAGAGTCAAAGGACATGCATTTTTCAAGCCTCGGATGCATCTTACTAGATGTCCTA**TAG**

FIGURE 72

MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSFLDLVVELEKLNLVAPDQLDLLEKCLKNIHRIDLKTKIQKY
KQSVQGAGTSYRNVLQAAIQKSLKDPSNNFREEPVKKSIQESEAFLPQSIPEERYKMKSKPLGICLIIDCIGNET
ELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRRM
FMGDSCPYLAGKPKMFFIQNYVVSDGQLEDSSLLEVDGPAMKNVEFKAQKRGLCTVHREADFFWSLCTADMSLLE
QSHSSPSLYLQCLSQKLRQERGTIPGSGITESKDMHFSSLGCILLDVL

FIGURE 73

TGAAGATCAGCTATTAGAAGAGAAAGATCAGTTAAGTCCTTTGGACCTGATCAGCTTGATACAAGAACTACTGAT
TTCAACTTCTTTGGCTTAATTCTCTCGGAAACG**ATG**AAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATC
GTTTTGGGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGAAAACCTTAAGAAATATTTTAAT
GCAGGTCATTCAGATGTAGCGGATAATGGAACTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGTGAC
AGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACTTTTTAAAAACTTTAAAGATGACCAGAGCATC
CAAAAGAGTGTGGAGACCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAGAAACGAGATGAC
TTCGAAAAGCTGACTAATTATTCGGTAACTGACTTGAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTG
ATGGCTGAACTGTCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGATGCTGTTTCAAGGTCGAAGAGCA
TCCCAG**TAA**TGGTTGTCCTGCCTGCAATATTTGAATTTTAAATCTAAATCTATTTATTAATATTTAACATTATTT
ATATGGGGAATATATTTTTAGACTCATCAATCAAATAAGTATTTATAATAGCAACTTTTGTGTAATGAAAATGAA
TATCTATTAATATATGTATTATTTATAATTCCTATATCCTGTGACTGTCTCACTTAATCCTTTGTTTTCTGACTA
ATTAGGCAAGGCTATGTGATTACAAGGCTTTATCTCAGGGGCCAACTAGGCAGCCAACCTAAGCAAGATCCCATG
GGTTGTGTGTTTATTTCACTTGATGATACAATGAACACTTATAAGTGAAGTGATACTATCCAGTTACTGCCGGTT
TGAAAATATGCCTGCAATCTGAGCCAGTGCTTTAATGGCATGTCAGACAGAACTTGAATGTGTCAGGTGACCCTG
ATGAAAACATAGCATCTCAGGAGATTTCATGCCTGGTGCTTCCAAATATTGTTGACAACTGTGACTGTACCCAAA
TGGAAAGTAACTCATTTGTTAAAATTATCAATATCTAATATATATGAATAAAGTGTAAGTTCACAACT

FIGURE 74

MKYTSYILAFQLCIVLGSLGCYCQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSF
YFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAAKTG
KRKRSQMLFQGRRASQ

FIGURE 75A

GAGTTGTGCCTGGAGTGATGTTTAAGCCAATGTCAGGGCAAGGCAACAGTCCCTGGCCGTCCTCCAGCACCTTTG
TAATGCATATGAGCTCGGGAGACCAGTACTTAAAGTTGGAGGCCCGGGAGCCCAGGAGCTGGCGGAGGGCGTTCG
TCCTGGGAGCTGCACTTGCTCCGTCGGGTCGCCGGCTTCACCGGACCGCAGGCTCCCGGGGCAGGGCCGGGGCCA
GAGCTCGCGTGTCGGCGGGACATGCGCTGCGTCGCCTCTAACCTCGGGCTGTGCTCTTTTTCCAGGTGGCCCGCC
GGTTTCTGAGCCTTCTGCCCTGCGGGGACACGGTCTGCACCCTGCCCGCGGCCACGGACC**ATG**ACCATGACCCTC
CACACCAAAGCATCTGGGATGGCCCTACTGCATCAGATCCAAGGGAACGAGCTGGAGCCCCTGAACCGTCCGCAG
CTCAAGATCCCCCTGGAGCGGCCCCTGGGCGAGGTGTACCTGGACAGCAGCAAGCCCGCCGTGTACAACTACCCC
GAGGGCGCCGCCTACGAGTTCAACGCCGCGGCCGCCGCCAACGCGCAGGTCTACGGTCAGACCGGCCTCCCCTAC
GGCCCCGGGTCTGAGGCTGCGGCGTTCGGCTCCAACGGCCTGGGGGGTTTCCCCCCACTCAACAGCGTGTCTCCG
AGCCCGCTGATGCTACTGCACCCGCCGCCGCAGCTGTCGCCTTTCCTGCAGCCCCACGGCCAGCAGGTGCCCTAC
TACCTGGAGAACGAGCCCAGCGGCTACACGGTGCGCGAGGCCGGCCCGCCGGCATTCTACAGGCCAAATTCAGAT
AATCGACGCCAGGGTGGCAGAGAAAGATTGGCCAGTACCAATGACAAGGGAAGTATGGCTATGGAATCTGCCAAG
GAGACTCGCTACTGTGCAGTGTGCAATGACTATGCTTCAGGCTACCATTATGGAGTCTGGTCCTGTGAGGGCTGC
AAGGCCTTCTTCAAGAGAAGTATTCAAGGACATAACGACTATATGTGTCCAGCCACCAACCAGTGCACCATTGAT
AAAAACAGGAGGAAGAGCTGCCAGGCCTGCCGGCTCCGCAAATGCTACGAAGTGGGAATGATGAAAGGTGGGATA
CGAAAAGACCGAAGAGGAGGGAGAATGTTGAAACACAAGCGCCAGAGAGATGATGGGGAGGGCAGGGGTGAAGTG
GGGTCTGCTGGAGACATGAGAGCTGCCAACCTTTGGCCAAGCCCGCTCATGATCAAACGCTCTAAGAAGAACAGC
CTGGCCTTGTCCCTGACGGCCGACCAGATGGTCAGTGCCTTGTTGGATGCTGAGCCCCCCATACTCTATTCCGAG
TATGATCCTACCAGACCCTTCAGTGAAGCTTCGATGATGGGCTTACTGACCAACCTGGCAGACAGGGAGCTGGTT
CACATGATCAACTGGGCGAAGAGGGTGCCAGGCTTTGTGGATTTGACCCTCCATGATCAGGTCCACCTTCTAGAA
TGTGCCTGGCTAGAGATCCTGATGATTGGTCTCGTCTGGCGCTCCATGGAGCACCCAGTGAAGCTACTGTTTGCT
CCTAACTTGCTCTTGGACAGGAACCAGGGAAAATGTGTAGAGGGCATGGTGGAGATCTTCGACATGCTGCTGGCT
ACATCATCTCGGTTCCGCATGATGAATCTGCAGGGAGAGGAGTTTGTGTGCCTCAAATCTATTATTTGCTTAAT
TCTGGAGTGTACACATTTCTGTCCAGCACCCTGAAGTCTCTGGAAGAGAAGGACCATATCCACCGAGTCCTGGAC
AAGATCACAGACACTTTGATCCACCTGATGGCCAAGGCAGGCCTGACCCTGCAGCAGCAGCACCAGCGGCTGGCC
CAGCTCCTCCTCATCCTCTCCCACATCAGGCACATGAGTAACAAAGGCATGGAGCATCTGTACAGCATGAAGTGC
AAGAACGTGGTGCCCCTCTATGACCTGCTGCTGGAGATGCTGGACGCCCACCGCCTACATGCGCCCACTAGCCGT
GGAGGGGCATCCGTGGAGGAGACGGACCAAAGCCACTTGGCCACTGCGGGCTCTACTTCATCGCATTCCTTGCAA
AAGTATTACATCACGGGGGAGGCAGAGGGTTTCCCTGCCACAGTC**TGA**GAGCTCCCTGGCTCCCACACGGTTCAG
ATAATCCCTGCTGCATTTTACCCTCATCATGCACCACTTTAGCCAAATTCTGTCTCCTGCATACACTCCGGCATG
CATCCAACACCAATGGCTTTCTAGATGAGTGGCCATTCATTTGCTTGCTCAGTTCTTAGTGGCACATCTTCTGTC
TTCTGTTGGGAACAGCCAAAGGGATTCCAAGGCTAAATCTTTGTAACAGCTCTCTTTCCCCCTTGCTATGTTACT
AAGCGTGAGGATTCCCGTAGCTCTTCACAGCTGAACTCAGTCTATGGGTTGGGGCTCAGATAACTCTGTGCATTT
AAGCTACTTGTAGAGACCCAGGCCTGGAGAGTAGACATTTTGCCTCTGATAAGCACTTTTTAAATGGCTCTAAGA
ATAAGCCACAGCAAAGAATTTAAAGTGGCTCCTTTAATTGGTGACTTGGAGAAAGCTAGGTCAAGGGTTTATTAT
AGCACCCTCTTGTATTCCTATGGCAATGCATCCTTTTATGAAAGTGGTACACCTTAAAGCTTTTATATGACTGTA
GCAGAGTATCTGGTGATTGTCAATTCACTTCCCCCTATAGGAATACAAGGGGCCACACAGGGAAGGCAGATCCCC
TAGTTGGCCAAGACTTATTTTAACTTGATACACTGCAGATTCAGAGTGTCCTGAAGCTCTGCCTCTGGCTTTCCG
GTCATGGGTTCCAGTTAATTCATGCCTCCCATGGACCTATGGAGAGCAACAAGTTGATCTTAGTTAAGTCTCCCT
ATATGAGGGATAAGTTCCTGATTTTTGTTTTTATTTTTGTGTTACAAAAGAAAGCCCTCCCTCCCTGAACTTGCA
GTAAGGTCAGCTTCAGGACCTGTTCCAGTGGGCACTGTACTTGGATCTTCCCGGCGTGTGTGTGCCTTACACAGG
GGTGAACTGTTCACTGTGGTGATGCATGATGAGGGTAAATGGTAGTTGAAAGGAGCAGGGGCCCTGGTGTTGCAT
TTAGCCCTGGGGCATGGAGCTGAACAGTACTTGTGCAGGATTGTTGTGGCTACTAGAGAACAAGAGGGAAAGTAG
GGCAGAAACTGGATACAGTTCTGAGCACAGCCAGACTTGCTCAGGTGGCCCTGCACAGGCTGCAGCTACCTAGGA
ACATTCCTTGCAGACCCCGCATTGCCTTTGGGGGTGCCCTGGGATCCCTGGGGTAGTCCAGCTCTTATTCATTTC
CCAGCGTGGCCCTGGTTGGAAGAAGCAGCTGTCAAGTTGTAGACAGCTGTGTTCCTACAATTGGCCCAGCACCCT
GGGGCACGGGAGAAGGGTGGGACCGTTGCTGTCACTACTCAGGCTGACTGGGGCCTGGTCAGATTACGTATGCC
CTTGGTGGTTTAGAGATAATCCAAAATCAGGGTTTGGTTTGGGGAAGAAAATCCTCCCCCTTCCTCCCCCGCCCC

FIGURE 75B

GTTCCCTACCGCCTCCACTCCTGCCAGCTCATTTCCTTCAATTTCCTTTGACCTATAGGCTAAAAAAGAAAGGCT
CATTCCAGCCACAGGGCAGCCTTCCCTGGGCCTTTGCTTCTCTAGCACAATTATGGGTTACTTCCTTTTTCTTAA
CAAAAAAGAATGTTTGATTTCCTCTGGGTGACCTTATTGTCTGTAATTGAAACCCTATTGAGAGGTGATGTCTGT
GTTAGCCAATGACCCAGGTAGCTGCTCGGGCTTCTCTTGGTATGTCTTGTTTGGAAAAGTGGATTTCATTCATTT
CTGATTGTCCAGTTAAGTGATCACCAAAGGACTGAGAATCTGGGAGGGCAAAAAAAAAAAAAAAAGTTTTTATGT
GCACTTAAATTTGGGGACAATTTTATGTATCTGTGTTAAGGATATGCTTAAGAACATAATTCTTTTGTTGCTGTT
TGTTTAAGAAGCACCTTAGTTTGTTTAAGAAGCACCTTATATAGTATAATATATATTTTTTTGAAATTACATTGC
TTGTTTATCAGACAATTGAATGTAGTAATTCTGTTCTGGATTTAATTTGACTGGGTTAACATGCAAAAACCAAGG
AAAAATATTTAGTTTTTTTTTTTTTTTTTGTATACTTTTCAAGCTACCTTGTCATGTATACAGTCATTTATGCCT
AAAGCCTGGTGATTATTCATTTAAATGAAGATCACATTTCATATCAACTTTTGTATCCACAGTAGACAAAATAGC
ACTAATCCAGATGCCTATTGTTGGATATTGAATGACAGACAATCTTATGTAGCAAAGATTATGCCTGAAAAGGAA
AATTATTCAGGGCAGCTAATTTTGCTTTTACCAAAATATCAGTAGTAATATTTTTGGACAGTAGCTAATGGGTCA
GTGGGTTCTTTTTAATGTTTATACTTAGATTTTCTTTTAAAAAAATTAAAATAAAACAAAAAAAATTTCTAGGAC
TAGACGATGTAATACCAGCTAAAGCCAAACAATTATACAGTGGAAGGTTTTACATTATTCATCCAATGTGTTTCT
ATTCATGTTAAGATACTACTACATTTGAAGTGGGCAGAGAACATCAGATGATTGAAATGTTCGCCCAGGGGTCTC
CAGCAACTTTGGAAATCTCTTTGTATTTTTACTTGAAGTGCCACTAATGGACAGCAGATATTTTCTGGCTGATGT
TGGTATTGGGTGTAGGAACATGATTTAAAAAAAAAACTCTTGCCTCTGCTTTCCCCCACTCTGAGGCAAGTTAAA
ATGTAAAAGATGTGATTTATCTGGGGGGCTCAGGTATGGTGGGGAAGTGGATTCAGGAATCTGGGGAATGGCAAA
TATATTAAGAAGAGTATTGAAAGTATTTGGAGGAAAATGGTTAATTCTGGGTGTGCACCAAGGTTCAGTAGAGTC
CACTTCTGCCCTGGAGACCACAAATCAACTAGCTCCATTTACAGCCATTTCTAAAATGGCAGCTTCAGTTCTAGA
GAAGAAAGAACAACATCAGCAGTAAAGTCCATGGAATAGCTAGTGGTCTGTGTTTCTTTTCGCCATTGCCTAGCT
TGCCGTAATGATTCTATAATGCCATCATGCAGCAATTATGAGAGGCTAGGTCATCCAAAGAGAAGACCCTATCAA
TGTAGGTTGCAAAATCTAACCCCTAAGGAAGTGCAGTCTTTGATTTGATTTCCCTAGTAACCTTGCAGATATGTT
TAACCAAGCCATAGCCCATGCCTTTTGAGGGCTGAACAAATAAGGGACTTACTGATAATTTACTTTTGATCACAT
TAAGGTGTTCTCACCTTGAAATCTTATACACTGAAATGGCCATTGATTTAGGCCACTGGCTTAGAGTACTCCTTC
CCCTGCATGACACTGATTACAAATACTTTCCTATTCATACTTTCCAATTATGAGATGGACTGTGGGTACTGGGAG
TGATCACTAACACCATAGTAATGTCTAATATTCACAGGCAGATCTGCTTGGGGAAGCTAGTTATGTGAAAGGCAA
ATAAAGTCATACAGTAGCTCAAAAGGCAACCATAATTCTCTTTGGTGCAAGTCTTGGGAGCGTGATCTAGATTAC
ACTGCACCATTCCCAAGTTAATCCCCTGAAAACTTACTCTCAACTGGAGCAAATGAACTTTGGTCCCAAATATCC
ATCTTTTCAGTAGCGTTAATTATGCTCTGTTTCCAACTGCATTTCCTTTCCAATTGAATTAAAGTGTGGCCTCGT
TTTTAGTCATTTAAAATTGTTTTCTAAGTAATTGCTGCCTCTATTATGGCACTTCAATTTTGCACTGTCTTTTGA
GATTCAAGAAAAAATTTCTATTCATTTTTTTGCATCCAATTGTGCCTGAACTTTTAAAATATGTAAATGCTGCCAT
GTTCCAAACCCATCGTCAGTGTGTGTGTTTAGAGCTGTGCACCCTAGAAACAACATACTTGTCCCATGAGCAGGT
GCCTGAGACACAGACCCCTTTGCATTCACAGAGAGGTCATTGGTTATAGAGACTTGAATTAATAAGTGACATTAT
GCCAGTTTCTGTTCTCTCACAGGTGATAAACAATGCTTTTTGTGCACTACATACTCTTCAGTGTAGAGCTCTTGT
TTTATGGGAAAAGGCTCAAATGCCAAATTGTGTTTGATGGATTAATATGCCCTTTTGCCGATGCATACTATTACT
GATGTGACTCGGTTTTGTCGCAGCTTTGCTTTGTTTAATGAAACACACTTGTAAACCTCTTTTGCACTTTGAAAA
AGAATCCAGCGGGATGCTCGAGCACCTGTAAACAATTTTCTCAACCTATTTGATGTTCAAATAAAGAATTAAACT

FIGURE 76

MTMTLHTKASGMALLHQIQGNELEPLNRPQLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAAANAQVYGQ
TGLPYGPGSEAAAFGSNGLGGFPPLNSVSPSPLMLLHPPPQLSPFLQPHGQQVPYYLENEPSGYTVREAGPPAFY
RPNSDNRRQGGRERLASTNDKGSMAMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATN
QCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRAANLWPSPLMIKR
SKKNSLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQ
VHLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKS
IILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQHQRLAQLLLILSHIRHMSNKGMEHL
YSMKCKNVVPLYDLLLEMLDAHRLHAPTSRGGASVEETDQSHLATAGSTSSHSLQKYYITGEAEGFPATV

FIGURE 77

CGTGCTGTAGCTGGTTCTTACGTCCAACCTGGGGGCAGTCTGCCCAGATCGCCTGCCTGGCCTCGCCTCTGCCCA
TCAGACACTTGGTGCTGGAATCTCCGAGGCTGGGAGGGACTGGGAGCGCCCCAGTTCTGTGTCCTCCCCACACAG
CCCCTTTTATGTAACTTGACTAAGATCAAGCAGTTAGTAAATGGTAGAAAGAATATT**<u>TGA</u>**ATCTACCTAGTGAGT
CTCTAGTGCATGCTTTTGTCCGGTATCCTGGAAAGCCTCCCACAAAAAGCTAATCTTTGCCCCATTCAAAACATG
CACCCTGAAGAAGCTGTTTGTACAGGATTGGGTTTATTCTGTTATTAAGACAAAGGCATCATGGCCTTTGGGTGA
GAGGCCCGTATGTGTTTGGGATTTGGCAATCAGCATTCCATCTCTGTCATCACCATTATTGAGAAAATAGATGGA
TTGGTTCCCTCTCTGCAGTCCTGTGGAGCAGTTGGACTGCTCTCTCTGCTCTCAGGATGATACTGTGAGAACAAT
TTAAATATGCTAAGCACATGTCAGGAAACAGTTTTGTGGTCTTTGGACACTCGCTGTAGCCATTCCGTTCCATTT
CAGGTGATTTTATTCATTTCATTTGTAGAATAAAATAAATCCATTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNTATACACCACTAAAGCCTCCCATTAAACCCATAGAAGACTTAAAGAGCTAAAGAGGCTATTN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNATTATTAGGCACGGCATCTTGTTTTACACA
ACGTGTTTGATCTTCACTTCTTCTTAATATTTGGTGTTTGATCTTCTCACAAGTGGTTTTGCTTGC

FIGURE 78

RAVAGSYVQPGGSLPRSPAWPRLCPSDTWCWNLRGWEGLGAPQFCVLPTQPLLCNLTKIKQLVNGRKNI

FIGURE 79

ACAGGGGTGAAGGCCCAGAGACCAGCAGAACGGCATCCCAGCCACGACGGCCACTTTGCTCTGTCTGCTGTCCGC
CACGGCCCTGCTCTGTTCCCTGGGACACCCCCGCCCCCACCTCCTCAGGCTGCCTGATCTGCCCAGCTTTCCAGC
TTTCCTCTGGATTCCGGCCTCTGGTCATCCCTCCCCACCCTCTCTCCAAGGCCCTCTCCTGGTCTCCCTTCTTCT
AGAACCCCTTCCTCCACCTCCCTCTCTGCAGAACTTCTCCTTTACCCCCCACCCCCCACCACTGCCCCCTTTCCT
TTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCCAGACCATAGGAGAG**ATG**TGGGAGGCTCAGTTCCTGGGCTT
GCTGTTTCTGCAGCCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGGGC
CCAGGAGGGGGCTCCTGCCCAGCTCCCCTGCAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGC
AGGGGTCACTTGGCAGCATCAGCCAGACAGTGGCCCGCCCGCTGCCGCCCCCGGCCATCCCCTGGCCCCCGGCCC
TCACCCGGCGGCGCCCTCCTCCTGGGGGCCCAGGCCCCGCCGCTACACGGTGCTGAGCGTGGGTCCCGGAGGCCT
GCGCAGCGGGAGGCTGCCCCTGCAGCCCCGCGTCCAGCTGGATGAGCGCGGCCGGCAGCGCGGGGACTTCTCGCT
ATGGCTGCGCCCAGCCCGGCGCGCGGACGCCGGCGAGTACCGCGCCGCGGTGCACCTCAGGGACCGCGCCCTCTC
CTGCCGCCTCCGTCTGCGCCTGGGCCAGGCCTCGATGACTGCCAGCCCCCCAGGATCTCTCAGAGCCTCCGACTG
GGTCATTTTGAACTGCTCCTTCAGCCGCCCTGACCGCCCAGCCTCTGTGCATTGGTTCCGGAACCGGGGCCAGGG
CCGAGTCCCTGTCCGGGAGTCCCCCCATCACCACTTAGCGGAAAGCTTCCTCTTCCTGCCCCAAGTCAGCCCCAT
GGACTCTGGGCCCTGGGGCTGCATCCTCACCTACAGAGATGGCTTCAACGTCTCCATCATGTATAACCTCACTGT
TCTGGGTCTGGAGCCCCCAACTCCCTTGACAGTGTACGCTGGAGCAGGTTCCAGGGTGGGGCTGCCCTGCCGCCT
GCCTGCTGGTGTGGGGACCCGGTCTTTCCTCACTGCCAAGTGGACTCCTCCTGGGGGAGGCCCTGACCTCCTGGT
GACTGGAGACAATGGCGACTTTACCCTTCGACTAGAGGATGTGAGCCAGGCCCAGGCTGGGACCTACACCTGCCA
TATCCATCTGCAGGAACAGCAGCTCAATGCCACTGTCACATTGGCAATCATCACAGTGACTCCCAAATCCTTTGG
GTCACCTGGATCCCTGGGGAAGCTGCTTTGTGAGGTGACTCCAGTATCTGGACAAGAACGCTTTGTGTGGAGCTC
TCTGGACACCCCATCCCAGAGGAGTTTCTCAGGACCTTGGCTGGAGGCACAGGAGGCCCAGCTCCTTTCCCAGCC
TTGGCAATGCCAGCTGTACCAGGGGGAGAGGCTTCTTGGAGCAGCAGTGTACTTCACAGAGCTGTCTAGCCCAGG
TGCCCAACGCTCTGGGAGAGCCCCAGGTGCCCTCCCAGCAGGCCACCTCCTGCTGTTTCTCACCCTTGGTGTCCT
TTCTCTGCTCCTTTTGGTGACTGGAGCCTTTGGCTTTCACCTTTGGAGAAGACAGTGGCGACCAAGACGATTTTC
TGCCTTAGAGCAAGGGATTCACCCTCCGCAGGCTCAGAGCAAGATAGAGGAGCTGGAGCAAGAACCGGAGCCGGA
GCCGGAGCCGGAACCGGAGCCCGAGCCCGAGCCCGAGCCGGAGCAGCTCTGACCTGGAGC**TGA**GGCAGCCAGCAG
ATCTCAGCAGCCCAGTCCAAATAAACGTCCTGTCTAGCAGC

FIGURE 80

MWEAQFLGLLFLQPLWVAPVKPLQPGAEVPVVWAQEGAPAQLPCSPTIPLQDLSLLRRAGVTWQHQPDSGPPAAA
PGHPLAPGPHPAAPSSWGPRPRRYTVLSVGPGGLRSGRLPLQPRVQLDERGRQRGDFSLWLRPARRADAGEYRAA
VHLRDRALSCRLRLRLGQASMTASPPGSLRASDWVILNCSFSRPDRPASVHWFRNRGQGRVPVRESPHHHLAESF
LFLPQVSPMDSGPWGCILTYRDGFNVSIMYNLTVLGLEPPTPLTVYAGAGSRVGLPCRLPAGVGTRSFLTAKWTP
PGGGPDLLVTGDNGDFTLRLEDVSQAQAGTYTCHIHLQEQQLNATVTLAIITVTPKSFGSPGSLGKLLCEVTPVS
GQERFVWSSLDTPSQRSFSGPWLEAQEAQLLSQPWQCQLYQGERLLGAAVYFTELSSPGAQRSGRAPGALPAGHL
LLFLTLGVLSLLLLVTGAFGFHLWRRQWRPRRFSALEQGIHPRQAQTQDRGAGARTGAGAGAGTGARARARAGAA
LTWS

FIGURE 81

GGCGTCCGCGCGCTGCACA**ATG**GCGGCTCTGAAGAGTTGGCTGTCGCGCAGCGTAACTTCATTCTTCAGGTACAG
ACAGTGTTTGTGTGTTCCTGTTGTGGCTAACTTTAAGAAGCGGTGTTTCTCAGAATTGATAAGACCATGGCACAA
AACTGTGACGATTGGCTTTGGAGTAACCCTGTGTGCGGTTCCTATTGCACAGAAATCAGAGCCTCATTCCCTTAG
TAGTGAAGCATTGATGAGGAGAGCAGTGTCTTTGGTAACAGATAGCACCTCTACCTTTCTCTCTCAGACCACATA
TGCGTTGATTGAAGCTATTACTGAATATACTAAGGCTGTTTATACCTTAACTTCTCTTTACCGACAATATACAAG
TTTACTTGGGAAAATGAATTCAGAGGAGGAAGATGAAGTGTGGCAGGTGATCATAGGAGCCAGAGCTGAGATGAC
TTCAAAACACCAAGAGTACTTGAAGCTGGAAACCACTTGGATGACTGCAGTTGGTCTTTCAGAGATGGCAGCAGA
AGCTGCATATCAAACTGGCGCAGATCAGGCCTCTATAACCGCCAGGAATCACATTCAGCTGGTGAAACTGCAGGT
GGAAGAGGTGCACCAGCTCTCCCGGAAAGCAGAAACCAAGCTGGCAGAAGCACAGATAGAAGAGCTCCGTCAGAA
AACACAGGAGGAAGGGGAGGAGCGGGCTGAGTCGGAGCAGGAGGCCTACCTGCGTGAGGAT**TGA**GGGCCTGAGCA
CACTGCCCTGTCTCCCCACTCAGTGGGGAAAGCAGGGGCAGATGCCACCCTGCCCAGGGTTGGCATGACTGTCTG
TGCACCGAGAAGAGGCGGCAGGTCCTGCCCTGGCCAATCAGGCGAGACGCCTTTGTGAGCTGTGAGTGCCTCCTG
TGGTCTCAGGCTTGCGCTGGACCTGGTTCTTAGCCCTTGGGCACTGCACCCTGTTTAACATTTCACCCCACTCTG
TACAGCTGCTCTTACCCATTTTTTTACCTCACACCCAAAGCATTTTGCCTACCTGGGTCAGAGAGAGGAGTCCT
TTTTGTCATGCCCTTAAGTTCAGCAACTGTTTAACCTGTTTTCAGTCTTATTTACGTCGTCAAAAATGATTTAGT
ACTTGTTCCCTCTGTTGGGATGCCAGTTGTGGCAGGGGGAGGGGAACCTGTCCAGTTTGTACGATTTCTTTGTAT
GTATTTCTGATGTGTTCTCTGATCTGCCCCCACTGTCCTGTGAGGACAGCTGAGGCCAAGGAGTGAAAAACCTAT
TACTACTAAGAGAAGGGGTGCAGAGTGTTTACCTGGTGCTCTCAACAGGACTTAACATCAACAGGACTTAACACA
GAAAAAAA

FIGURE 82

MAALKSWLSRSVTSFFRYRQCLCVPVVANFKKRCFSELIRPWHKTVTIGFGVTLCAVPIAQKSEPHSLSSEALMR
RAVSLVTDSTSTFLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEVWQVIIGARAEMTSKHQEY
LKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQIEELRQKTQEEGE
ERAESEQEAYLRED

FIGURE 83

ACTTTCCTGCCCCTTCCCCGGCCAAGCCCAACTCCGGATCTCGCTCTCCACCGGATCTCACCCGCCACACCCGGA
CAGGCGGCTGGAGGAGGCGGGCGTCTAAAATTCTGGGAAGCAGAACCTGGCCGGAGCCACTAGACAGAGCCGGGC
CTAGCCCAGAGAC**ATG**GAGAGTTGCTACAACCCAGGTCTGGATGGTATTATTGAATATGATGATTTCAAATTGAA
CTCCTCCATTGTGGAACCCAAGGAGCCAGCCCCAGAAACAGCTGATGGCCCCTACCTGGTGATCGTGGAACAGCC
TAAGCAGAGAGGCTTCCGATTTCGATATGGCTGTGAAGGCCCCTCCCATGGAGGACTGCCCGGTGCCTCCAGTGA
GAAGGGCCGAAAGACCTATCCCACTGTCAAGATCTGTAACTACGAGGGACCAGCCAAGATCGAGGTGGACCTGGT
AACACACAGTGACCCACCTCGTGCTCATGCCCACAGTCTGGTGGGCAAGCAATGCTCGGAGCTGGGGATCTGCGC
CGTTTCTGTGGGGCCCAAGGACATGACTGCCCAATTTAACAACCTGGGTGTCCTGCATGTGACTAAGAAGAACAT
GATGGGGACTATGATACAAAAACTTCAGAGGCAGCGGCTCCGCTCTAGGCCCCAGGGCCTTACGGAGGCCGAGCA
GCGGGAGCTGGAGCAAGAGGCCAAAGAACTGAAGAAGGTGATGGATCTGAGTATAGTGCGGCTGCGCTTCTCTGC
CTTCCTTAGAGCCAGTGATGGCTCCTTCTCCCTGCCCCTGAAGCCAGTCACCTCCCAGCCCATCCATGATAGCAA
ATCTCCGGGGGCATCAAACCTGAAGATTTCTCGAATGGACAAGACAGCAGGCTCTGTGCGGGGTGGAGATGAAGT
TTATCTGCTTTGTGACAAGGTGCAGAAAGATGACATTGAGGTTCGGTTCTATGAGGATGATGAGAATGGATGGCA
GGCCTTTGGGGACTTCTCTCCCACAGATGTGCATAAACAGTATGCCATTGTGTTCCGGACACCCCCCTATCACAA
GATGAAGATTGAGCGGCCTGTAACAGTGTTTCTGCAACTGAAACGCAAGCGAGGAGGGGACGTGTCTGATTCCAA
ACAGTTCACCTATTACCCTCTGGTGGAAGACAAGGAAGAGGTGCAGCGGAAGCGGAGGAAGGCCTTGCCCACCTT
CTCCCAGCCCTTCGGGGGTGGCTCCCACATGGGTGGAGGCTCTGGGGGTGCAGCCGGGGGCTACGGAGGAGCTGG
AGGAGGTGAGGGGGTACTGATGGAGGGAGGGGTAAAGGTAAGAGAAGCTGTGGAGGAAAAAAATCTGGGGGAGGC
CGGGCGTGGCTTGCACGCCTGTAATCCAGCCTTTGGGAGGCCAAGGCAGGCAGTTACC**TGA**GATCAGGAGTTCAA
GACCAGCTTGGCCAACAGCGTGAAACCTCGTCTCTACTAAAAATACAAACATTAGCTGGGCATGGTGGCAGGCGC
CTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCTGGGAGACAAGAGGTTGCAGTAAGC
TGAGATCACACCACTGCACTCCAGGCTGGGCAATAAGAGCGAAACTCCGTCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

MESCYNPGLDGIIEYDDFKLNSSIVEPKEPAPETADGPYLVIVEQPKQRGFRFRYGCEGPSHGGLPGASSEKGRK
TYPTVKICNYEGPAKIEVDLVTHSDPPRAHAHSLVGKQCSELGICAVSVGPKDMTAQFNNLGVLHVTKKNMMGTM
IQKLQRQRLRSRPQGLTEAEQRELEQEAKELKKVMDLSIVRLRFSAFLRASDGSFSLPLKPVTSQPIHDSKSPGA
SNLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSPTDVHKQYAIVFRTPPYHKMKIE
RPVTVFLQLKRKRGGDVSDSKQFTYYPLVEDKEEVQRKRRKALPTFSQPFGGGSHMGGGSGGAAGGYGGAGGGEG
VLMEGGVKVREAVEEKNLGEAGRGLHACNPAFGRPRQAVT

FIGURE 85A

CACTGTGCTTTCAGCTTGAGTGACAGAGTGAGACCCTCC**TGA**CTCAAAACAAAAAACATGGTTTCTCCTCTCTCT
CCTGTCTTCTTACTCTCTATCCCATTTGATGTAGTGATTTTTAAATGCTTTTGTAAGTTAATTCTTAACACAAAA
GAGACATTGTAATGAGGCACACCACTAAAGTGAGCATGCCCAATTAAAACCAGTGTAATATAGGATAAGAAAATC
TGATTTTTCAAAAAAGATACTCTACATAAAGAATCCTTCATATAAAAAGTTCTTTCTTGTAGTACATTTAAAGTT
TTAATTCACTCATGTATAACTGAGAGTTCCTTTGAGCCCTTTTTAGGCAGGGAGGCATGTCTGTCATCTAGCGTG
TGGCCCAGTAAGTGATTATTACATTGGAATCAGTTTTTCAGTCTTTTAAAATAAATTCTGTGCCATAAGAATAAA
AGATAAAGAGAAAAATTAATGTTAACTATTTTTAGCTTATTATAACTATGTCAACAAGTGTTTATTAATACCTAT
TATGGGAAAGTCACTGTGGTTGGCATTGAAAATTACATCATCTTTAAAGCAGTATTTGTCCCCAGATGGACTCAT
CACTAGCAAAGACTAGGTTCATTGGAAGGCATAGGGTGAGAGAATGGGAAGATGGAGTGGAGGCGGGTTGTTAAA
GTGCTGTCAGTGAGTGATTTTGTCTACTTGAATAATGGTCCATGTTTGGGGGCATATTGTGTTTCATAAGAAGTG
AAAGGTATTTGCAAAGTAAGCTACAAATGACCCATAAATCTGTTAACAACAGTCCTTAATATGCAAAGATGAAAA
ACAAGCATTACTGCTACCCAAAGGGAACTGGTGCTTGGTGATGTGCAGATGGGGCTGTTGGTTAAGAGAGCTATT
ACAGGTTTTCTCTCTTAGGTTTCATAGGAGGTAGTTACTGAGATGAGATTGTTTTATCTTTTTGAATACAGATCT
CTTGTCTTGAGTTAGTTCTGAGGATGGGAGTAATAAAGGAGTTTTTTGTTTTTTTGTTTGTTTGTTTGTTTTGGC
TCCTTAGTAATACTCCTCTGACATTTATTTCTATTATTCTTCAAAGAAAGGAAACCAACTGAAATGTTTGCTTTA
ACAAACATTTTAATAAGTTCTCTGGGTTTTTTTTTCCCCTTTTAAAAAAATTAGCATATACCATAGCAATAAAAG
AACTAATGTTAACTATTGTATGCTACAACTTAAGTGATTTTTCTAAAGAAGCACAATGTCATTGAAAGTATTATT
GAAAAGGATCATAGTCACATTGAATTTGTGAAGGCCAAAGAAATTGAAGGGAGTGATATTTTCATTTTATGATAT
TCACATATTTAGTAAATTTTGTGTACAAGAATACCAGGCAGAGTGTTTTACCCATGGAAACAGGTTTCAGATTAC
TTTGTTTTTACTGTTAGAGTCTCAAGTTTAGAAATGCTAACACTTAAATCAGTTTTTTTCTCACTATACTTGAAG
ATTGTTAATATTTTGATATCTTCCTAGCTTGATGAATTTAAACATATCTTCAGATCTGTGACAGTGACAGCCAAT
AGGACTGATAATATTAGCTTCAAACCAATAATATCCAGGGTTAAAATAAAAATCATAGTGAAAGTACGATTGTAA
AATTATGCTATATTAACTTTTAAGTCTGTAATAACTTGACATCAAAATGTTATGTAATTACCATAAATAATGGCT
AGCGAGAACATCTTTGGAAATTCTCAAATTACCTTTCTTACTACACTGTTTGCAGAATGAATGTAGAAATGATCC
TGTTAGCTTTCTGAATGTTCTGTGGTTGAATGTGTTTTTGCTTAAATAAAGCTTTTGGTATTTGTTTAAATTACA
CTTCTTGAGAAGTGGAAATTTTAGGATCATCTTTGCTTTGTTTCAGTTTTGTGATTTTTGAAATGAATGTTTAGT
TTACTGAGCCAGTTGGTCATTTCTTCCTCATGTCGTTAAGTCCAGTGAGTAAGCCTGAACTGTGAATAAATTACC
AAAAACTTGCTTAGAATTTCATTTTGAAGCAATTTGCTAATATTTGAAGTGTATACACATTTGTAGTTATGTTAA
AAATTGTATTGTACTAAGAATGTAATCAATGTCTACTTTAGTTGTAAACATTTCTGATGTCAAAACTTTATTCAT
TACTGTTGATTTTAAGAATACGAAATCACTGCCTAAATATTACCAAAAGCCACTGTCTCTACCCGAACTTCCCAG
TTTGGGAAAGAATCGTTAGATAAAACAAAGGCTCTGCCCTTTCTGATACCAAACTCCACAGATACTTTCTCACAT
CTTTTAAAACATTTTGCAATAACATATTGTTTATAGGAAGTTTACAGGGTATGCAATGATTAAAACTTTTAAGTG
AATTGATAGTTGCAAAAGAAAGGATAATATTTAAGGTCAGTGAGTAGCAAGACAATCTAAAGTTTCTGTAATATC
TGGCTCTCTGTTAATTATAGAGCAAAGTTTCCCTTACAGAATCCTTTTATGAACAGCAAGCTAGAGTCTATCCCT
AGTGGTTATAGCACCTGCTGCGTTTTTCAGGAGACAGTTAGGCCAGGGTGATTTGAATGGATAGATGTGCTGTTT
TGCCTGCTTGTAGAATTCAGCCCAGTCTTTGGCNNNNNNNNNNNNNNNNNNNCTCCACCTCTCCCTCTCTCTTCT
TCTGCACCAGAGCCTAAGGCTGCGCCACCAAGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGACATATCAAATTTGACAG
GTATTGTATACCCTTTGGATCTTTAGGAATTAATTTTTGCCTCTGTCACTCAGCTTTGTATATTTTGAAATGGAG
ATAAGTATAGGGAGGTCTTGGAAGGAAAATTGCCAGAATTCCCAAACCATGTAACACTCATTGAGAATTCCAGAT
CCATTATATCTAAAGGGCAAGTGAAGGAAACAGTATTGTGAACTGGGTATAACTCCTTGGTTCTTAACTAGTACA
TTCTTAATCTGTGAGACCCAAAGGTTGATAAACAATAATTTAAGATTGTACAGTACTCTAAACGTCTGCAAAGGT
CTAGATGTTATCAGTATCACTAGTTTTTATTTCTGCCAGTAGCTCCCTTTTAGGTTACATTGTTGTCCTCTTTCC
AGTGTGGCATCTGTCATTGGTTTTTCACTATGGCAAGTTCATTAAAAAGCTTGCTCCATTGTTATCTTCAAGTAA
TGCCCATAAGGAGATGGAAGATATCTGAGACAATTAAGGCTTTAGCTTCTAGGCAAGAGAAATAACGTTGCATTA

FIGURE 85B

AATTTCAAGTTTCTTTCTGCTAGACTTGAATGTGTCTAGCCACTCTAATTTATGGGGGCTTTTGGTTTTTTCCTA
TTGTACTTTGTATGTAGAATTGTTTTGAAATATCAAGCATATTTACTTTGAATTTGAACTCTTTCTTAATTTTGT
ATTTATCCTTTGAATAAAATGTAAATCCAATATTTATTATT

FIGURE 86

HCAFSLSDRVRPS

FIGURE 87

GGGGCAGACGTGGGACGGGAAGGACGGCTGCCGGGACTGGCGCGCGGGGACACTGGGCCGACGCGTGGAGTAGCG
GGGAGAGCGGGAAGCCTGAGGGGGCGGGGCCGGCGCGAGGCCGTGGGTGCGGCACGAGGATGCCGGCGGCGGGAC
AGCGCCCGTAGGCAGCCCCACGGGCAGGGCGCGCGGGCGGGGCGGGGCGGGCCGGGCCAGAGGAGCTCCCGGC**AT**
GTCGCAAGGGCTCCCGGCCGCCGGCAGCGTCCTGCAGAGGAGCGTCGCGGCGCCCGGGAACCAGCCGCAGCCGCA
GCCGCAGCAGCAGAGCCCTGAGGATGATGACAGGAAGGTCCGAAGGAGAGAAAAAAACCGAGTTGCTGCTCAGAG
AAGTCGGAAGAAGCAGACCCAGAAGGCTGACAAGCTCCATGAGGAATATGAGAGCCTGGAGCAAGAAAACACCAT
GCTGCGGAGAGAGATCGGGAAGCTGACAGAGGAGCTGAAGCACCTGACAGAGGCACTGAAGGAGCACGAGAAGAT
GTGCCCGCTGCTGCTCTGCCCTATGAACTTTGTGCCAGTGCCTCCCCGGCCGGACCCTGTGGCCGGCTGCTTGCC
CCGA**TGA**AGCCGGGGACACTCCTCTGCCCAGCAAGGAGCCTTGGTCATTTTCATACCTGGGAGGAAGGCTTTTCC
TTCACAATTGTATACAGGGGGCACCTGTGGCCAGGCCTCCTCCTGGGAGCTCCAGGACCAGCCAGCTGTGTTCCC
TGCAGACTGGGCTCAGCCCGACATCCAACAGGCGCCAAACTCACAGAGCCCTTGTGCAGATCCAGCATGGAGGCC
ACCCTCAGGAGTGACTTCTCATCCACCCTGGCAGCTAGTAGGTTCTGCTGTTATGCAGAGCCATTTCCTCTAGAA
TTTGGATAATAAAGATGCTTATTGTCTCTCCCTTCTCCAGTTCTGGAATTTACAGGCACAATACACTTCCTTTT
CCTGG

FIGURE 88

MSQGLPAAGSVLQRSVAAPGNQPQPQPQQQSPEDDDRKVRRREKNRVAAQRSRKKQTQKADKLHEEYESLEQENT
MLRREIGKLTEELKHLTEALKEHEKMCPLLLCPMNFVPVPPRPDPVAGCLPR

FIGURE 89

GGGCGGGGTGCCGCATCCCCAGCCCGCCGCC**ATG**GCCGCCTACAAACTGGTGCTGATCCGGCACGGCGAGAGCGC
ATGGAACCTGGAGAACCGCTTCAGCGGCTGGTACGACGCCGACCTGAGCCCGGCGGGCCACGAGGAGGCGAAGCG
CGGCGGGCAGGCGCTACGAGATGCTGGCTATGAGTTTGACATCTGCTTCACCTCAGTGCAGAAGAGAGCGATCCG
GACCCTCTGGACAGTGCTAGATGCCATTGATCAGATGTGGCTGCCAGTGGTGAGGACTTGGCGCCTCAATGAGCG
GCACTATGGGGGTCTAACCGGTCTCAATAAAGCAGAAACTGCTGCAAAGCATGGTGAGGCCCAGGTGAAGATCTG
GAGGCGCTCCTATGATGTCCCACCACCTCCGATGGAGCCCGACCATCCTTTCTACAGCAACATCAGTAAGGATCG
CAGGTATGCAGACCTCACAGAAGATCAGCTACCCTCCTGTGAGAGTCTGAAGGATACTATTGCCAGAGCTCTGCC
CTTCTGGAATGAAGAAATAGTTCCCCAGATCAAGGAGGGGAAACGTGTACTGATTGCAGCCCATGGCAACAGCCT
CCGGGGCATTGTCAAGCATCTGGAGGGTCTCTCTGAAGAGGCTATCATGGAGCTGAACCTGCCGACTGGTATTCC
CATTGTCTATGAATTGGACAAGAACTTGAAGCCTATCAAGCCCATGCAGTTTCTGGGGGATGAAGAGACGGTGCG
CAAAGCCATGGAAGCTGTGGCTGCCCAGGGCAAGGCCAAGAAG**TGA**AGGCCGGCGGGGAGGATACTGTCCCCAGG
AGCACCCTCCCTGCCCGTCTTGTCCCTCTGCCCCTCCCACCTGCACATGTCACACTGACCACATCTGTAGACATC
TTGAGTTGTAGCTGCAGACGGGGACCAGTGGCTCCCATTTTCATTTTAGCCATTTTGTCGCCTGCACCCACTCCC
TTCATACAATCTAGTCAGAATAGCAGTTCTAGAGCACAGGTTCTCAGTCTAAGCTATGGAAAAGCTCCCCTTATC
CAACAGAGTTTAAAAGTAGTGACTTGGGTTTTTGCGAGTGCTTTGTTTACTAAGGACTTTGGGGAGGAACCATGC
TAAGCCATGACCAGTGAGGAGAAGCAACAGAGCCTGTCTGTCCCCATGAGCGGAGTCTGTCCTCTGCTCTTCTGC
AGTCAGGTCACTGCCTACTGCCTGGGGGCTCTAGTCATTCCAGTGGAAGACGAATGTAACCTGCGTGGTGATGTG
ACAACTGTTTCCTCCCTGACCCCAGAGGATCTGGCTCTAGGTTGGGATCAATCCTGAATTTCGTTATGTGTTAAT
TTACTTTTATTAAAAAAGTATAGTATATATAATACAAAACAATAACCCTTCTGGGGTTTCTTGTGGCGGTTGAAA
TAGTCCCACATGTGGTCATCAGAAATAGCATTCCTCATACCAATATAGGATCAGCTCCTTGACCTCTGAGGGGTC
AGGAGTGCTTCCTGGTGTGTGTATTAGAATCCCTTCCTGCCTTGTTTCATGGCAGTGAAATGCCTCTTGGTCCTG
TCCAGTGTATCTTTCACTGATTTCTGAATCATGTTCTAGTTGCTTGACCCTGCCACATGGGTCCAGTGTTCATCT
GAGCATAACTGTACTAAATCCTTTTTCCATATCAGTATAATAAAGGAGTGATGTGCAAT

FIGURE 90

MAAYKLVLIRHGESAWNLENRFSGWYDADLSPAGHEEAKRGGQALRDAGYEFDICFTSVQKRAIRTLWTVLDAID
QMWLPVVRTWRLNERHYGGLTGLNKAETAAKHGEAQVKIWRRSYDVPPPPMEPDHPFYSNISKDRRYADLTEDQL
PSCESLKDTIARALPFWNEEIVPQIKEGKRVLIAAHGNSLRGIVKHLEGLSEEAIMELNLPTGIPIVYELDKNLK
PIKPMQFLGDEETVRKAMEAVAAQGKAKK

FIGURE 91

GCGGCCGCTTTCGATTTCGCTTTCCCCTAA**ATG**GCTGAGCTTCTCGCCAGCGCAGGATCAGCCTGTTCCTGGGAC
TTTCCGAGAGCCCCGCCCTCGTTCCCTCCCCCAGCCGCCAGTAGGGGAGGACTCGGCGGTACCCGGAGCTTCAGG
CCCCACCGGGGCGCGGAGAGTCCCAGACCCGGCCGGGACCGGGACGGCGTCCGAGTGCCAATGGCTAGCTCTAGG
TGTCCCGCTCCCCGCGGGTGCCGCTGCCTCCCCGGAGCTTCTCTCGCATGGCTGGGGACAGTACTGCTACTTCTC
GCCGACTGGGTGCTGCTCCGGACCGCGCTGCCCCGCATATTCTCCCTGCTGGTGCCCACCGCGCTGCCACTGCTC
CGGGTCTGGGCGGTGGGCCTGAGCCGCTGGGCCGTGCTCTGGCTGGGGGCCTGCGGGGTCCTCAGGGCAACGGTT
GGCTCCAAGAGCGAAAACGCAGGTGCCCAGGGCTGGCTGGCTGCTTTGAAGCCATTAGCTGCGGCACTGGGCTTG
GCCCTGCCGGGACTTGCCTTGTTCCGAGAGCTGATCTCATGGGGAGCCCCCGGGTCCGCGGATAGCACCAGGCTA
CTGCACTGGGGAAGTCACCCTACCGCCTTCGTTGTCAGTTATGCAGCGGCACTGCCCGCAGCAGCCCTGTGGCAC
AAACTCGGGAGCCTCTGGGTGCCCGGCGGTCAGGGCGGCTCTGGAAACCCTGTGCGTCGGCTTCTAGGCTGCCTG
GGCTCGGAGACGCGCCGCCTCTCGCTGTTCCTGGTCCTGGTGGTCCTCTCCTCTCTTGGGGAGATGGCCATTCCA
TTCTTTACGGGCCGCCTCACTGACTGGATTCTACAAGATGGCTCAGCCGATACCTTCACTCGAAACTTAACTCTC
ATGTCCATTCTCACCATAGCCAGTGCAGTGCTGGAGTTCGTGGGTGACGGGATCTATAACAACACCATGGGCCAC
GTGCACAGCCACTTGCAGGGAGAGGTGTTTGGGGCTGTCCTGCGCCAGGAGACGGAGTTTTTCCAACAGAACCAG
ACAGGTAACATCATGTCTCGGGTAACAGAGGACACGTCCACCCTGAGTGATTCTCTGAGTGAGAATCTGAGCTTA
TTTCTGTGGTACCTGGTGCGAGGCCTATGTCTCTTGGGGATCATGCTCTGGGGATCAGTGTCCCTCACCATGGTC
ACCCTGATCACCCTGCCTCTGCTTTTCCTTCTGCCCAAGAAGGTGGGAAAATGGTACCAGTTGCTGGAAGTGCAG
GTGCGGGAATCTCTGGCAAAGTCCAGCCAGGTGGCCATTGAGGCTCTGTCGGCCATGCCTACAGTTCGAAGCTTT
GCCAACGAGGAGGGCGAAGCCCAGAAGTTTAGGGAAAAGCTGCAAGAAATAAAGACACTCAACCAGAAGGAGGCT
GTGGCCTATGCAGTCAACTCCTGGACCACTAGTATTTCAGGTATGCTGCTGAAAGTGGGAATCCTCTACATTGGT
GGGCAGCTGGTGACCAGTGGGGCTGTAAGCAGTGGGAACCTTGTCACATTTGTTCTCTACCAGATGCAGTTCACC
CAGGCTGTGGAGGTACTGCTCTCCATCTACCCCAGAGTACAGAAGGCTGTGGGCTCCTCAGAGAAAATATTTGAG
TACCTGGACCGCACCCCTCGCTGCCCACCCAGTGGTCTGTTGACTCCCTTACACTTGGAGGGCCTTGTCCAGTTC
CAAGATGTCTCCTTTGCCTACCCAAACCGCCCAGATGTCTTAGTGCTACAGGGGCTGACATTCACCCTACGCCCT
GGCGAGGTGACGGCGCTGGTGGGACCCAATGGGTCTGGGAAGAGCACAGTGGCTGCCCTGCTGCAGAATCTGTAC
CAGCCCACCGGGGGACAGCTGCTGTTGGATGGGAAGCCCCTTCCCCAATATGAGCACCGCTACCTGCACAGGCAG
GTGGCTGCAGTGGGACAAGAGCCACAGGTATTTGGAAGAAGTCTTCAAGAAAATATTGCCTATGGCCTGACCCAG
AAGCCAACTATGGAGGAAATCACAGCTGCTGCAGTAAAGTCTGGGGCCCATAGTTTCATCTCTGGACTCCCTCAG
GGCTATGACACAGAGGTAGACGAGGCTGGGAGCCAGCTGTCAGGGGGTCAGCGACAGGCAGTGGCGTTGGCCCGA
GCATTGATCCGGAAACCGTGTGTACTTATCCTGGATGATGCCACCAGTGCCCTGGATGCAAACAGCCAGTTACAG
GTGGAGCAGCTCCTGTACGAAAGCCCTGAGCGGTACTCCCGCTCAGTGCTTCTCATCACCCAGCACCTCAGCCTG
GTGGAGCAGGCTGACCACATCCTCTTTCTGGAAGGAGGCGCTATCCGGGAGGGGGGAACCCACCAGCAGCTCATG
GAGAAAAAGGGGTGCTACTGGGCCATGGTGCAGGCTCCTGCAGATGCTCCAGAA**TGA**AAGCCTTCTCAGACCTGC
GCACTCCATCTCCCTCCCTTTTCTTCTCTCTGTGGTGGAGAACCACAGCTGCAGAGTAGCAGCTGCCTCCAGGAT
GAGTTACTTGAAATTTGCCTTGAGTGTGTTACCTCCTTTCCAAGCTCCTCGTGATAATGCAGACTTCCTGGAGTA
CAAACACAGGATTTGTAATTCCTACTGTAACGGAGTTTAGAGCCAGGGCTGATGCTTTGGTGTGGCCAGCACTCT
GAAACTGAGAAATGTTCAGAATGTACGGAAAGATGATCAGCTATTTTCAACATAACTGAAGGCATATGCTGGCCC
ATAAACACCCTGTAGGTTCTTGATATTTATAATAAAATTGGTGTTTTGT

FIGURE 92

MAELLASAGSACSWDFPRAPPSFPPPAASRGGLGGTRSFRPHRGAESPRPGRDRDGVRVPMASSRCPAPRGCRCL
PGASLAWLGTVLLLLADWVLLRTALPRIFSLLVPTALPLLRVWAVGLSRWAVLWLGACGVLRATVGSKSENAGAQ
GWLAALKPLAAALGLALPGLALFRELISWGAPGSADSTRLLHWGSHPTAFVVSYAAALPAAALWHKLGSLWVPGG
QGGSGNPVRRLLGCLGSETRRLSLFLVLVVLSSLGEMAIPFFTGRLTDWILQDGSADTFTRNLTLMSILTIASAV
LEFVGDGIYNNTMGHVHSHLQGEVFGAVLRQETEFFQQNQTGNIMSRVTEDTSTLSDSLSENLSLFLWYLVRGLC
LLGIMLWGSVSLTMVTLITLPLLFLLPKKVGKWYQLLEVQVRESLAKSSQVAIEALSAMPTVRSFANEEGEAQKF
REKLQEIKTLNQKEAVAYAVNSWTTSISGMLLKVGILYIGGQLVTSGAVSSGNLVTFVLYQMQFTQAVEVLLSIY
PRVQKAVGSSEKIFEYLDRTPRCPPSGLLTPLHLEGLVQFQDVSFAYPNRPDVLVLQGLTFTLRPGEVTALVGPN
GSGKSTVAALLQNLYQPTGGQLLLDGKPLPQYEHRYLHRQVAAVGQEPQVFGRSLQENIAYGLTQKPTMEEITAA
AVKSGAHSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQLQVEQLLYESPE
RYSRSVLLITQHLSLVEQADHILFLEGGAIREGGTHQQLMEKKGCYWAMVQAPADAPE

FIGURE 93

GGGATCCCGGGGCCGCCGCGTCGCTCGGGCCCCGCC**ATG**GCCGTCACCATCACGCTCAAAACGCTGCAGCAGCAG
ACCTTCAAGATCCGCATGGAGCCTGACGAGACGGTGAAGGTGCTAAAGGAGAAGATAGAAGCTGAGAAGGGTCGT
GATGCCTTCCCCGTGGCTGGACAGAAACTCATCTATGCCGGCAAGATCTTGAGTGACGATGTCCCTATCAGGGAC
TATCGCATCGATGAGAAGAACTTTGTGGTCGTCATGGTGACCAAGACCAAAGCCGGCCAGGGTACCTCAGCACCC
CCAGAGGCCTCACCCACAGCTGCCCCAGAGTCCTCTACATCCTTCCCGCCTGCCCCCACCTCAGGCATGTCCCAT
CCCCCACCTGCCGCCAGAGAGGACAAGAGCCCATCAGAGGAATCCGCCCCCACGACGTCCCCAGAGTCTGTGTCA
GGCTCTGTTCCCTCTTCAGGTAGCAGCGGGCGAGAGGAAGACGCGGCCTCCACGCTAGTGACGGGCTCTGAGTAT
GAGACGATGCTGACGGAGATCATGTCCATGGGCTATGAGCGAGAGCGGGTCGTGGCCGCCCTGAGAGCCAGCTAC
AACAACCCCCACCGAGCCGTGGAGTATCTGCTCACGGGAATTCCTGGGAGCCCCGAGCCGGAACACGGTTCTGTC
CAGGAGAGCCAGGTATCGGAGCAGCCGGCCACGGAAGCAGCAGGAGAGAACCCCCTGGAGTTCCTGCGGGACCAG
CCCCAGTTCCAGAACATGCGGCAGGTGATTCAGCAGAACCCTGCGCTGCTGCCCGCCCTGCTCCAGCAGCTGGGC
CAGGAGAACCCTCAGCTTTTACAGCAAATCAGCCGGCACCAGGAGCAGTTCATCCAGATGCTGAACGAGCCCCCT
GGGGAGCTGGCGGACATCTCAGATGTGGAGGGGGAGGTGGGCGCCATAGGAGAGGAGGCCCCGCAGATGAACTAC
ATCCAGGTGACGCCGCAGGAGAAAGAAGCTATAGAGAGGTTGAAGGCCCTGGGCTTCCCAGAGAGCCTGGTCATC
CAGGCCTATTTCGCGTGTGAAAAAAATGAGAACTTGGCTGCCAACTTCCTCCTGAGTCAGAACTTTGATGACGAG
TGATGCCAGGAAGCCAGGCCACCGAAGCCCCCACCCTACCCTTATTCCATGAAAGTTTTATAAAAGAAAAAATAT
ATATATATTCATGTTTATTTAAGAAATGGAAAAAAAAATCAAAAATCTTAAAAAAAACAAGCAAACAGTCCAGCTT
CCTGTCCTCCTAAAGTGGCCCCTGTTCCCATCTCCCGGGCCAGACAGCTGTCCCCCCGTCCTCCTCCCCAGCCCA
GCCTGCTCAGAGAAGCTGGCAGGACTGGGAGGCGACAGATGGGCCCCTCTTGGCCTCTGTCCCAGCTCTCTGCAG
CCAGACGGAAAGGCGGCTGCTTGCCTCTCCATCCTCCGAAAAACCCCTGAGGACCCCCCCCCATCCTCTTCTAGG
ATGAGGGGAAGCTGGAGCCCCAACTTTGATCCTCCATTGGAGTGGCCCAAATCTTTCCATCTAGGGCAAGTCCTG
AAAGGCCCAAGGCCCCCTCCCAGTCTGGCCTTGGCCTCCAGCCTGGAGAAGGGCTAACATCAGCTCATTGTCAAG
GCCACCCCCACCCCAGAACAGAACCGTGTCTCTGATAAAGGTTTTGAAGTGAATAAAGTTTTAAAAACT

FIGURE 94

MAVTITLKTLQQQTFKIRMEPDETVKVLKEKIEAEKGRDAFPVAGQKLIYAGKILSDDVPIRDYRIDEKNFVVVM
VTKTKAGQGTSAPPEASPTAAPESSTSFPPAPTSGMSHPPPAAREDKSPSEESAPTTSPESVSGSVPSSGSSGRE
EDAASTLVTGSEYETMLTEIMSMGYERERVVAALRASYNNPHRAVEYLLTGIPGSPEPEHGSVQESQVSEQPATE
AAGENPLEFLRDQPQFQNMRQVIQQNPALLPALLQQLGQENPQLLQQISRHQEQFIQMLNEPPGELADISDVEGE
VGAIGEEAPQMNYIQVTPQEKEAIERLKALGFPESLVIQAYFACEKNENLAANFLLSQNFDDE

FIGURE 95

GTCACTCGTATAAAAACCTATGCTTTGAAGGTTCTCGTGTGTCTCGGCCTGCAGGTCTCGCTCAGAGCTGTGTCC
CTGAACATCCACCCTGCTGGGGTGGCTTGACGCACTTCTGTGCAAATCTGTTCGCTCGCAACCCTACCTACCTCT
CTCCCGAACCGGAGAAAACCTTCGGCGGGGTCCTTCCGGGTTTTGTGTCGAATCTGCGGCGGCGACCCGGCGCCG
CGTCACGCGGTGGTGAATGTGCGGCAGTACGCGCGCCGCGTCGTTTACGCGGCGATTTCATCATGCTCCGAGCCG
GCGGCGCGCGCCGCTTCCGTCGCCACCCTCTCTGGACAGCCCAGGGCCGCAGGCTCATGCCCTCTCCGCGTCCAG
TGCTGCTTAGAGGTGCTCGCGCCGCTCTGCTGCTGCTGCTGCCGCCCCGGCTCTTAGCCCGACCCTCGCTCCTCC
TCCGCCGGTCCCTCAGCGCGGCCTCCTGCGCCCCGATCTCCTTGCCCGCCGCCGCCTCCCGGAGCAGC**ATG**GACG
GCGCGGGGGCTGAGGAGGTGCTGGCACCTCTGAGGCTAGCAGTGCGCCAGCAGGGAGATCTTGTGCGAAAACTCA
AAGAAGATAAAGCACCCCAAGTAGACGTAGACAAAGCAGTGGCTGAGCTCAAAGCCCGCAAGAGGGTTCTGGAAG
CAAAGGAGCTGGCGTTACAGCCCAAAGATGATATTGTAGACCGAGCAAAAATGGAAGATACCCTGAAGAGGAGGT
TTTTCTATGATCAAGCTTTTGCTATTTATGGAGGTGTTAGTGGTCTGTATGACTTTGGGCCAGTTGGCTGTGCTT
TGAAGAACAATATTATTCAGACCTGGAGGCAGCACTTTATCCAAGAGGAACAGATCCTGGAGATCGATTGCACCA
TGCTCACCCCTGAGCCAGTTTTAAAGACCTCTGGCCATGTAGACAAATTTGCTGACTTCATGGTGAAAGACGTAA
AAAATGGAGAATGTTTTCGTGCTGACCATCTATTAAAAGCTCATTTACAGAAATTGATGTCTGATAAGAAGTGTT
CTGTCGAAAAGAAATCAGAAATGGAAAGTGTTTTGGCCCAGCTTGATAACTATGGACAGCAAGAACTTGCGGATC
TTTTTGTGAACTATAATGTAAAATCTCCCATTACTGGAAATGATCTATCCCCTCCAGTGTCTTTTAACTTAATGT
TCAAGACTTTCATTGGGCCTGGAGGAAACATGCCTGGGTACTTGAGACCAGAAACTGCACAGGGGATTTTCTTGA
ATTTCAAACGACTTTTGGAGTTCAACCAAGGAAAGTTGCCTTTTGCTGCTGCCCAGATTGGAAATTCTTTTAGAA
ATGAGATCTCCCCTCGATCTGGACTGATCAGAGTCAGAGAATTCACAATGGCAGAAATTGAGCACTTTGTAGATC
CCAGTGAGAAAGACCACCCCAAGTTCCAGAATGTGGCAGACCTTCACCTTTATTTGTATTCAGCAAAAGCCCAGG
TCAGCGGACAGTCCGCTCGGAAAATGCGCCTGGGAGATGCTGTTGAACAGGGTGTGATTAATAACACAGTATTAG
GCTATTTCATTGGCCGCATCTACCTCTACCTCACGAAGGTTGGAATATCTCCAGATAAACTCCGCTTCCGGCAGC
ACATGGAGAATGAGATGGCCCATTATGCCTGTGACTGTTGGGATGCAGAATCCAAAACATCCTACGGTTGGATTG
AGATTGTTGGATGTGCTGATCGTTCCTGTTATGACCTCTCCTGTCATGCACGAGCCACCAAAGTCCCACTTGTAG
CTGAGAAACCTCTGAAAGAACCCAAAACAGTCAATGTTGTTCAGTTTGAACCCAGTAAGGGAGCAATTGGTAAGG
CATATAAGAAGGATGCAAAACTGGTGATGGAGTATCTTGCCATTTGTGATGAGTGCTACATTACAGAAATGGAGA
TGCTGCTGAATGAGAAAGGGGAATTCACAATTGAAACTGAAGGGAAAACATTTCAGTTAACAAAAGACATGATCA
ATGTGAAGAGATTCCAGAAAACACTATATGTGGAAGAAGTTGTTCCGAATGTAATTGAACCTTCCTTCGGCCTGG
GTAGGATCATGTATACGGTATTTGAACATACATTCCATGTACGAGAAGGAGATGAACAGAGAACATTCTTCAGTT
TCCCTGCTGTAGTTGCTCCATTCAAATGTTCCGTCCTCCCACTGAGCCAAAACCAGGAGTTCATGCCATTTGTCA
AGGAATTATCGGAAGCCCTGACCAGGCATGGAGTATCTCACAAAGTAGACGATTCCTCTGGGTCAATCGGAAGGC
GCTATGCCAGGACTGATGAGATTGGCGTGGCTTTTGGTGTCACCATTGACTTTGACACAGTGAACAAGACCCCCC
ACACTGCAACTCTGAGGGACCGTGACTCAATGCGGCAGATAAGAGCAGAGATCTCTGAGCTGCCCAGCATAGTCC
AAGACCTAGCCAATGGCAACATCACATGGGCTGATGTGGAGGCCAGGTATCCTCTGTTTGAAGGGCAAGAGACTG
GTAAAAAAGAGACAATCGAGGAA**TGA**GGACAATTTTGACAACTTTTGACCACTTGCGCTAATAAAAAAAAAAAAA
CTACTCTTATGTCCACTTTACAAAAGAAAACAGCATTGTGATTACTCCCAGGGACCGTATTTTATCTTCAGTGGC
TGCCTGATTTTACCCCCACAATTAAAGTTGAAGGAATCCTGA

FIGURE 96

MDGAGAEEVLAPLRLAVRQQGDLVRKLKEDKAPQVDVDKAVAELKARKRVLEAKELALQPKDDIVDRAKMEDTLK
RRFFYDQAFAIYGGVSGLYDFGPVGCALKNNIIQTWRQHFIQEEQILEIDCTMLTPEPVLKTSGHVDKFADFMVK
DVKNGECFRADHLLKAHLQKLMSDKKCSVEKKSEMESVLAQLDNYGQQELADLFVNYNVKSPITGNDLSPPVSFN
LMFKTFIGPGGNMPGYLRPETAQGIFLNFKRLLEFNQGKLPFAAAQIGNSFRNEISPRSGLIRVREFTMAEIEHF
VDPSEKDHPKFQNVADLHLYLYSAKAQVSGQSARKMRLGDAVEQGVINNTVLGYFIGRIYLYLTKVGISPDKLRF
RQHMENEMAHYACDCWDAESKTSYGWIEIVGCADRSCYDLSCHARATKVPLVAEKPLKEPKTVNVVQFEPSKGAI
GKAYKKDAKLVMEYLAICDECYITEMEMLLNEKGEFTIETEGKTFQLTKDMINVKRFQKTLYVEEVVPNVIEPSF
GLGRIMYTVFEHTFHVREGDEQRTFFSFPAVVAPFKCSVLPLSQNQEFMPFVKELSEALTRHGVSHKVDDSSGSI
GRRYARTDEIGVAFGVTIDFDTVNKTPHTATLRDRDSMRQIRAEISELPSIVQDLANGNITWADVEARYPLFEGQ
ETGKKETIEE

FIGURE 97

TCCCCGCCCTTCTCTTTTCTACAGTATCTGTTACCTCAGTCAGATTGAGGATGCACATATACTGGGAAAATAATC
GACTTCCAGCGTCCCTCATGTAGTCTCTACCTGATTCAGGAATCTCTAACCCAGTATCGGAACGTTAAGCGGCTT
CTCCGCTTTCCTGCCGTGAGAAACTCGAGGTGACCAACCTCCGTTTCCGGTTGGCTCCGGTTGCAGAGTTGAGTG
TCCTGAGAGGTCAGATTGCTGTCAGAC**ATG**GCCCATGAACATGGACATGAGCATGGACATCATAAAATGGAACTT
CCAGATTATAGACAATGGAAGATAGAAGGGACACCATTAGAAACTATCCAGAAGAAGCTGGCTGCAAAAGGGCTA
AGGGATCCATGGGGCCGCAATGAAGCTTGGAGATACATGGGTGGCTTTGCAAAGAGTGTTTCCTTTTCTGATGTA
TTCTTTAAAGGATTCAAATGGGGATTTGCTGCATTTGTGGTAGCTGTAGGAGCTGAATATTACCTGGAGTCCCTG
AATAAAGATAAGAAGCATCAC**TGA**AGATAATACCTGGAAGCATCATAGTGGTTTCTTAACTCTCCAAAATAAGAT
TTCTTCTCTGTAGCCTACTTGTCTGGTTTATCCCTTACAGAATATTAGTAAAGATTTAATCAATTAAAATATATA
TAAAAAAAAAAAAAAAAA

FIGURE 98

MAHEHGHEHGHHKMELPDYRQWKIEGTPLETIQKKLAAKGLRDPWGRNEAWRYMGGFAKSVSFSDVFFKGFKWGF
AAFVVAVGAEYYLESLNKDKKHH

FIGURE 99

GCTGCGCCCCACGCCAGCCCGCGCCCCGC**ATG**GCTGCCGCCGGGGCCAGGCCTGTGGAGCTGGGCTTCGCCGAGT
CGGCGCCGGCGTGGCGACTGCGCAGCGAGCAGTTCCCCAGCAAGGTGGGCGGGCGGCCGGCATGGCTGGGCGCGG
CCGGGCTGCCGGGGCCCCAGGCCCTGGCCTGCGAGCTGTGCGGCCGCCCGCTCTCCTTCCTGCTGCAGGTGTATG
CGCCGCTGCCTGGCCGCCCGGACGCCTTCCACCGCTGCATCTTCCTCTTCTGCTGCCGCGAGCAGCCGTGCTGTG
CCGGCTTGCGAGTTTTTAGGAATCAACTACCCAGGAAAAACGATTTTTACTCATATGAGCCACCTTCTGAGAATC
CTCCCCCAGAAACAGGAGAATCAGTGTGTCTCCAGCTTAAGTCTGGTGCTCATCTCTGCAGGGTTTGTGGCTGTT
TAGGCCCCAAAACGTGCTCCAGATGCCACAAAGCATATTACTGCAGCAAGGAGCATCAGACCCTAGACTGGAGAT
TGGGACATAAGCAGGCTTGTGCACAACCAGATCATCTGGACCATATAATTCCAGACCACAACTTCCTTTTTCCAG
AATTTGAAATTGTAATAGAAACAGAAGATGAGATTATGCCTGAGGTTGTGGAAAAGGAAGATTACTCAGAGATTA
TAGGGAGCATGGGTGAAGCACTTGAGGAAGGACTGGATTCCATGGCAAAACATGAATCCAGGGAAGATAAAATTT
TTCAGAAGTTTAAAACTCAGATAGCCCTTGAACCAGAACAGATTCTTAGATATGGCAGAGGTATTGCCCCCATCT
GGATTTCTGGTGAAAATATTCCTCAAGAAAAGGATATTCCAGATTGCCCCTGTGGTGCCAAGAGAATATTGGAAT
TCCAGGTCATGCCTCAGCTCTTAAACTACCTGAAGGCTGACAGACTGGGCAAGAGCATTGACTGGGGCATCCTGG
CTGCTTTCACCTGTGCTGAGAGCTGCAGCTTGGGTACTGGTTATACAGAAGAATTTGTGTGGAAGCAGGATGTAA
CAGATACACCG**TAA**AGGCATCTTAAAGCCTTGAAAAATGTTAATAATCTTTTATACCTTGCAATTCCATTTCTGG
GATTTTATCCTAAGGAAATACTTATACCAAAAATAGAGGTGCAGAGATGTTGACGGATTGCTTACACAGTGTCTA
CTTATTAGTGAAACAAAAGTGTCCAGTGACAGGGAATTAAATAAATTTTGGTACATCCACAAAAAAAAAAAAAAA
AAAAAAA

FIGURE 100

MAAAGARPVELGFAESAPAWRLRSEQFPSKVGGRPAWLGAAGLPGPQALACELCGRPLSFLLQVYAPLPGRPDAF
HRCIFLFCCREQPCCAGLRVFRNQLPRKNDFYSYEPPSENPPPETGESVCLQLKSGAHLCRVCGCLGPKTCSRCH
KAYYCSKEHQTLDWRLGHKQACAQPDHLDHIIPDHNFLFPEFEIVIETEDEIMPEVVEKEDYSEIIGSMGEALEE
GLDSMAKHESREDKIFQKFKTQIALEPEQILRYGRGIAPIWISGENIPQEKDIPDCPCGAKRILEFQVMPQLLNY
LKADRLGKSIDWGILAAFTCAESCSLGTGYTEEFVWKQDVTDTP

FIGURE 101

TGGGCAATTAACCAAGCCATAGCCAATGAATATGAAGTCCGGAGAAAGCTGCTAATAAAACGTTTGGATGTCACT
GTACAATCCTTTGGCTGGTCTGACAGAGCTAAGAGCCAGACAGAAAAATTAGCCAAGGTTTACCAGCCGAAACGT
TCAGTCTTATCCCCTAAAACTACTATTTCTGTTGCCCATCTTTTGGCTGCAAGGCAGGACTTGTCAAAGATTTTA
AGGACAAGCAGCGGCTCTATAAGAGAAAAGACTGCCTGTGCCATCAATAAGGTGTTGATGGGCAGGGTGCCTGAC
AGAGGTGGTAGACCCAATGAAATCGAACCTCCACCCCCAGAGATGCCACCGTGGCAGAAGAGGCAAGATGGCCCC
CAGCAGCAAACAGGAGGCCGAGTAGGAGGGAGAGGTGGCTATGAACATTCCTCATACGGAGGACGAGGAGGTCAT
GAACAAGGAGGCGGGAGAGGTGGACGTGGTGGCTATGACCATGGTGGCCGAGGGGGAGGAAGAGGAAATAAGCAT
CAAGGAGGCTGGACAGATGGAGGGAGTGGTGGAGGAGGTGGCTACCAAGATGGTGGTTATCGAGATTCAGGTTTC
CAGCCAGGTGGCTATCATGGTGGCCACAGCAGTGGTGGCTATCAAGGCGGAGGTTATGGTGGCTTCCAAACATCT
TCTTCATATACAGGAAGTGGATACCAGGGTGGTGGCTACCAGCAGGACAATAGATACCAAGATGGCGGGCACCAT
GGTGATCGTGGTGGTGGTCGTGGTGGGCGAGGTGGTCGTGGAGGCCGAGGTGGTCGTGCAGGCCAGGGAGGAGGC
TGGGGAGGAAGAGGGAGCCAGAATTATCACCAAGGGGGTCAATTTGAACAGCATTTCCAGCATGGAGGTTATCAG
TATAATCATTCTGGATTTGGACAGGGAAGACATTACACTAGT**TGA**GGCTACCGAACTTTACATTTTGCTAGAGCT
CAAGTAATAGAAACTTAGTTTCAGAATCCTGAATTCAGCACCTATTTTGAATTAATGTGAGACCACAGGTGGCAG
GCAGATTCCTGCTTGGCATAAGCATTTGTAGGTCTTCATTCAATTCTGTTAGATTTTTTTATTGGACTTACATAA
TGCCGTTTATTTGAGAAACACATAACATCTCTCCTTCCTATGAAAAATTTTTTAAAAGGTGGTTAAAATTGCCTT
TAATTGCCCAGTAGACTAATTCCACAGTCAGAACATGCAAACTTTTTTGAAGAAATTACTTGAATAAGTAGTTTT
CATGTTTTCAATATGCAGTTTTGAAAATGAGGATTCACCTAGACTTTTTTAGATTTACTACTAGGAAACCTTCCT
CATATGAATAACCATTTATATGTGTTTTGCTTAAAGTATTCCAATGCCTATTTTCCAAGCACAGTTCTGCCCCCC
GGTTGACTTTTATGCCACGTGTGCTTCATGATGGAACTTTTAGGTCAGTTCCTATTAAATGAGCTCTTCTGCAGA
TAGCACATTCAGTAGCCTTATTTTGTTGATGGAATACTGTATCATATGCTCAACTCTGAAAACCTTGAACACGGC
CAAAATCCATAAAGATTATAAAAGCAAACTAAGTTGTGAAGCTATAGTACATGTAGGCATTTAGTTAAGTATAGC
AATTCAAACTGACCTGCATCCATCCAAAACAAATTCCTCCTTCAACCTTATTTTTACTTGAAATTTGCTAGAAGA
AATAGCAAACCGAAATTTGTTTTATGCATGAGTTAATACCACTGGCTCAGCAAATACAAGTTAGTTTGCTTTAAG
CAGGTAACTTTTTTTGTAATGGAAGAAATGCACTACAAAGTTAAGACAGATTTTTGCTAAGTGCAGGAGGCCCTT
TATTATTGCTGCAGAAAACAAAAGCCTGGCTGAGTTGATGTTTTACATTCTCCCTTACTGAAATCTACATGACAT
GATGCTTCTTGCTGGGTTTTTGTACATGTAAACATTGTCAAGCTGTGAAAGAAAATGGCTGGAGGTGTGCTTTGT
GTGAAAGGTGAGCAATAAAGTATCTGTTAAGTTCAAAAAAAAAAAAAAAAAAA

FIGURE 102

WAINQAIANEYEVRRKLLIKRLDVTVQSFGWSDRAKSQTEKLAKVYQPKRSVLSPKTTISVAHLLAARQDLSKIL
RTSSGSIREKTACAINKVLMGRVPDRGGRPNEIEPPPPEMPPWQKRQDGPQQQTGGRVGGRGGYEHSSYGGRGGH
EQGGGRGGRGGYDHGGRGGGRGNKHQGGWTDGGSGGGGGYQDGGYRDSGFQPGGYHGGHSSGGYQGGGYGGFQTS
SSYTGSGYQGGGYQQDNRYQDGGHHGDRGGGRGGRGGRGGRGGRAGQGGGWGGRGSQNYHQGGQFEQHFQHGGYQ
YNHSGFGQGRHYTS

FIGURE 103

GGGGGGGGAGATGCAGTAGCCGAAAACTGCGCGGAGGCACGAGAGGCCGGGGAGAGCGTTCTGGGTCCGAGGGTC
CAGGTAGGGGTTGAGCCACCATCTGACCGCAAGCTGCGTCGTGTCGCCTTCTCTGCAGGCACC**ATG**AGCCAGGAC
ACCGAGGTGGATATGAAGGAGGTGGAGCTGAATGAGTTAGAGCCCGAGAAGCAGCCGATGAACGCGGCGTCTGGG
GCGGCCATGTCCCTGGCGGAAGCCGAGAAGAATGGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGGCG
GCAGCCGCGGCTAAGTTCACGGGCCTGTCCAAGGAGGAGCTGCTGAAGGTGGCAGGCAGCCCCGGCTGGGTACGC
ACCCGCTGGGCACTGCTGCTGCTCTTCTGGCTCGGCTGGCTCGGCATGCTTGCTGGTGCCGTGGTGATAATCGTG
CGAGCGCCGCGTTGTCGCGAGCTACCGGCGCAGAAGTGGTGGCACACGGGCCCCCTCTACCGCATCGGCGACCTT
CAGGCCTTCCAGGGCCACGGCGCGGGCAACCTGGCGGGTCTGAAGGGGCGTCTCGATTACCTGAGCTCTCTGAAG
GTGAAGGGCCTTGTGCTGGGTCCAATTCACAAGAACCAGAAGGATGATGTCGCTCAGACTGACTTGCTGCAGATC
GACCCCAATTTTGGCTCCAAGGAAGATTTTGACAGTCTCTTGCAATCGGCTAAAAAAAAGAGCATCCGTGTCATT
CTGGACCTTACTCCCAACTACCGGGGTGACAACTCGTGGTTCTCCACTCAGGTTGACACTGTGGCCACCAAGGTG
AAGGATGCTCTGGAGTTTTGGCTGCAAGCTGGCGTGGATGGGTTCCAGGTTCGGGACATAGAGAATCTGAAGGAT
GCATCCTCATTCTTGGCTGAGTGGCAAAATATCACCAAGGGCTTCAGTGGAGACAGGCTCTTGATTGCGGGGACT
AACTCCTCCGACCTTCAGCAGATCCTGAGCCTACTCGAATCCAACAAAGACTTGCTGTTGACTAGCTCATACCTG
TCTGATTCTGGTTCTACTCCCCAGCATACAAAATCCCTAGTCACACAGTATTTGAATGCCACTGGCAATCGCTGG
TGCAGCTGGAGTTTGTCTCAGGCAAGGCTCCTGACTTCCTTCTTGCCGGCTCAACTTCTCCGACTCTACCAGCTG
ATGCTCTTCACCCTGCCAGGGACCCCTCTTTTCAGCTACGGGGATGAGATTGGCCTGGATGCAGCTGCCCTTCCT
CCACAGCCTATGGAGGCTCCAGTCATGCTGTGGGATGAGTCCAGCTTCCCTGACATCCCAGGGGCTGTAAGTGCC
AACATGACTGTGAAGGGCCAGAGTGAAGACCCTGGCTCCCTCCTTTCCTTGTTCCGGCGGCTGAGTGACCAGCGG
AGTAAGGAGCGCTCCCTACTGCATGGGGACTTCCACGCGTTCTCCGCTGGGCCTGGACTCTTCTCCTATATCCGC
CACTGGGACCAGAATGAGCGTTTTCTGGTAGTGCTTAACTTTGGGGATGTGGGCCTCTCGGCTGGACTGCAGGCC
TCCGACCTGCCTGCCAGCGCCAGCCTGCCAGCCAAGGCTGACCTCCTGCTCAGCACCCAGCCAGGCCGTGAGGAG
GGCTCCCCTCCTGAGCTGGGACGCCTGAAACTGGAGCCTCACGAAGGGCTGCTGCTCCGCTTCCCCTACGCGGCC
TGACCTCAGCCTGACATGGACCCACTACCCTTCTCCTTTCCTTCCCAGGCCCTTTGGCTTCTGATTTTTTTTCTC
TTTTTTAAAACAAACAAACAAACTGTTGCAGATTATGAGTGAACCCCAAATAGGGTGTTTT

FIGURE 104

MSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAEAEKNGLVKIKVAEDEAEAAAAAKFTGLSKEELLKVAGSP
GWVRTRWALLLLFWLGWLGMLAGAVVIIVRAPRCRELPAQKWWHTGPLYRIGDLQAFQGHGAGNLAGLKGRLDYL
SSLKVKGLVLGPIHKNQKDDVAQTDLLQIDPNFGSKEDFDSLLQSAKKKSIRVILDLTPNYRGDNSWFSTQVDTV
ATKVKDALEFWLQAGVDGFQVRDIENLKDASSFLAEWQNITKGFSGDRLLIAGTNSSDLQQILSLLESNKDLLLT
SSYLSDSGSTPQHTKSLVTQYLNATGNRWCSWSLSQARLLTSFLPAQLLRLYQLMLFTLPGTPLFSYGDEIGLDA
AALPPQPMEAPVMLWDESSFPDIPGAVSANMTVKGQSEDPGSLLSLFRRLSDQRSKERSLLHGDFHAFSAGPGLF
SYIRHWDQNERFLVVLNFGDVGLSAGLQASDLPASASLPAKADLLLSTQPGREEGSPPELGRLKLEPHEGLLLRF
PYAA

FIGURE 105A

GATCAATACTGAGGCCGCGTCGACCCCCTTGAGCCGAGACCCCCCCCAGCCCAGCCCCCACCCCACCCCCCGCA
CACGCCCCACCCCCCCCACGACCCAGCCTCATACCGCACCAGCTGAGGCACCCAAGAGGATTACCCCCTGGGGCC
CTCTCCCGCCCCCCAAAAAAGAGAAGATCCCCTCTCCTGGCCCATCCCTTCCCTTCTTCCCTCCCCCCTCCCCCC
GAACTTTCCCTCTCGCATGCTTTTCCCCTGCACCACGGATCGCCTCTCGGATGCCGCTTGCCTGGAAGCTGCGTT
AGGAGCGAGCGGCGGCGGTGGCGGCGGTGGCGGCGGCGGCGGCAGCTCGGGAGTGCT**ATG**ACCGGCAAACTCGCC
GAGAAGCTGCCGGTGACCATGAGCAGTTTGCTAAACCAACTGCCTGACAATCTGTACCCCGAGGAGATCCCCAGC
GCGCTCAACCTCTTCTCCGGCAGCAGCGACTCGGTAGTCCATTACAATCAGATGGCTACAGAGAATGTAATGGAC
ATCGGTCTGACCAACGAGAAGCCCAACCCGGAACTCTCTTACTCCGGCTCCTTCCAGCCAGCCCCCGGGAACAAG
ACCGTGACCTACTTGGGAAAGTTCGCCTTCGACTCCCCTTCCAACTGGTGCCAGGACAACATCATTAGCCTCATG
AGCGCCGGCATCTTGGGGGTGCCCCCGGCTTCAGGGGCGCTAAGCACGCAGACGTCCACGGCCAGCATGGTGCAG
CCACCGCAGGGTGACGTGGAGGCCATGTATCCCGCGCTACCCCCCTACTCCAACTGCGGCGACCTCTACTCAGAG
CCCGTGTCTTTCCACGACCCCCAGGGCAATCCCGGGCTCGCCTATTCCCCCCAGGATTACCAATCGGCCAAGCCG
GCGTTGGACAGCAATCTCTTCCCCATGATTCCTGACTACAACCTCTACCACCACCCCAACGACATGGGCTCCATT
CCGGAGCACAAGCCCTTCCAGGGCATGGACCCCATCCGGGTCAACCCGCCCCCTACTACCCCTCTGGAGACCATC
AAGGCATTCAAAGACAAGCAGATCCACCCGGGCTTTGGCAGCCTGCCCCAGCCGCCGCTCACCCTCAAGCCCATC
CGGCCCCGCAAGTACCCCAACCGGCCTAGCAAGACACCGCTCCACGAACGGCCCCACGCGTGCCCGGCCGAGGGC
TGCGACCGCCGTTTCAGCCGTTCGGACGAGCTGACCCGGCACCTGCGCATCCACACGGGCCACAAGCCCTTCCAG
TGCCGGATCTGCATGCGGAGCTTCAGCCGCAGCGACCACCTCACCACTCACATCCGCACTCATACGGGCGAGAAG
CCCTTTGCCTGCGAGTTCTGCGGGCGCAAGTTTGCGCGCAGCGACGAGCGCAAGCGCCACGCCAAGATCCACCTC
AAGCAAAAGGAGAAGAAGGCGGAGAAGGGCGGTGCACCCTCTGCATCCTCGGCGCCCCCCGTGTCGCTGGCCCCC
GTGGTCACCACCTGCGCC**TGA**GGATCGGGCCCCCAGATCCCCACTTTTCCCCTCCAGTGCCTCCCGGCTGCTAGC
CTGAAAGCAGCGGGAAAGCCAGCCACGGAGGCGTAGGGGCCGCGCCCTGGCCTCTCCATGGACGTGCGGCCCCTT
GCTTCCCCTTCGATGCCCCCGGTTCCCAACCTTTCACGCCGGCCAGCGGTCAGGGGCCAGGGCTGGAGGCGCCTT
CCCCTCGCGGTCCCCCACTTAGCCAAGGCGTGGGGGCGGAAAGGTGGCGTCTAGCCCGCTTTGTTCAGTTCGGAT
CGCCTTGATCCAGGGGCCGCCGGGCCGCGCCAAGGACCTGCAAGGGACTGAAGGCGGAGCCCATCCAACCCTCGC
CCGACCCAAACACCTCATTGTTTCCCCCACGTCTCCCTCTATACCCCCTCGAAGACTCGAGAGGGGGAGGGGGTA
AGGAGCGCACCAAAGCGCAGAGCTTGCTGCCCGCCGCACGCACGCGCGCCTGCGTGCGGGGATGCGCGCGAGTGT
GTGCGTGCTCGCGTGTGTGTGTATGTGTGTGTGTGAGTGTGTGTGTGTGCGCGCGCGCAAGCGTGTGTGTTTAAG
ACTCTTGAGCTGAACTGGGCTGTGTTTACCCCAAACTCTTCCCCACCTCGGGTCCCCAAGCCGCTGGGAGATGTC
CCATGCTGGGGGTCCGCACGTGGCTGGAGGAGGTGGTCTTCCATCCGCTCTGAAATCATGTTTCTTAGAGAAATG
CCTCGGATGCCGCCGACGCGGTGCTGCTGCCGCCGCTTCGGGTTTGGCCCCTCAGAACCCCTCCTTTTCTGAGCG
CTTCCCTCTTAGGCCTCAGGGCAGTTTGATCTGTGGGGAGAAAGAGCAGCCATCGCTGAGCCTGCCTTTTAAAAT
ATATGTGTATTTCCTTAGCCCCACTCTAAGAAATCTATGTTCCTGAGTTTGCCCCCTGCCCTCCCACTCCTTCCC
CTTTTCCCCTCTAAACCTTCTCCCATCTCTTTCAAAATCTTTTCCCAGAAAGGCAGGCTTCAACCAGCCACTCCA
GCTTTGTGTCTTCTCTCAATTACATAGCAATTTCTCCTTCCCACCATCATGGGGAAGCTGGCTCTGCTTTTGCCC
TTTGTCATCACCAACACAACAGATAGAATTTAAATATAAGTATATGGTGTGCGTGTGTATGTATGTGTATGTATA
TGCATGCATGTGTATAAAGATGCACATGCGTACATATACATAACATACACACAATATGTATTCCTAGCAAAATAA
AATCTCTAAGGTACTTGGTTATCCAGTGCAGTGCACCGGAATAAAGAGAATTTGTAGGCGTATACAGCTTTAAAT
GATTTATTTTTTATGAAAATGTTAACTGATGAGATTATATCTACATACGTGTGTTATGTGTGTGGATATAGATGC
ACACATATCTGTACATATACATGTGAGTGTACATATATACACATATACACATCTATGTATGGATATGTGTGTATA
CACATATACACATCTCTGTCCAAAATTTCCTCAAAGATATGGGGATTTTTTCATGAATCCATGTGGATGAATGAG
GTGTCTCCTTTCCATACCCAGTCTCACCTTCTCCCCACCCTACCTCACCTCTTCTCAGGCACCCCTCTTCCCCAG
CTGTCCTGCCAGCCCTTCTCGTACAGGGTGGCTCCTTTGAAGTGGAGTAATAGGGAAGGTTGCTCTCTGCCACAG
CTTGCAGCATGGTCTTGACTGAATGTACTGTTCCTGTTAGCGTTACTTCTCCTGTGGTCAGTAAGTTGCCCAGAG
AGAAGGAACAAAGGTCTGGAGTTTACAGAATGTCTGTTTTTAAAGTCACTTTATGCGTTTTCCACTTTTTTCTTT
TTTAAGAAAAAGAAGTACCATTTTTGTTTTGTTTTGTTTTGATTTTTGGTGGTGGATAAATAATACTAAAAGGAC
TCTAGTGGAAAGGGGGGATATCGAAGAGCAGGGGGTTGTGAATTTCCAGGTACTTGGACTTTTTGTAGAAGTAGA
GAGAAGAAGATGAAGTTTGCCAGGAGGGCCCATATTTTTTCAGCTGAAGGGTAAAATCTTTCTTTGCAGAGACAG

FIGURE 105B

TATTTTGCTGAATACTTTTTATAATGTGATGATTATTAAAAAAGCAAAAATTTTGGTCACTTCCAAGCTAGAAGG
AGGAATCAGATACCCTTTAATATTTTTTCCTCGCTCCTTCTGGTATATGCATGTCACTGCATGATAATTGAGTTT
TCCTTTGTTTTAATAAAACTGTTCTCAGACATTAAGCTAAACTAAGAGAAAAATAACTTTGTTGCCAAAAGGTTG
TGCTATCCAGATTTTTTATATGTCTGCATGTTTAAAAAAAAAAAAGCAACAAAAGAAAATGCACTCTAACTTATG
TGAACTGAGAGAAAAAAAATCAGGTTTTAAACAGGAAAACCTATGGGGAATGATATTTTTTGAAAGACTTTTGTAT
AAAGTTGAGTACTTAGAAAAAAGACAAACCAGATGTAATATATTTTGTGGATGTTTTTATTTCTTGGATTTATAG
TACCTTATACTAAGGTTAAAAAAATATGCTTGATATTGTGAAAAGGTGAAATTCTTCACCAACATTTCATTTGCT
CCTTTGTCATATTGTAATGCCAATATAATATAGTTAATGAAAACAGCATTTTTAAAAACCGAAATATTGAAATGG
TGTAATGTTGTACCATTTGCACTGTGAGCAAATGCTAATACAGTAAATATATTGTGTTTGCTGACAATCAAAAAA
AAAAAAAAAAAAAA

FIGURE 106

MTGKLAEKLPVTMSSLLNQLPDNLYPEEIPSALNLFSGSSDSVVHYNQMATENVMDIGLTNEKPNPELSYSGSFQ
PAPGNKTVTYLGKFAFDSPSNWCQDNIISLMSAGILGVPPASGALSTQTSTASMVQPPQGDVEAMYPALPPYSNC
GDLYSEPVSFHDPQGNPGLAYSPQDYQSAKPALDSNLFPMIPDYNLYHHPNDMGSIPEHKPFQGMDPIRVNPPPT
TPLETIKAFKDKQIHPGFGSLPQPPLTLKPIRPRKYPNRPSKTPLHERPHACPAEGCDRRFSRSDELTRHLRIHT
GHKPFQCRICMRSFSRSDHLTTHIRTHTGEKPFACEFCGRKFARSDERKRHAKIHLKQKEKKAEKGGAPSASSAP
PVSLAPVVTTCA

FIGURE 107

CTGCACCAATACACTGAGTGAAGGAAGAGAGACAGAGGATCAAGGGCTTTAGACAGCACTCCTTCAATATGCAAT
CACAGAGAAAGATGCGCCTGATCCAAGTTAATATCTCTAAGGTGAGAGCCTTCTTAGAGTCAGTTTGTTGCAAAT
TTCACCTACTCTGTTCTTTTCCATCCATCCCCCTGAGTCAGTTGGTTGAAGGGAGTTATTTTTTCAAGTGGAATT
CAAACAAAGCTCAAACCAGAACTGTAAATAGTGATTGCAGGAATTATTTTCTAAACTGCTTTGCCCTTTCCTCTC
ACTGCCTTTTATAGCCAATATAAATGTCTCTTTGCACACCTTTTGTTGTGGTTTTATATTGTAACACCATTTTTC
TTTGAAACTATTGTATTTAAAGTAAGGTTTCATATTATGTCAGCAAGTAATTAACTTATGTTTAAAAGGTGGCCA
TATCATGTACCAAAAGTTGCTGAAGTTTCTCTTCTAGCTGGTAAAGTAGGAGTTTGCATGACTTCACACTTTTTT
TGCGTAGTTTCTTCTGTTGTATGATGGCGTGAGTGTGTGTCTTGGGTACCGCTGTGTACTACTGTGTGCCTAGAT
TCCATGCACTCTCGTTGTGTTTGAAGTAAATATTGGAGACCGGAGGGTAACAGGTTGGCCTGTTGATTACAGCTA
GTAATCGCTGTGTCTTGTTCCGCCCCCTCCCTGACACCCCAGCTTCCCAGGATGTGGAAAGCCTGGATCTCAGCT
CCTTGCCCCATATCCCTTCTGTAATTTGTACCTAAAGAGTGTGATTATCCTAATTCAAGAGTCACTAAAACTCAT
CACATTATCATTGCATATCAGCAAAGGGTAAAGTCCTAGCACCAATTGCTTCACATACCAGCATGTTCCATTTCC
AATTTAGAATTAGCCACATAATAAAATCTTAGAATCTTCCTTGAGAAAGAGCTGCCTGAGATGTAGTTTTGTTAT
ATGGTTCCCCACCGACCATTTTTGTGCTTTTTTCTTGTTTTGTTTTGTTTTGACTGCACTGTGAGTTTTGTAGTG
TCCTCTTCTTGCCAAAACAAACGCGAGATGAACTGGACTTATGTAGACAAATCGTGATGCCAGTGTATCCTTCCT
TTCTTCAGTTCCAGCAATAATGAATGGTCAACTTTTTTAAAATCTAGATCTCTCTCATTCATTTCAATGTATTTT
TACTTTAAGATGAACCAAAATTATTAGACTTATTTAAGATGTACAGGCATCAGAAAAAAGAAGCACATAATGCTT
TTGGTGCGATGGCACTCACTGTGAACATGTGTAACCACATATTAATATGCAATATTGTTTCCAATACTTTCTAAT
ACAGTTTTTTATAATGTTGTGTGTGGTGATTGTTCAGGTCGAATCTGTTGTATCCAGTACAGCTTTAGGTCTTCA
GCTGCCCTTCTGGCGAGTACATGCACAGGATTGTAAATGAGAAATGCAGTCATATTTCCAGTCTGCCTCTATGAT
GATGTTAAATTATTGCTGTTTAGCTGTGAACAAGGGATGTACCACTGGAGGAATAGAGTATCCTTTTGTACACAT
TTTGAAATGCTTCTTCTGTAGTGATAGAACAAATAAATGCAACGAATACTCTGTCTGCCCTATCCCGTGAAGTCC
ACACTGGCGTAAGAGAAGGCCCAGCAGAGCAGGAATCTGCCTAGACTTTCTCCCAATGAGATCCCAATATGAGAG
GGAGAAGAGATGGGCCTCAGGACAGCTGCAATACCACTTGGGAACACATGTGGTGTCTTGATGTGGCCAGCGCAG
CAGTTCAGCACAACGTACCTCCCATCTACAACAGTGCTGGACGTGGGAATTCTAAGTCCCAGTCTTGAGGGTGGG
TGGAGATGGAGGGCAACAAGAGATACATTTCCAGTTCTCCACTGCAGCATGCTTCAGTCATTCTGTGAGTGGCCG
GGCCCAGGGCCCTCACAATTTCACTACCTTGTCTTTTACATAGTCATAAGAATTATCCTCAACATAGCCTTTTGA
CGCTGTAAATCTTGAGTATTCATTTACCCTTTTCTGATCTCCTGGAAACAGCTGCCTGCCTGCATTGCACTTCTC
TTCCCGAGGAGTGGGGTAAATTTAAAAGTCAAGTTATAGTTTGGATGTTAGTATAGAATTTTGAAATTGGGAATT
AAAAATCAGGACTGGGGACTGGGAGACCAAAAAATTTCTGATCCCATTTCTGATGG**ATG**TGTCACACCTTTTCTGT
CAAAATAAAATGTCTTGGAGGTTATGACTCCTTGGTGAAAAAAA

FIGURE 108

MCHTFSVKIKCLGGYDSLVK

FIGURE 109

TGCTGCGAACCACGTGGGTCCCGGGCGCGTTTCGGGTGCTGGCGGCTGCAGCCGGAGTTCAAACCTAAGCAGCTG
GAAGGAACC**ATG**GCCAACTGTGAGCGTACCTTCATTGCGATCAAACCAGATGGGGTCCAGCGGGGTCTTGTGGGA
GAGATTATCAAGCGTTTTGAGCAGAAAGGATTCCGCCTTGTTGGTCTGAAATTCATGCAAGCTTCCGAAGATCTT
CTCAAGGAACACTACGTTGACCTGAAGGACCGTCCATTCTTTGCCGGCCTGGTGAAATACATGCACTCAGGGCCG
GTAGTTGCCATGGTCTGGGAGGGGCTGAATGTGGTGAAGACGGGCCGAGTCATGCTCGGGGAGACCAACCCTGCA
GACTCCAAGCCTGGGACCATCCGTGGAGACTTCTGCATACAAGTTGGCAGGAACATTATACATGGCAGTGATTCT
GTGGAGAGTGCAGAGAAGGAGATCGGCTTGTGGTTTCACCCTGAGGAACTGGTAGATTACACGAGCTGTGCTCAG
AACTGGATCTATGAA**TGA**CAGGAGGGCAGACCACATTGCTTTTCACATCCATTTCCCCTCCTTCCCATGGGCAGA
GGACCAGGCTGTAGGAAATCTAGTTATTTACAGGAACTTCATCATAATTTGGAGGGAAGCTCTTGGAGCTGTGAG
TTCTCCCTGTACAGTGTTACCATCCCCGACCATCTGATTAAAATGCTTCCTCCCAGC

FIGURE 110

MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPFFAGLVKYMHSGPVVA
MVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWI
YE

FIGURE 111A

GCGAGCGCAGCGGAGCCTGGAGAGAAGGCGCTGGGCTGCGAGGGCGCGAGGGCGCGAGGGCAGGGGGCAACCGGA
CCCCGCCCGCACCC**<u>ATG</u>**GCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCTCTGGGCTGCGGCGC
ACGCCTTGCCCGCCCAGGTGGCATTTACACCCTACGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACT
ATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCT
CGGACACCGTGTGTGACTCCTGTGAGGACAGCACATACACCCAGCTCTGGAACTGGGTTCCCGAGTGCTTGAGCT
GTGGCTCCCGCTGTAGCTCTGACCAGGTGGAAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCA
GGCCCGGCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCGCCCGG
GCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGACGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCA
ACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCATCCCTGGGAATGCAAGCA
TGGATGCAGTCTGCACGTCCACGTCCCCCACCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCCAGCCAGTGT
CCACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGG
GCCCCAGCCCCCCAGCTGAAGGGAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGACAGCCT
TGGGTCTACTAATAATAGGAGTGGTGAACTGTGTCATCATGACCCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGA
GAGAAGCCAAGGTGCCTCACTTGCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAGCAGCACCTGCTGA
TCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGAGAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGA
ACCAGCCACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGCCAGCACCGGGAGCTCAGATTCTT
CCCCTGGTGGCCATGGGACCCAGGTCAATGTCACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCTCAC
AGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCCAGCCCCTCGGAGTCCCCGAAGGACGAGCAGG
TCCCCTTCTCCAAGGAGGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGGGGAGCACCGAAG
AGAAGCCCCTGCCCCTTGGAGTGCCTGATGCTGGGATGAAGCCCAGT**<u>TAA</u>**CCAGGCCGGTGTGGGCTGTGTCGTA
GCCAAGGTGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTTCCAGGCCCCCACCACTAGGAC
TCTGAGGCTCTTTCTGGGCCAAGTTCCTCTAGTGCCCTCCACAGCCGCAGCCTCCCTCTGACCTGCAGGCCAAGA
GCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCCTCTCGGAAGGCTGGCTGGGCATGGACGT
TCGGGGCATGCTGGGGCAAGTCCCTGACTCTCTGTGACCTGCCCCGCCCAGCTGCACCTGCCAGCCTGGCTTCTG
GAGCCCTTGGGTTTTTTGTTTGTTTGTTTGTTTGTTTGTTTGTTTCTCCCCCTGGGCTCTGCCCAGCTCTGGCTT
CCAGAAAACCCCAGCATCCTTTTCTGCAGAGGGGCTTTCTGGAGAGGAGGGATGCTGCCTGAGTCACCCATGAAG
ACAGGACAGTGCTTCAGCCTGAGGCTGAGACTGCGGGATGGTCCTGGGGCTCTGTGTAGGGAGGAGGTGGCAGCC
CTGTAGGGAACGGGGTCCTTCAAGTTAGCTCAGGAGGCTTGGAAAGCATCACCTCAGGCCAGGTGCAGTGGCTCA
CGCCTATGATCCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTTAGGAGTTCGAGACCAGCCTGGC
CAACATGGTAAAACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGCGTGGTGGCGGGCACCTATAGTCCCAG
CTACTCAGAAGCCTGAGGCTGGGAAATCGTTTGAACCCGGGAAGCGGAGGTTGCAGGGAGCCGAGATCACGCCAC
TGCACTCCAGCCTGGGCGACAGAGCGAGAGTCTGTCTCAAAAGAAAAAAAAAAAAGCACCGCCTCCAAATGCTAA
CTTGTCCTTTTGTACCATGGTGTGAAAGTCAGATGCCCAGAGGGCCCAGGCAGGCCACCATATTCAGTGCTGTGG
CCTGGGCAAGATAACGCACTTCTAACTAGAAATCTGCCAATTTTTTAAAAAAGTAAGTACCACTCAGGCCAACAA
GCCAACGACAAAGCCAAACTCTGCCAGCCACATCCAACCCCCCACCTGCCATTTGCACCCTCCGCCTTCACTCCG
GTGTGCCTGCAGCCCCGCGCCTCCTTCCTTGCTGTCCTAGGCCACACCATCTCCTTTCAGGGAATTTCAGGAACT
AGAGATGACTGAGTCCTCGTAGCCATCTCTCTACTCCTACCTCAGCCTAGACCCTCCTCCTCCCCCAGAGGGGTG
GGTTCCTCTTCCCCACTCCCCACCTTCAATTCCTGGCCCCAAACGGGCTGCCCTGCCACTTTGGTACATGGCCA
GTGTGATCCCAAGTGCCAGTCTTGTGTCTGCGTCTGTGTTGCGTGTCGTGGGTGTGTGTAGCCAAGGTCGGTAAG
TTGAATGGCCTGCCTTGAAGCCACTGAAGCTGGGATTCCTCCCCATTAGAGTCAGCCTTCCCCCTCCCAGGGCCA
GGGCCCTGCAGAGGGGAAACCAGTGTAGCCTTGCCCGGATTCTGGGAGGAAGCAGGTTGAGGGGCTCCTGGAAAG
GCTCAGTCTCAGGAGCATGGGGATAAAGGAGAAGGCATGAAATTGTCTAGCAGAGCAGGGGCAGGGTGATAAATT
GTTGATAAATTCCACTGGACTTGAGCTTGGCAGCTGAACTATTGGAGGGTGGGAGAGCCCAGCCATTACCATGGA
GACAAGAAGGGTTTTCCACCCTGGAATCAAGATGTCAGACTGGCTGGCTGCAGTGACGTGCACCTGTACTCAGGA
GGCTGAGGGGAGGATCACTGGAGCCCAGGAGTTTGAGGCTGCAGCGAGCTATGATCGCGCCACTACACTCCAGCC
TGAGCAACAGAGTGAGACCCTGTCTCTTAAAGAAAAAAAAAGTCAGACTGCTGGGACTGGCCAGGTTTCTGCCCA
CATTGGACCCACATGAGGACATGATGGAGCGCACCTGCCCCCTGGTGGACAGTCCTGGGAGAACCTCAGGCTTCC
TTGGCATCACAGGGCAGAGCCGGGAAGCGATGAATTTGGAGACTCTGTGGGGCCTTGGTTCCCTTGTGTGTGTGT

FIGURE 111B

GTTGATCCCAAGACAATGAAAGTTTGCACTGTATGCTGGACGGCATTCCTGCTTATCAATAAACCTGTTTGTTTT
AAAAAAAA

FIGURE 112

MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVC
DSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA
RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQ
HTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV
PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGH
GTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
LGVPDAGMKPS

FIGURE 113A

GCCCTGCTTCCCCTTGCACCTGCGCCGGGCGGCC**ATG**GACTTGTACAGCACCCCGGCCGCTGCGCTGGACAGGTT
CGTGGCCAGAAGGCTGCAGCCGCGGAAGGAGTTCGTAGAGAAGGCGCGGCGCGCTCTGGGCGCCCTGGCCGCTGC
CCTGAGGGAGCGCGGGGGCCGCCTCGGTGCTGCTGCCCCGCGGGTGCTGAAAACTGTCAAGGGAGGCTCCTCGGG
CCGGGGCACAGCTCTCAAGGGTGGCTGTGATTCTGAACTTGTCATCTTCCTCGACTGCTTCAAGAGCTATGTGGA
CCAGAGGGCCCGCCGTGCAGAGATCCTCAGTGAGATGCGGGCATCGCTGGAATCCTGGTGGCAGAACCCAGTCCC
TGGTCTGAGACTCACGTTTCCTGAGCAGAGCGTGCCTGGGGCCCTGCAGTTCCGCCTGACATCCGTAGATCTTGA
GGACTGGATGGATGTTAGCCTGGTGCCTGCCTTCAATGTCCTGGGTCAGGCCGGCTCCGCGGTCAAACCCAAGCC
ACAAGTCTACTCTACCCTCCTCAACAGTGGCTGCCAAGGGGGCGAGCATGCGGCCTGCTTCACAGAGCTGCGGAG
GAACTTTGTGAACATTCGCCCAGCCAAGTTGAAGAACCTAATCTTGCTGGTGAAGCACTGGTACCACCAGGTGTG
CCTACAGGGGTTGTGGAAGGAGACGCTGCCCCCGGTCTATGCCCTGGAATTGCTGACCATCTTCGCCTGGGAGCA
GGGCTGTAAGAAGGATGCTTTCAGCCTAGGCGAAGGCCTCCGAACTGTCCTGGGCCTGATCCAACAGCATCAGCA
CCTGTGTGTTTTCTGGACTGTCAACTATGGCTTCGAGGACCCTGCAGTTGGGCAGTTCTTGCAGCGGCACGTTAA
GAGACCCAGGCCTGTGATCCTGGACCCAGCTGACCCCACATGGGACCTGGGGAATGGGGCAGCCTGGCACTGGGA
TTTGCATGCCCAGGAGGCAGCATCCTGCTATGACCACCCATGCTTTCTGAGGGGGATGGGGGACCCAGTGCAGTC
TTGGAAGGGGCCGGGCCTTCCACGTGCTGGATGCTCAGGTTTGGGCCACCCCATCCAGCTAGACCCTAACCAGAA
GACCCCTGAAAACAGCAAGAGCCTCAATGCTGTGTACCCAAGAGCAGGGAGCAAACCTCCCTCATGCCCAGCTCC
TGGCCCCACTGCGGAGCCAGCATCGTACCCCTCTGTGCCGGGAATGGCCTTGGACCTGTCTCAGATCCCCACCAA
GGAGCTGGACCGCTTCATCCAGGACCACCTGAAGCCGAGCCCCCAGTTCCAGGAGCAGGTGAAAAAGGCCATCGA
CATCATCTTGCGCTGCCTCCATGAGAACTGTGTTCACAAGGCCTCAAGAGTCAGTAAAGGGGGCTCATTTGGCCG
GGGCACAGACCTAAGGGATGGCTGTGATGTTGAACTCATCATCTTCCTCAACTGCTTCACGGACTACAAGGACCA
GGGGCCCCGCCGCGCAGAGATCCTTGATGAGATGCGAGCGCACGTAGAATCCTGGTGGCAGGACCAGGTGCCCAG
CCTGAGCCTTCAGTTTCCTGAGCAGAATGTGCCTGAGGCTCTGCAGTTCCAGCTGGTGTCCACAGCCCTGAAGAG
CTGGACGGATGTTAGCCTGCTGCCTGCCTTCGATGCTGTGGGGCAGCTCAGTTCTGGCAGCAAACCAAATCCCCA
GGTCTACTCGAGGCTCCTCACCAGTGGCTGCCAGGAGGGCGAGCATAAGGCCTGCTTCGCAGAGCTGCGGAGGAA
CTTCATGAACATTCGCCCTGTCAAGCTGAAGAACCTGATTCTGCTGGTGAAGCACTGGTACCGCCAGGTTGCGGC
TCAGAACAAAGGAAAAGGACCAGCCCCTGCCTCTCTGCCCCCAGCCTATGCCCTGGAGCTCCTCACCATCTTTGC
CTGGGAGCAGGGCTGCAGGCAGGATTGTTTCAACATGGCCCAAGGCTTCCGGACGGTGCTGGGGCTCGTGCAACA
GCATCAGCAGCTCTGTGTCTACTGGACGGTCAACTATAGCACTGAGGACCCAGCCATGAGAATGCACCTTCTTGG
CCAGCTTCGAAAACCCAGACCCCTGGTCCTGGACCCCGCTGATCCCACCTGGAACGTGGGCCACGGTAGCTGGGA
GCTGTTGGCCCAGGAAGCAGCAGCGCTGGGGATGCAGGCCTGCTTTCTGAGTAGAGACGGGACATCTGTGCAGCC
CTGGGATGTGATGCCAGCCCTCCTTTACCAAACCCCAGCTGGGGACCTTGACAAGTTCATCAGTGAATTTCTCCA
GCCCAACCGCCAGTTCCTGGCCCAGGTGAACAAGGCCGTTGATACCATCTGTTCATTTTTGAAGGAAAACTGCTT
CCGGAATTCTCCCATCAAAGTGATCAAGGTGGTCAAGGGTGGCTCTTCAGCCAAAGGCACAGCTCTGCGAGGCCG
CTCAGATGCCGACCTCGTGGTGTTCCTCAGCTGCTTCAGCCAGTTCACTGAGCAGGGCAACAAGCGGGCCGAGAT
CATCTCCGAGATCCGAGCCCAGCTGGAGGCATGTCAACAGGAGCGGCAGTTCGAGGTCAAGTTTGAAGTCTCCAA
ATGGGAGAATCCCCGCGTGCTGAGCTTCTCACTGACATCCCAGACGATGCTGGACCAGAGTGTGGACTTTGATGT
GCTGCCAGCCTTTGACGCCCTAGGCCAGCTGGTCTCTGGCTCCAGGCCCAGCTCTCAAGTCTACGTCGACCTCAT
CCACAGCTACAGCAATGCGGGCGAGTACTCCACCTGCTTCACAGAGCTACAACGGGACTTCATCATCTCTCGCCC
TACCAAGCTGAAGAGCCTGATCCGGCTGGTGAAGCACTGGTACCAGCAGTGTACCAAGATCTCCAAGGGGAGAGG
CTCCCTACCCCCACAGCACGGGCTGGAACTCCTGACTGTGTATGCCTGGGAGCAGGGCGGGAAGGACTCCCAGTT
CAACATGGCTGAGGGCTTCCGCACGGTCCTGGAGCTGGTCACCCAGTACCGCCAGCTCTGTATCTACTGGACCAT
CAACTACAACGCCAAGGACAAGACTGTTGGAGACTTCCTGAAACAGCAGCTTCAGAAGCCCAGGCCTATCATCCT
GGATCCGGCTGACCCGACAGGCAACCTGGGCCACAATGCCCGCTGGGACCTGCTGGCCAAGGAAGCTGCAGCCTG
CACATCTGCCCTGTGCTGCATGGGACGGAATGGCATCCCCATCCAGCCATGGCCAGTGAAGGCTGCTGTG**TGA**AG
TTGAGAAAATCAGCGGTCCTACTGGATGAAGAGAAGATGGACACCAGCCCTCAGCATGAGGAAATTCAGGGTCCC
CTACCAGATGAGAGAGATTGTGTACATGTGTGTGTGAGCACATGTGTGCATGTGTGTGCACACGTGTGCATGTGT
GTGTTTTAGTGAATCTGCTCTCCCAGCTCACACACTCCCCTGCCTCCCATGGCTTACACACTAGGATCCAGACTC
CATGGTTTGACACCAGCCTGCGTTTGCAGCTTCTCTGTCACTTCCATGACTCTATCCTCATACCACCACTGCTGC

FIGURE 113B

TTCCCACCCAGCTGAGAATGCCCCCTCCTCCCTGACTCCTCTCTGCCCATGCAAATTAGCTCACATCTTTCCTCC
TGCTGCAATCCATCCCTTCCTCCCATTGGCCTCTCCTTGCCAAATCTAAATACTTTATATAGGGATGGCAGAGAG
TTCCCATCTCATCTGTCAGCCACAGTCATTTGGTACTGGCTACCTGGAGCCTTATCTTCTGAAGGGTTTTAAAGA
ATGGCCAATTAGCTGAGAAGAATTATCTAATCAATTAGTGATGTCTGCCATGGATGCAGTAGAGGAAAGTGGTGG
TACAAGTGCCATGATTGATTAGCAATGTCTGCACTGGATATGGAAAAAAGAAGGTGCTTGCAGGTTTACAGTGTA
TATGTGGGCTATTGAAGAGCCCTCTGAGCTCGGTTGCTAGCAGGAGAGCATGCCCATATTGGCTTACTTTGTCTG
CCACAGACACAGACAGAGGGAGTTGGGACATGCATGCTATGGGGACCCTCTTGTTGGACACCTAATTGGATGCCT
CTTCATGAGAGGCCTCCTTTTCTTCACCTTTTATGCTGCACTCCTCCCCTAGTTTACACATCTTGATGCTGTGGC
TCAGTTTGCCTTCCTGAATTTTTATTGGGTCCCTGTTTTCTCTCCTAACATGCTGAGATTCTGCATCCCCACAGC
CTAAACTGAGCCAGTGGCCAAACAACCGTGCTCAGCCTGTTTCTCTCTGCCCTCTAGAGCAAGGCCCACCAGGTC
CATCCAGGAGGCTCTCCTGACCTCAAGTCCAACAACAGTGTCCACACTAGTCAAGGTTCAGCCCAGAAAACAGAA
AGCACTCTAGGAATCTTAGGCAGAAAGGGATTTTATCTAAATCACTGGAAAGGCTGGAGGAGCAGAAGGCAGAGG
CCACCACTGGACTATTGGTTTCAATATTAGACCACTGTAGCCGAATCAGAGGCCAGAGAGCAGCCACTGCTACTG
CTAATGCCACCACTACCCCTGCCATCACTGCCCCACATGGACAAAACTGGAGTCGAGACCTAGGTTAGATTCCTG
CAACCACAAACATCCATCAGGGATGGCCAGCTGCCAGAGCTGCGGGAAGACGGATCCCACCTCCCTTTCTTAGCA
GAATCTAAATTACAGCCAGACCTCTGGCTGCAGAGGAGTCTGAGACATGTATGATTGAATGGGTGCCAAGTGCCA
GGGGGCGGAGTCCCCAGCAGATGCATCCTGGCCATCTGTTGCGTGGATGAGGGAGTGGGTCTATCTCAGAGGAAG
GAACAGGAAACAAAGAAAGGAAGCCACTGAACATCCCTTCTCTGCTCCACAGGAGTGTCTTAGACAGCCTGACTC
TCCACAAACCACTGTTAAAACTTACCTGCTAGGAATGCTAGATTGAATGGGATGGGAAGAGCCTTCCCTCATTAT
TGTCATTCTTGGAGAGAGGTGAGCAACCAAGGGAAGCTCCTCTGATTCACCTAGAACCTGTTCTCTGCCGTCTTT
GGCTCAGCCTACAGAGACTAGAGTAGGTGAAGGGACAGAGGACAGGGCTTCTAATACCTGTGCCATATTGACAGC
CTCCATCCCTGTCCCCCATCTTGGTGCTGAACCAACGCTAAGGGCACCTTCTTAGACTCACCTCATCGATACTGC
CTGGTAATCCAAAGCTAGAACTCTCAGGACCCCAAACTCCACCTCTTGGATTGGCCCTGGCTGCTGCCACACACA
TATCCAAGAGCTCAGGGCCAGTTCTGGTGGGCAGCAGAGACCTGCTCTGCCAAGTTGTCCAGCAGCAGAGTGGCC
CTGGCCTGGGCATCACAAGCCAGTGATGCTCCTGGGAAGACCAGGTGGCAGGTCGCAGTTGGGTACCTTCCATTC
CCACCACACAGACTCTGGGCCTCCCCGCAAAATGGCTCCAGAATTAGAGTAATTATGAGATGGTGGGAACCAGAG
CAACTCAGGTGCATGATACAAGGAGAGGTTGTCATCTGGGTAGGGCAGAGAGGAGGGCTTGCTCATCTGAACAGG
GGTGTATTTCATTCCAGGCCCTCAGTCTTTGGCAATGGCCACCCTGGTGTTGGCATATTGGCCCCACTGTAACTT
TTGGGGGCTTCCCGGTCTAGCCACACCCTCGGATGGAAAGACTTGACTGCATAAAGATGTCAGTTCTCCCTGAGT
TGATTGATAGGCTTAATGGTCACCCTAAAAACACCCACATATGCTTTTCGATGGAACCAGATAAGTTGACGCTAA
AGTTCTTATGGAAAAATACACACGCAATAGCTAGGAAAACACAGGGAAAGAAGAGTTCTGAGCAGGGCCTAGTCT
TAGCCAATATTAAAACATACTATGAAGCCTCTGATACTTAAACAGCATGGCGCTGGTACGTAAATAGACCAATGC
AGTTAGGTGGCTCTTTCCAAGACTCTGGGGAAAAAAGTAGTAAAAAGCTAAATGCAATCAATCAGCAATTGAAAG
CTAAGTGAGAGAGCCAGAGGGCCTCCTTGGTGGTAAAAGAGGGTTGCATTTCTTGCAGCCAGAAGGCAGAGAAAG
TGAAGACCAAGTCCAGAACTGAATCCTAAGAAATGCAGGACTGCAAAGAAATTGGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTTTAATTTTTAAAAAGTTTTTATTCGGAATCCGCG

FIGURE 114

MDLYSTPAAALDRFVARRLQPRKEFVEKARRALGALAAALRERGGRLGAAAPRVLKTVKGGSSGRGTALKGGCDS
ELVIFLDCFKSYVDQRARRAEILSEMRASLESWWQNPVPGLRLTFPEQSVPGALQFRLTSVDLEDWMDVSLVPAF
NVLGQAGSAVKPKPQVYSTLLNSGCQGGEHAACFTELRRNFVNIRPAKLKNLILLVKHWYHQVCLQGLWKETLPP
VYALELLTIFAWEQGCKKDAFSLGEGLRTVLGLIQQHQHLCVFWTVNYGFEDPAVGQFLQRHVKRPRPVILDPAD
PTWDLGNGAAWHWDLHAQEAASCYDHPCFLRGMGDPVQSWKGPGLPRAGCSGLGHPIQLDPNQKTPENSKSLNAV
YPRAGSKPPSCPAPGPTAEPASYPSVPGMALDLSQIPTKELDRFIQDHLKPSPQFQEQVKKAIDIILRCLHENCV
HKASRVSKGGSFGRGTDLRDGCDVELIIFLNCFTDYKDQGPRRAEILDEMRAHVESWWQDQVPSLSLQFPEQNVP
EALQFQLVSTALKSWTDVSLLPAFDAVGQLSSGTKPNPQVYSRLLTSGCQEGEHKACFAELRRNFMNIRPVKLKN
LILLVKHWYRQVAAQNKGKGPAPASLPPAYALELLTIFAWEQGCRQDCFNMAQGFRTVLGLVQQHQQLCVYWTVN
YSTEDPAMRMHLLGQLRKPRPLVLDPADPTWNVGHGSWELLAQEAAALGMQACFLSRDGTSVQPWDVMPALLYQT
PAGDLDKFISEFLQPNRQFLAQVNKAVDTICSFLKENCFRNSPIKVIKVVKGGSSAKGTALRGRSDADLVVFLSC
FSQFTEQGNKRAEIISEIRAQLEACQQERQFEVKFEVSKWENPRVLSFSLTSQTMLDQSVDFDVLPAFDALGQLV
SGSRPSSQVYVDLIHSYSNAGEYSTCFTELQRDFIISRPTKLKSLIRLVKHWYQQCTKISKGRGSLPPQHGLELL
TVYAWEQGGKDSQFNMAEGFRTVLELVTQYRQLCIYWTINYNAKDKTVGDFLKQQLQKPRPIILDPADPTGNLGH
NARWDLLAKEAAACTSALCCMGRNGIPIQPWPVKAAV

FIGURE 115A

GAAGTATAAGTGGGATTTTCACCAAAACCCTATCCTTCCCCAGACTCCAGTGACAGTTTAACGGTCAGCTGCATC
AAGGCTTGTGTACTGTGCAGTCTTAAAAGGCACCACTCCTGTCCATCTCGGTGAAATTGATGGTGGAGCAAAAGG
GAGTTTAGGTGGTTCCGGTCTGGGGAGAAGACGTGCAGGGTTTCAGATGCGAAAGTCGCACCCAACCGCTTCACT
CGGGCTCTAGGCCATCCGCAGGGGCCCTGCTTCCTTCCACCTGCGAGCTTTTTCTGCAGAATGCGGGAAGCCGCC
GCCGCCGCCACAGAGGAGGGGGCGGAGGCAGAGGCGGAGGCGGCACCCAGGGGCCGGGGCAGGGGAGGCCGGGAC
CATCGCAGTGACAATTTATTTTCCTGCAGCAGCGGCAGCAGGGACGGTTGCTGCAGGTTCGGGGTCGGCCGGCCT
GCGCGTGGGCTTGCGAGGACGCTGTTCGTCCCCTGCGCTGGGGTGTCCGACAGCGAGGAGGAGAACGACGCACGG
AGCCCGCGCGACTGGAACCAGCAAAGCTCCATCTGTCGGCAGAGGAGAAGGGGGAGGAGGCACGGCCGAGGCAAA
CGAGCGGACGCCTCGTCGCCGGGTGCCGGTATCACCCCGCTGCAACGCCTTCCAGCAAAAGCCACCGCGGCCCGG
GTTGCAGCAGCCGGACGGATGCCAAGGCCACACGGCAGCCACGGGGGCAGCCGTCGCAGTCGCCGTCCCACACGG
GCTGCGGACACCAAGGGTTGCTAATGAAGTGATTGAGAAGAAACAGTGAACATCCTCATTTCACAGATAAGACAA
CATGGATCAGCCTTTTACTGTGAATTCTCTGAAAAAGTTAGCTGCTATGCCTGACCATACAGATGTTTCCCTAAG
CCCAGAAGAGCGAGTCCGTGCCCTAAGCAAGCTTGGTTGTAATATCACCATCAGTGAAGACATCACTCCACGACG
TTACTTTAGGTCTGGAGTAGAGATGGAGAGGATGGCGTCTGTGTATTTGGAAGAAGGAAATTTGGAAAATGCCTT
TGTTCTTTATAATAAATTTATAACCTTATTTGTAGAAAAGCTTCCTAACCATCGAGATTACCAGCAATGTGCAGT
ACCTGAAAAGCAGGATATTATGAAGAAACTGAAGGAGATTGCATTCCCAAGGACAGATGAATTGAAAAACGACCT
TTTAAAGAAATATAACGTAGAATACCAAGAATATTTGCAAAGCAAAAACAAATATAAAGCTGAAATTCTCAAAAA
ATTGGAGCATCAGAGATTGATAGAGGCAGAAAGGAAGCGGATTGCTCAGATGCGCCAGCAGCAGCTAGAATCGGA
GCAGTTTCTGTTTTTCGAAGATCAACTCAAGAAGCAAGAGTTAGCCCGAGGTCAAATGCGAAGTCAGCAAACCTC
AGGGCTGTCAGAGCAGATTGATGGGAGCGCTTTGTCCTGCTTTTCCACACACCAGAACAATTCCTTGCTGAATGT
ATTTGCAGATCAACCTAATAAAAGTGATGCAACCAATTATGCTAGCCACTCTCCTCCTGTAAACAGGGCCTTAAC
GCCAGCTGCTACTCTAAGTGCTGTTCAGAATTTAGTGGTTGAAGGACTGCGATGTGTAGTTTTGCCAGAAGATCT
TTGCCACAAATTTCTGCAACTGGCAGAATCTAATACAGTGAGAGGAATAGAAACCTGTGGAATACTCTGTGGAAA
ACTGACACATAATGAATTTACTATTACCCATGTAATTGTGCCAAAGCAGTCTGCGGGACCAGACTATTGTGACAT
GGAGAATGTAGAGGAATTATTCAATGTTCAGGATCAACATGATCTCCTCACTCTAGGATGGATCCATACACATCC
CACTCAAACTGCATTTTTATCCAGCGTTGATCTTCACACTCACTGTTCCTATCAACTCATGTTGCCAGAGGCCAT
TGCCATTGTTTGCTCACCAAAGCATAAAGACACTGGCATCTTCAGGCTCACCAATGCTGGCATGCTTGAGGTTTC
TGCTTGTAAAAAAAAGGGCTTTCATCCACACACCAAGGAGCCCAGGCTGTTCAGTATTCAGAAATTCCTTTCTGG
GATAATTTCTGGCACTGCTTTGGAGATGGAGCCCCTGAAAATTGGCTATGGACCAAATGGATTCCCACTCTTGGG
GATCTCTAGGTCATCATCACCATCTGAACAGCTCTGAGAGAGACAAGAAGTGGAATGGAGAAGGTGATTAGGTAA
TCCAAGAATTGCCAGGCGAACAATTGTGAAAATCTTTCATAGAGTTCCCGATGAAAACAACTCTTTCTTGTTAGC
CATTATCTCTGCCTTTCCTTTCTAAAGAAAAACACGTCATTTCATCTTGATTATCAGTTTCTCAAGTACTCATGG
ATGTGAGGCCAGGTACCCTGTCACCTTGGCTCTGTTTGGGATGCAATGTTGTGTTTGTCACCACTTCCCATTCCC
CAAAAGCATCTTTAACATAGACCATTCATTCTTCAGATTCAAAATGCTTAAGCTGAACTAACCTCAAAGGGCCCT
CATTAATTTACAGACATTTGAATAACACCCATATTCATTTCTGCTACTGAACCAAAGCCTTTTCCAAAAAAATCA
TCTAGCAAACTGTTTTTGCCAGGCCAAATATTAACAGGTATATATATTTGCATACATAAATATTTACCTCTATGT
CTTGTGTGTTTTTGTTATGAGACAGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGGCACAGTCTCAGCTCA
CTGCAACCTCCACCTCCCAGGTTCAAGCGATTCTCATGCCTCAGCCTCCCGAGTAGCGAGGACTACAGGCGTGCA
CCACCACGCCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTACCCTGTTGGCCAGGGTGGTCTCGAATT
CCTGACCTCTGATGATCTGCCCGCCTGGACCTCTCAAAGTGCTGGGATTACAGACATGAGCCACTGTGCCCTGCC
TCTGTTTTGTGTATTTACATAAATACATGTCTCCAGAGCTTTAAATTCTTCTTAAATTTTAAAACTAGAACTAAA
CCAGACATTGAGAGGACCCAGAAATATACCCTGACTAACGTGGGTGGAATTTCATTTGGCTTGACTCTTTGGTGA
AAAAAAAAAAAAATCAGGCTCTCAAGGACTCAATTTGGTGAACCAATGCCAAATAGAAAAATGTTCTTGACATTTT
CCCCAAAATAGATGTCTAAAGATTTTGCACTTCAAATTGGTACTTTATGTATTAAAAGTGATATTGAAACTAAAT
TCCTACCCAATTAGTTGAAAAATATGAAAAAAGCAATTGCTAGAGAATGCAATTTATTAAATGTTGGTGGTCTTT
TAAAAAATGAATTCCTCTTGTAGCCAGTGAGATCAGTTATTTATTTATTTATTTTAATAGTAACAAGGTCTCACT
ATATTGTCCAGGCTGATCTTGAACTCCTGGCCTCAAGCTGTCCTCCCATCTCAGCTTCCCAAAGTGCTGAGATTA
TAGGCATGAGCCACCATGCCTGGCTAGTTAATGGTTATTAAGTAATACAAACATTTCTGTGAATTCCACCAGATC

FIGURE 115B

ATTGACTTTGGCATAGTTCACTTAAGACTTTGTTTGATAAAATAAATCTCTTTCACTCTAATTAGGAAGCATTTT
TGGGATCCTGATTAATGCTCTAATATTGTGGGGCCAAAAAATATGTGGAACGTGGCCCTGCAGTTAGATGAGCTG
AGATCACTATAGTACTATATAGCGCTCTAAATCCTAAATGCTAGATCACTGTAATACTGTACAGATCAGCCACTT
GCTGGCTTGTGACTCTGGGCCATTTACTTCACCTCTCAAAAGGCATATTTAAAGTGAGGAAAATAATAAGTTTAT
TTTGGAAATTCAGTTAGATGATGCAAATTGTTTACTGTAATTTCTAGCATGTAGTTCGTGCTCCATGCATTTAAC
TGTTATTACAGGTTGTATTAGTATCACATTAAATTACCCACTGAAGTGAAAGTGAAACCAGAATGCTGTCAACGA
TT

FIGURE 116

DNMDQPFTVNSLKKLAAMPDHTDVSLSPEERVRALSKLGCNITISEDITPRRYFRSGVEMERMASVYLEEGNLEN
AFVLYNKFITLFVEKLPNHRDYQQCAVPEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQEYLQSKNKYKAEIL
KKLEHQRLIEAERKRIAQMRQQQLESEQFLFFEDQLKKQELARGQMRSQQTSGLSEQIDGSALSCFSTHQNNSLL
NVFADQPNKSDATNYASHSPPVNRALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGILC
GKLTHNEFTITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWIHTHPTQTAFLSSVDLHTHCSYQLMLPE
AIAIVCSPKHKDTGIFRLTNAGMLEVSACKKKGFHPHTKEPRLFSIQKFLSGIISGTALEMEPLKIGYGPNGFPL
LGISRSSSPSEQL

FIGURE 117

ATCCCCTCCGGTTTTCCTCAGTCTCCACGTACGTCCCTCAAAGCGCGTCCTAAAACCCGGATAACCGGAGCGCTC
CCC**ATG**GACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGGAAATTTGGTGAG
CGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTAAAAGAGCGAGGGGATCAAACAGTACTT
ATTCTTCATGCAAAAGTTGCACAGAAGTCATATGGAAATGAAAAAAGGTTTTTTTGCCCACCTCCTTGTGTATAT
CTTATGGGCAGCGGATGGAAGAAAAAAAAAGAACAAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCG
TGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGAAGGAAAGAACTATTGCACA
GCCAAAACATTGTATATATCTGACTCAGACAAGCGAAAGCACTTCATTTTTTCTGTAAAGATGTTCTATGGCAAC
AGTGATGACATTGGTGTGTTCCTCAGCAAGCGGATAAAAGTCATCTCCAAACCTTCCAAAAAGAAGCAGTCATTG
AAAAATGCTGACTTATGCATTGCCTCAGGAACAAAGGTGGCTCTGTTTAATCGACTACGATCCCAGACAGTTAGT
ACCAGATACTTGCATGTAGAAGGAGGTAATTTTCATGCCAGTTCACAGCAGTGGGGAGCCTTTTTTATTCATCTC
TTGGATGATGATGAATCAGAAGGAGAAGAATTCACAGTCCGAGATGTCTACATCCATTATGGACAAACATGCAAA
CTTGTGTGCTCAGTTACTGGCATGGCACTCCCAAGATTGATAATTATGAAAGTTGATAAGCATACCGCATTATTG
GATGCAGATGATCCTGTGTCACAACTCCATAAATGTGCATTTTACCTTAAGGATACAGAAAGAATGTATTTGTGC
CTTTCTCAAGAAAGAATAATTCAATTTCAGGCCACTCCATGTCCAAAAGAACCAAATAAAGAGATGATAAATGAT
GGCGCTTCCTGGACAATCATTAGCACAGATAAGGCAGAGTATACATTTTATGAGGGAATGGGCCCTGTCCTTGCC
CCAGTCACTCCTGTGCCTGTGGTAGAGAGCCTTCAGTTGAATGGCGGTGGGGACGTAGCAATGCTTGAACTTACA
GGACAGAATTTCACTCCAAATTTACGAGTGTGGTTTGGGGATGTAGAAGCTGAAACTATGTACAGGTGTGGAGAG
AGTATGCTCTGTGTCGTCCCAGACATTTCTGCATTCCGAGAAGGTTGGAGATGGGTCCGGCAACCAGTCCAGGTT
CCAGTAACTTTGGTCCGAAATGATGGAATCATTTATTCCACCAGCCTTACCTTTACCTACACACCAGAACCAGGG
CCACGGCCACATTGCAGTGTAGCAGGAGCAATCCTTCCAGCCAATTCAAGCCAGGTGCCCCCTAACGAATCAAAC
ACAAACAGCGAGGGAAGTTACACAAACGCCAGCACAAATTCAACCAGTGTCACATCATCTACAGCCACAGTGGTA
TCCTA

FIGURE 118

MDHTEGLPAEEPPAHAPSPGKFGERPPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPPPCVYL
MGSGWKKKKEQMERDGCSEQESQPCAFIGIGNSDQEMQQLNLEGKNYCTAKTLYISDSDKRKHFIFSVKMFYGNS
DDIGVFLSKRIKVISKPSKKKQSLKNADLCIASGTKVALFNRLRSQTVSTRYLHVEGGNFHASSQQWGAFFIHLL
DDDESEGEEFTVRDVYIHYGQTCKLVCSVTGMALPRLIIMKVDKHTALLDADDPVSQLHKCAFYLKDTERMYLCL
SQERIIQFQATPCPKEPNKEMINDGASWTIISTDKAEYTFYEGMGPVLAPVTPVPVVESLQLNGGGDVAMLELTG
QNFTPNLRVWFGDVEAETMYRCGESMLCVVPDISAFREGWRWVRQPVQVPVTLVRNDGIIYSTSLTFTYTPEPGP
RPHCSVAGAILPANSSQVPPNESNTNSEGSYTNASTNSTSVTSSTATVVS

FIGURE 119

GGTAAAGAGACAACTTACAGATTGGGAGAATATATTTCCAAACTATTGTTGGGGCTCAGAAACGGATACCCTAAC
ATATAGTGATTTGACAGGTGGAACTAAAGAAGACTCGAGGTCTCTC<u>**TGA**</u>CCTCCTCCTCAACCTCTGTTTCTTAA
TCCTCTGTTTTCCCAGAGCACAGGAGGAAGTTCTCTGAAGTTCCTTTATCTGCTTTAAGTTCAGACTCACCAAAT
AAGAAAACAGTTAATTCTGGTGCCTTCCATGGGTTTTCATTAACTGAAGTCATATTGTAGGAAAAAGAATGAAGT
CTCTTAACCCACCTGGATAGATTTTTCTCACAAACCATTGTCTTCTCTGCAAGCCCAGTAGACTTTGTCCCAGGC
CATTTATGTGATCTTCACCCCATTAAGTTCTCCCCAAATTATTTACTCTTCCCCCAAAATCACCCACACTTCCCC
ATCTCCCTCTCCCCTAAGGACAAGGGTATATCACCATCTATACCCCATTGCTTGGTGGGGTGATCACTCTGATTC
TCTGCATGCATTTTTATAGATTTGTTTGCCATTTATCCTATTAATCTGCATTCTGTCAATTGTGGCAAGTTATCA
GCATATTTTTTAACTTTTAATTATTATTAATGGAAAGACACTTCTGTATACACTGGAAATCTCAGGAAATTTCTT
TTTTCCTTAAGCTTAATTGAAATGTTTACTTTTCAGTAAAATTTCAAGCTTGAGTAATGTTCATGCCTGCTTTTC
ATTGAAATAGAATGAAAAGGTTGCACAATATTATTTTCATGAAATTACTTCTAGTATAATTCTGAATAAACACTT
TGAAAGGCAGTGAACTGTAAATATATTACAGCTATCTCTTATTCTTCAGGGCGGGTCTCAATTATGTAAAAGATG
ATTGGCTTTCTGTTTTAAGTAATAGTCATTTTGAAAACACTTTAAAACTGTCAAGTGAAG

FIGURE 120

VKRQLTDWENIFPNYCWGSETDTLTYSDLTGGTKEDSRSL

FIGURE 121

CGGCAGCCAGCTGAGAGCA**ATG**GGAAATGGGGAGTCCCAGCTGTCCTCGGTGCCTGCTCAGAAGCTGGGTTGGTT
TATCCAGGAATACCTGAAGCCCTACGAAGAATGTCAGACACTGATCGACGAGATGGTGAACACCATCTGTGACGT
CTGCAGGAACCCCGAACAGTTCCCCCTGGTGCAGGGAGTGGCCATAGGTGGCTCCTATGGACGGAAAACAGTCTT
AAGAGGCAACTCCGATGGTACCCTTGTCCTTTTCTTCAGTGACTTAAAACAATTCCAGGATCAGAAGAGAAGCCA
ACGTGACATCCTCGATAAAACTGGGGATAAGCTGAAGTTCTGTCTGTTCACGAAGTGGTTGAAAAACAATTTCGA
GATCCAGAAGTCCCTTGATGGGTCCACCATCCAGGTGTTCACAAAAAATCAGAGAATCTCTTTCGAGGTGCTGGC
CGCCTTCAACGCTCTGAGCTTAAATGATAATCCCAGCCCCTGGATCTATCGAGAGCTCAAAAGATCCTTGGATAA
GACAAATGCCAGTCCTGGTGAGTTTGCAGTCTGCTTCACTGAACTCCAGCAGAAGTTTTTTGACAACCGTCCTGG
AAAACTAAAGGATTTGATCCTCTTGATAAAGCACTGGCATCAACAGTGCCAGAAAAAAATCAAGGATTTACCCTC
GCTGTCTCCGTATGCCCTGGAGCTGCTTACGGTGTATGCCTGGGAACAGGGGTGCAGAAAAGACAACTTTGACAT
TGCTGAAGGCGTCAGAACGGTTCTGGAGCTGATCAAATGCCAGGAGAAGCTGTGTATCTATTGGATGGTCAACTA
CAACTTTGAAGATGAGACCATCAGGAACATCCTGCTGCACCAGCTCCAATCAGCGAGGCCAGTAATCTTGGATCC
AGTTGACCCAACCAATAATGTGAGTGGAGATAAAATATGCTGGCAATGGCTGAAAAAAGAAGCTCAAACCTGGTT
GACTTCTCCCAACCTGGATAATGAGTTACCTGCACCATCTTGGAATGTCCTGCCTGCACCACTCTTCACGACCCC
AGGCCACCTTCTGGATAAGTTCATCAAGGAGTTTCTCCAGCCCAACAAATGCTTCCTAGAGCAGATTGACAGTGC
TGTTAACATCATCCGTACATTCCTTAAAGAAAACTGCTTCCGACAATCAACAGCCAAGATCCAGATTGTCCGGGG
AGGATCAACCGCCAAAGGCACAGCTCTGAAGACTGGCTCTGATGCCGATCTCGTCGTGTTCCATAACTCACTTAA
AAGCTACACCTCCCAAAAAAACGAGCGGCACAAAATCGTCAAGGAAATCCATGAACAGCTGAAAGCCTTTTGGAG
GGAGAAGGAGGAGGAGCTTGAAGTCAGCTTTGAGCCTCCCAAGTGGAAGGCTCCCAGGGTGCTGAGCTTCTCTCT
GAAATCCAAAGTCCTCAACGAAAGTGTCAGCTTTGATGTGCTTCCTGCCTTTAATGCACTGGGTCAGCTGAGTTC
TGGCTCCACACCCAGCCCCGAGGTTTATGCAGGGCTCATTGATCTGTATAAATCCTCGGACCTCCCGGGAGGAGA
GTTTTCTACCTGTTTCACAGTCCTGCAGCGAAACTTCATTCGCTCCCGGCCCACCAAACTAAAGGATTTAATTCG
CCTGGTGAAGCACTGGTACAAAGAGTGTGAAAGGAAACTGAAGCCAAAGGGGTCTTTGCCCCCCAAAGTATGCCTT
GGAGCTGCTCACCATCTATGCCTGGGAGCAGGGGAGTGGAGTGCCGGATTTTGACACTGCAGAAGGTTTCCGGAC
AGTCCTGGAGCTGGTCACACAATATCAGCAGCTCGGCATCTTCTGGAAGGTCAATTACAACTTTGAAGATGAGAC
CGTGAGGAAGTTTCTACTGAGCCAGTTGCAGAAAACCAGGCCTGTGATCTTGGACCCAGGCGAACCCACAGGTGA
CGTGGGTGGAGGGGACCGTTGGTGTTGGCATCTTCTGGACAAAGAAGCAAAGGTTAGGTTATCCTCTCCCTGCTT
CAAGGATGGGACTGGAAACCCAATACCACCTTGGAAAGTGCCGGTAAAAGTCATC**TAA**AGGAGGCGTTGTCTGGA
AATAGCCCTGTAACAGGCTTGAATCAAAGAACTTCTCCTACTGTAGCAACCTGAAATTAACTCAGACACAAATAA
AGGAAACCCAGCTCACAGGAGCTTAAACAGCTGGTCAGCCCCCCTAAGCCCCCACTACAAGTGATCCTCAGGCAG
GTAACCCCAGATTCATGCACTGTAGGGCTGGGCGCAGCATCCCTAGGTCTCTACCCAGTAGATGCCACTAGCCCT
CCTCTCCCAGTGACAACCAAAAGTCTTCACATGTTCAAACGTTCCCCTGGGTTCACAGATCTTTCTGCCTTTGGC
TTTTGGCTCCACCCTCTTTAGCTGTTAATTTGAGTACTTATGGCCCTGAAAGCGGCCACGGTGCCTCCAGATGGC
AGGTTTGCAATCCAAGCAGGAAGAAGGAAAAGATACCCAAAGGTCAAGAACACAGTGATTTTATTAGAAGTTTCA
TCCGCAAATTTTCTTCCATTTCATTGCTCAGAATGTCATGTGGTTACCTGTAACTTGAAGGTGGCTACAAAGATG
ACTGTGGAGGTGGTTGCACTTGCCACCCAAGGATGTCTGCCACACCTCTCCAAGCCCTCCTACCTACCAAGATAT
ACCTGATATATCCACCAGATATCTCCTCAGATATACTTGGTTCTCTCCACCAGGTTCTTTCTTTAAAGCAGGATT
CTCAACTTTGATACTTACTCACATTGGGCTAGACAGTTCTTTGTTTGGAGGCTCTCTTGTGCATGTAGGATGTTG
AGCAGCATGTGTGGCCTGTACCCAGTACATGCCACCCAGTTGTGACAATTAAAAGTGTCTTGAGACTTTATCATG
TGTCTTCTGCCCTAGGTGAGAACCCTTGCACTACAGGAACCCTACACCCAACCTGGGGGGAATGTAGGGAAGAGG
TGCCAAGCCAACCGTGGGGTTAGCTCTAATTATTAAGTTATGCATTATAAATAAATACCAAAAAATTG

FIGURE 122

MGNGESQLSSVPAQKLGWFIQEYLKPYEECQTLIDEMVNTICDVCRNPEQFPLVQGVAIGGSYGRKTVLRGNSDG
TLVLFFSDLKQFQDQKRSQRDILDKTGDKLKFCLFTKWLKNNFEIQKSLDGSTIQVFTKNQRISFEVLAAFNALS
LNDNPSPWIYRELKRSLDKTNASPGEFAVCFTELQQKFFDNRPGKLKDLILLIKHWHQQCQKKIKDLPSLSPYAL
ELLTVYAWEQGCRKDNFDIAEGVRTVLELIKCQEKLCIYWMVNYNFEDETIRNILLHQLQSARPVILDPVDPTNN
VSGDKICWQWLKKEAQTWLTSPNLDNELPAPSWNVLPAPLFTTPGHLLDKFIKEFLQPNKCFLEQIDSAVNIIRT
FLKENCFRQSTAKIQIVRGGSTAKGTALKTGSDADLVVFHNSLKSYTSQKNERHKIVKEIHEQLKAFWREKEEEL
EVSFEPPKWKAPRVLSFSLKSKVLNESVSFDVLPAFNALGQLSSGSTPSPEVYAGLIDLYKSSDLPGGEFSTCFT
VLQRNFIRSRPTKLKDLIRLVKHWYKECERKLKPKGSLPPKYALELLTIYAWEQGSGVPDFDTAEGFRTVLELVT
QYQQLGIFWKVNYNFEDETVRKFLLSQLQKTRPVILDPGEPTGDVGGGDRWCWHLLDKEAKVRLSSPCFKDGTGN
PIPPWKVPVKVI

FIGURE 123

CTACTACTACTAAATTCGCGGCCXCTCXGGAATTGGCGACTTCGATATTAACAAGG**ATG**GCGGCGGCCGCAGCAA
GTCGAGGAGTCGGGGCAAAGCTGGGCCTGCGTGAGATTCGCATCCACTTATGTCAGCGCTCGCCCGGCAGCCAGG
GCGTCAGGGACTTCATTGAGAAACGCTACGTGGAGCTGAAGAAGGCGAATCCCGACCTACCCATCCTAATCCGCG
AATGCTCCGATGTGCAGCCCAAGCTCTGGGCCCGCTACGCATTTGGCCAAGAGACGAATGTCCCTTTGAACAACT
TCAGTGCTGATCAGGTAACCAGAGCCCTGGAGAACGTTCTAAGTGGTAAAGCC**TGA**AGCCTCCACTGAGGATTAA
GAGCAACAGCCCCAGAGCCTGGGCTCTGCTGGACTTAGTATAATGTGAAAAAAATGTGTTCTCCTATTCCTCATA
AAGCTTGTGCTGTAAAATACTTTCTCAGGGTGTTCTTGTCCTCATCTACCCTCTAACCCCTTAATGGTGCAACCA
CTGAGGCAAAGTAGCTTAATATAAAAATTAAACTTTATTCTGGCCTCATCAAAAAAAAAAAAAAA

FIGURE 124

MAAAAASRGVGAKLGLREIRIHLCQRSPGSQGVRDFIEKRYVELKKANPDLPILIRECSDVQPKLWARYAFGQET
NVPLNNFSADQVTRALENVLSGKA

FIGURE 125

CTGGTGGGCGTCAGGGGCAGGCAACAGAGTGGCGGCCGCTACGGCCCTGGAACGGGGCCATGGAGAAGCTGCGGC
GAGTCCTGAGCGGCCAGGACGACGAGGAGCAGGGCCTGACTGCGCAGGTCCTGGATGCCTCATCCCTTAGTTTCA
ACACCAGATTGAAATGGTTTGCCATCTGCTTCGTATGTGGCGTTTTCTTTTCTATTCTTGGAACTGGATTGCTGT
GGCTTCCGGGCGGCATAAAGCTTTTTGCAGTGTTTTATACCCTCGGCAATCTTGCTGCGTTAGCCAGTACATGCT
TTTTAATGGGACCTGTGAAGCAACTGAAGAAAATGTGTGAAGCAACAAGATTGCTTGCAACAATTGTTATGCTTT
TGTGTTTCATATTTACCCTGTGTGCTGCTCTTTGGTGGCATAAGAAAGGACTGGCTGTGTTATTCTGCATATTGC
AGTTCTTGTCAATGACCTGGTATAGCCTGTCGTACATCCCATATGCAAGGGATGCAGTTATTAAATGCTGTTCTT
CTCTCCTAAGTTGAAAATCAGAAACTTGTGGAAAAGAGCACTTGAATGTTGGTACTCTATGTTTGGTGAAGTTTG
CTTTTCCCCATAAAACACTCCAGGAACAACTGACGTGACAGTTGAAGACCGTXTTGTACTAAGTCTCATTTTGTA
TACTGGTAAAAACTACATGCTTGATTAAACCATTAAATGCTTGTAACTTTAAATTCATTATGTGTCATTAATATA
CTTTTCCAAAGATAAGATTTTTAATCACTGCCAGTTGTAAATTATTTTTAGCCAATTTTTAAATCTTTTCAAAGC
AGCTTTGAAATGTGAATATTTAAAGGTAGACCTGTGCTGCAAGATAATTAAACTTTTTTGCTTTTAAAAAATGTC
TGCATXTXTAAGATTTXTTTTACTTTAAATGTGAAACTTATTTXAAGCTAAAAATTGCTTATTATATGTAATAAA
AATAATATATAAATCTTTACAATTTTGAAATAAACCCATCCTTGGAAAAATAAAT

FIGURE 126

GGRQGQATEWRPLRPWNGAMEKLRRVLSGQDDEEQGLTAQVLDASSLSFNTRLKWFAICFVCGVFFSILGTGLLW
LPGGIKLFAVFYTLGNLAALASTCFLMGPVKQLKKMCEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
FLSMTWYSLSYIPYARDAVIKCCSSLLS

FIGURE 127

TGTCGGGGACGGTAACCGGGACCCGTGCTCTGCTCCTGTCGCCTTCGCCTCCTGAATCCCTAGCCAT**ATG**CGTGA
GTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTGCTGGGAGCTCTACTGCCTGGAACA
CGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTT
CAGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTGATGAAGT
TCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTA
TGCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTTGGACCGAATTCGCAAGCTGGCTGACCA
GTGCACCCGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTCACCTCCCTGCT
CATGGAACGCCTGTCAGTTGATTATGGCAAGAAATCCAAGCTGGAGTTCTCCATTTACCCGGCACCCCAGGTTTC
CACAGCTGTAGTTGAGCCCTACAACTCCATCCTCACCACCCACACCACCCTGGAGCACTCTGATTGTGCCTTCAT
GGTAGACAATGAGGCCATCTATGACATCTGTCGTAGAAACCTCGATATCGAGCGCCCAACCTACACTAACCTTAA
CCGCCTTATTAGCCAGATTGTGTCCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTGAC
AGAATTCCAGACCAACCTGGTCCCCTACCCCCGCATCCACTTCCCTCTGGCCACATATGCCCCTGTCATCTCTGC
TGAGAAAGCCTACCATGAACAGCTTTCTGTAGCAGACATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGT
GAAATGTGACCCTGGCCATGGTAAATACATGGCTTGCTGCCTGTTGTACCGTGGTGACGTGGTTCCCAAAGATGT
CAATGCTGCCATTGCCACCATCAAAACCAAGCGCACGATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGT
TGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCT
GAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGC
CTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTCAGAGGCCCGTGAAGATATGGCTGCCCT
TGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATAC**TAA**TT
ATCCATTCCTTTTGGCCCTGCAGCATGTCATGCTCCCAGAATTTCAGCTTCAGCTTAACTGACAGATGTTAAAGC
TTTCTGGTTAGATTGTTTTCACTTGGTGATCATGTCTTTTCCATGTGTACCTGTAATATTTTTCCATCATATCTC
AAAGTAAAGTCATTAACATCA

FIGURE 128

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVI
DEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLADQCTRLQGFLVFHSFGGGTGSGFT
SLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYT
NLNRLISQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVADITNACFEPAN
QMVKCDPGHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGVDSVEGEGEEEGEE
Y

FIGURE 129

GGCACGAGGGTTTGCACCTCGCTGCTCCAGCCTCTGGGGCGCATTCCAACCTTCCAGCCTGCGACCTGCGGAGAA
AAAAAATTACTTATTTTCTTGCCCCATACATACCTTGAGGCGAGCAAAAAAATTAAATTTTAACC**ATG**AGGGAAA
TCGTGCACATCCAGGCTGGTCAGTGTGGCAACCAGATCGGTGCCAAGTTCTGGGAGGTGATCAGTGATGAACATG
GCATCGACCCCACCGGCACCTACCACGGGGACAGCGACCTGCAGCTGGACCGCATCTCTGTGTACTACAATGAAG
CCACAGGTGGCAAATATGTTCCTCGTGCCATCCTGGTGGATCTAGAACCTGGGACCATGGACTCTGTTCGCTCAG
GTCCTTTTGGCCAGATCTTTAGACCAGACAACTTTGTATTTGGTCAGTCTGGGGCAGGTAACAACTGGGCCAAAG
GCCACTACACAGAGGGCGCCGAGCTGGTTGATTCTGTCCTGGATGTGGTACGGAAGGAGGCAGAGAGCTGTGACT
GCCTGCAGGGCTTCCAGCTGACCCACTCACTGGGCGGGGGCACAGGCTCTGGAATGGGCACTCTCCTTATCAGCA
AGATCCGAGAAGAATACCCTGATCGCATCATGAATACCTTCAGTGTGGTGCCTTCACCCAAAGTGTCTGACACCG
TGGTCGAGCCCTACAATGCCACCCTCTCCGTCCATCAGTTGGTAGAGAATACTGATGAGACCTATTGCATTGACA
ACGAGGCCCTCTATGATATCTGCTTCCGCACTCTGAAGCTGACCACACCAACCTACGGGGATCTGAACCACCTTG
TCTCAGCCACCATGAGTGGTGTCACCACCTGCCTCCGTTTCCCTGGCCAGCTCAATGCTGACCTCCGCAAGTTGG
CAGTCAACATGGTCCCCTTCCCACGTCTCCATTTCTTTATGCCTGGCTTTGCCCCTCTCACCAGCCGTGGAAGCC
AGCAGTATCGAGCTCTCACAGTGCCGGAACTCACCCAGCAGGTCTTCGATGCCAAGAACATGATGGCTGCCTGTG
ACCCCCGCCACGGCCGATACCTCACCGTGGCTGCTGTCTTCCGTGGTCGGATGTCCATGAAGGAGGTCGATGAGC
AGATGCTTAACGTGCAGAACAAGAACAGCAGCTACTTTGTGGAATGGATCCCCAACAATGTCAAGACAGCCGTCT
GTGACATCCCACCTCGTGGCCTCAAGATGGCAGTCACCTTCATTGGCAATAGCACAGCCATCCAGGAGCTCTTCA
AGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCCGGAAGGCCTTCCTCCACTGGTACACAGGCGAGGGCATGG
ACGAGATGGAGTTCACCGAGGCTGAGAGCAACATGAACGACCTCGTCTCTGAGTATCAGCAGTACCAGGATGCCA
CCGCAGAAGAGGAGGAGGATTTCGGTGAGGAGGCCGAAGAGGAGGCC**TAA**GGCAGAGCCCCCATCACCTCAGGCT
TCTCAGTTCCCTTAGCCGTCTTACTCAACTGCCCCTTTCCTCTCCCTCAGAATTTGTGTTTGCTGCCTCTATCTT
GTTTTTTGTTTTTTCTTCTGGGGGGGGTCTAGAACAGTGCCTGGCACATAGTAGGCGCTCAATAAATACTTGTTT
GTTGAAAAAAAAAAAAAAAAAA

FIGURE 130

MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGTYHGDSDLQLDRISVYYNEATGGKYVPRAILVDLEPGTMDS
VRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKEAESCDCLQGFQLTHSLGGGTGSGMGTL
LISKIREEYPDRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDL
NHLVSATMSGVTTCLRFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQVFDAKNMM
AACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRGLKMAVTFIGNSTAIQ
ELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQDATAEEEEDFGEEAEEEA

FIGURE 131

ATCCAATACAGGAGTGACTTGGAACTCCATTCTATCACT**ATG**AAGAAAAGTGGTGTTCTTTTCCTCTTGGGCATC
ATCTTGCTGGTTCTGATTGGAGTGCAAGGAACCCCAGTAGTGAGAAAGGGTCGCTGTTCCTGCATCAGCACCAAC
CAAGGGACTATCCACCTACAATCCTTGAAAGACCTTAAACAATTTGCCCCAAGCCCTTCCTGCGAGAAAATTGAA
ATCATTGCTACACTGAAGAATGGAGTTCAAACATGTCTAAACCCAGATTCAGCAGATGTGAAGGAACTGATTAAA
AAGTGGGAGAAACAGGTCAGCCAAAAGAAAAAGCAAAAGAATGGGAAAAAACATCAAAAAAAGAAAGTTCTGAAA
GTTCGAAAATCTCAACGTTCTCGTCAAAAGAAGACTACA**TAA**GAGACCACTTCACCAATAAGTATTCTGTGTTAA
AAATGTTCTATTTTAATTATACCGCTATCATTCCAAAGGAGGATGGCATATAATACAAAGGCTTATTAATTTGAC
TAGAAAATTTAAAACATTACTCTGAAATTGTAACTAAAGTTAGAAAGTTGATTTTAAGAATCCAAACGTTAAGAA
TTGTTAAAGGCTATGATTGTCTTTGTTCTTCTACCACCCACCAGTTGAATTTCATCATGCTTAAGGCCATGATTT
TAGCAATACCCATGTCTACACAGATGTTCACCCAACCACATCCCACTCACAACAGCTGCCTGGAAGAGCAGCCCT
AGGCTTCCACGTACTGCAGCCTCCAGAGAGTATCTGAGGCACATGTCAGCAAGTCCTAAGCCTGTTAGCATGCTG
GTGAGCCAAGCAGTTTGAAATTGAGCTGGACCTCACCAAGCTGCTGTGGCCATCAACCTCTGTATTTGAATCAGC
CTACAGGCCTCACACACAATGTGTCTGAGAGATTCATGCTGATTGTTATTGGGTATCACCACTGGAGATCACCAG
TGTGTGGCTTTCAGAGCCTCCTTTCTGGCTTTGGAAGCCATGTGATTCCATCTTGCCCGCTCAGGCTGACCACTT
TATTTCTTTTTGTTCCCCTTTGCTTCATTCAAGTCAGCTCTTCTCCATCCTACCACAATGCAGTGCCTTTCTTCT
CTCCAGTGCACCTGTCATATGCTCTGATTTATCTGAGTCAACTCCTTTCTCATCTTGTCCCCAACACCCCACAGA
AGTGCTTTCTTCTCCCAATTCATCCTCACTCAGTCCAGCTTAGTTCAAGTCCTGCCTCTTAAATAAACCTTTTTG
GACACACAAATTATCTTAAAACTCCTGTTTCACTTGGTTCAGTACCACATGGGTGAACACTCAATGGTTAACTAA
TTCTTGGGTGTTTATCCTATCTCTCCAACCAGATTGTCAGCTCCTTGAGGGCAAGAGCCACAGTATATTTCCCTG
TTTCTTCCACAGTGCCTAATAATACTGTGGAACTAGGTTTTAATAATTTTTTAATTGATGTTGTTATGGGCAGGA
TGGCAACCAGACCATTGTCTCAGAGCAGGTGCTGGCTCTTTCCTGGCTACTCCATGTTGGCTAGCCTCTGGTAAC
CTCTTACTTATTATCTTCAGGACACTCACTACAGGGACCAGGGATGATGCAACATCCTTGTCTTTTTATGACAGG
ATGTTTGCTCAGCTTCTCCAACAATAAGAAGCACGTGGTAAAACACTTGCGGATATTCTGGACTGTTTTTAAAAA
ATATACAGTTTACCGAAAATCATATAATCTTACAATGAAAAGGACTTTATAGATCAGCCAGTGACCAACCTTTTC
CCAACCATACAAAAATTCCTTTTCCCGAAGGAAAAGGGCTTTCTCAATAAGCCTCAGCTTTCTAAGATCTAACAA
GATAGCCACCGAGATCCTTATCGAAACTCATTTTAGGCAAATATGAGTTTTATTGTCCGTTTACTTGTTTCAGAG
TTTGTATTGTGATTATCAATTACCACACCATCTCCCATGAAGAAAGGGAACGGTGAAGTACTAAGCGCTAGAGGA
AGCAGCCAAGTCGGTTAGTGGAAGCATGATTGGTGCCCAGTTAGCCTCTGCAGGATGTGGAAACCTCCTTCCAGG
GGAGGTTCAGTGAATTGTGTAGGAGAGGTTGTCTGTGGCCAGAATTTAAACCTATACTCACTTTCCCAAATTGAA
TCACTGCTCACACTGCTGATGATTTAGAGTGCTGTCCGGTGGAGATCCCACCCGAACGTCTTATCTAATCATGAA
ACTCCCTAGTTCCTTCATGTAACTTCCCTGAAAAATCTAAGTGTTTCATAAATTTGAGAGTCTGTGACCCACTTA
CCTTGCATCTCACAGGTAGACAGTATATAACTAACAACCAAAGACTACATATTGTCACTGACACACACGTTATAA
TCATTTATCATATATATACATACATGCATACACTCTCAAAGCAAATAATTTTTCACTTCAAAACAGTATTGACTT
GTATACCTTGTAATTTGAAATATTTTCTTTGTTAAAATAGAATGGTATCAATAAATAGACCATTAATCAG

FIGURE 132

MKKSGVLFLLGIILLVLIGVQGTPVVRKGRCSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKNGVQTCL
NPDSADVKELIKKWEKQVSQKKKQKNGKKHQKKKVLKVRKSQRSRQKKTT

FIGURE 133

TCTCGGCCCGGCATCATTGTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGCCCGCTGCAATCCGTGGA
GGAACGCGCCGCCGAGCCACCATCATGCCTGGGCACTTACAGGAAGGCTTCGGCTGCGTGGTCACCAACCGATTC
GACCAGTTATTTGACGACGAATCGGACCCCTTCGAGGTGCTGAAGGCAGCAGAGAACAAGAAAAAAGAAGCCGGC
GGGGGCGGCGTTGGGGGCCCTGGGGCCAAGAGCGCGACTCAGGCCGCGGCCCAGACCAACTCCAACGCGGCAGGC
AAACAGCTGCGCAAGGAGTCCCAGAAAGACCGCAAGAACCCGCTGCCCCCCAGCGTTGGCGTGGTTGACAAGAAA
GAGGAGACGCAGCCGCCCGTGGCGTTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACTT
CAGGGTGAAGGGAAAATAATTGATAGAAGACCAGAAAGGCGACCACCTCGTGAACGAAGATTCGAAAAGCCACTT
GAAGAAAAGGGTGAAGGAGGCGAATTTTCAGTTGATAGACCGATTATTGACCGACCTATTCGAGGTCGTGGTGGT
CTTGGAAGAGGTCGAGGGGGCCGTGGACGTGGAATGGGCCGAGGAGATGGATTTGATTCTCGTGGCAAACGTGAA
TTTGATAGGCATAGTGGAAGTGATAGATCTTCTTTTTCACATTACAGTGGCCTGAAGCACGAGGACAAACGTGGA
GGTAGCGGATCTCACAACTGGGGAACTGTCAAAGACGAATTAACTGACTTGGATCAATCAAATGTGACTGAGGAA
ACACCTGAAGGTGAAGAACATCATCCAGTGGCAGACACTGAAAATAAGGAGAATGAAGTTGAAGAGGTAAAAGAG
GAGGGTCCAAAAGAGATGACTTTGGATGAGTGGAAGGCTATTCAAAATAAGGACCGGGCAAAAGTAGAATTTAAT
ATCCGAAAACCAAATGAAGGTGCTGATGGGCAGTGGAAGAAGGGATTTGTTCTTCATAAATCAAAGAGTGAAGAG
GCTCATGCTGAAGATTCGGTTATGGACCATCATTTCCGGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATC
AATTTTGGAGACCTTGGCCGCCCAGGACGTGGCGGCAGGGGAGGACGAGGTGGACGTGGGCGTGGTGGGCGCCCA
AACCGTGGCAGCAGGACCGACAAGTCAAGTGCTTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCCAGCTCTG
GCTTAACTGGATGCCATAAGACAACCCTGGTTCCTTTGTGAACCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGA
TTCCAAACGACTAAGAAATTAAAAAAAAAAAGACTGTCATTCATACCATTCACACCTAAAGACTGAATTTTATCT
GTTTTAAAAATGAACTTCTCCCGCTACACAGAAGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTG
GTAGCAGGGATGTTTTCATAATTTTCAGAGATTATGCATTCTTCATGAATACTTTTGTATTGCTGCTTGCAAATA
TGCATTTCCAAACTTGAAATATAGGTGTGAACAGTGTGTACCAGTTTAAAGCTTTCACTTCATTTGTGTTTTTTA
ATTAAGGATTTAGAAGTTCCCCCAATTACAAACTGGTTTTAAATATTGGACATACTGGTTTTAATACCTGCTTTG
CATATTCACACATGGTCAACTGGGACATGTTAAACTTTGATTTGTCAAATTTTATGCTGTGTGGAATACTAACTA
TATGTATTTTAACTTAGTTTTAATATTTTCATTTTTGGGGAAAAATCTTTTTTCACTTCTCATGGATAGCTGTTA
TATATATATGCTAAATCTTTATATACAGAAATATCAGTACTTGAACCAATTCAAAGCACATTTGGGTTATTAACC
CTTGCTCCCTGCATGGCTCATTAGGGTCCAAATTATAACTGATTTACATT

FIGURE 134

MPGHLQEGFGCVVTNRFDQLFDDESDPFEVLKAAENKKKEAGGGGVGGPGAKSATQAAAQTNSNAAGKQLRKESQ
KDRKNPLPPSVGVVDKKEETQPPVAFKKEGIRRVGRRPDQQLQGEGKIIDRRPERRPPRERRFEKPLEEKGEGGE
FSVDRPIIDRPIRGRGGLGRGRGGRGRGMGRGDGFDSRGKREFDRHSGSDRSSFSHYSGLKHEDKRGGSGSHNWG
TVKDELTDLDQSNVTEETPEGEEHHPVADTENKENEVEEVKEEGPKEMTLDEWKAIQNKDRAKVEFNIRKPNEGA
DGQWKKGFVLHKSKSEEAHAEDSVMDHHFRKPANDITSQLEINFGDLGRPGRGGRGGRGGRGRGGRPNRGSRTDK
SSASAPDVDDPEAFPALA

FIGURE 135

GGCGGACCGAAGAACGCAGGAAGGGGGCCGGGGGACCCGCCCCCGGCCGGCCGCAGCC**<u>ATG</u>**AACTCCAACGTGG
AGAACCTACCCCCGCACATCATCCGCCTGGTGTACAAGGAGGTGACGACACTGACCGCAGACCCACCCGATGGCA
TCAAGGTCTTTCCCAACGAGGAGGACCTCACCGACCTCCAGGTCACCATCGAGGGCCCTGAGGGGACCCCATATG
CTGGAGGTCTGTTCCGCATGAAACTCCTGCTGGGGAAGGACTTCCCTGCCTCCCCACCCAAGGGCTACTTCCTGA
CCAAGATCTTCCACCCGAACGTGGGCGCCAATGGCGAGATCTGCGTCAACGTGCTCAAGAGGGACTGGACGGCTG
AGCTGGGCATCCGACACGTACTGCTGACCATCAAGTGCCTGCTGATCCACCCTAACCCCGAGTCTGCACTCAACG
AGGAGGCGGGCCGCCTGCTCTTGGAGAACTACGAGGAGTATGCGGCTCGGGCCCGTCTGCTCACAGAGATCCACG
GGGGCGCCGGCGGGCCCAGCGGCAGGGCCGAAGCCGGTCGGGCCCTGGCCAGTGGCACTGAAGCTTCCTCCACCG
ACCCTGGGGCCCCAGGGGGCCCGGGAGGGGCTGAGGGTCCCATGGCCAAGAAGCATGCTGGCGAGCGCGATAAGA
AGCTGGCGGCCAAGAAAAAGACGGACAAGAAGCGGGCGCTGCGGGCGCTGCGGCGGCTG**<u>TAG</u>**TGGGCTCTCTTCC
TCCTTCCACCGTGACCCCAACCTCTCCTGTCCCCTCCCTCCAACTCTGTCTCTAAGTTATTTAAATTATGGCTGG
GGTCGGGGAGGGTACAGGGGGCACTGGGACCTGGATTTGTTTTTCTAAATAAAGTTGGAAAAGCA

FIGURE 136

MNSNVENLPPHIIRLVYKEVTTLTADPPDGIKVFPNEEDLTDLQVTIEGPEGTPYAGGLFRMKLLLGKDFPASPP
KGYFLTKIFHPNVGANGEICVNVLKRDWTAELGIRHVLLTIKCLLIHPNPESALNEEAGRLLLENYEEYAARARL
LTEIHGGAGGPSGRAEAGRALASGTEASSTDPGAPGGPGGAEGPMAKKHAGERDKKLAAKKKTDKKRALRALRRL

FIGURE 137

CATTGATTCATAAAGGATCTTTATAAATCTTATTCTTTGTTGGCTATATAGTTGCCAATATCTTCTCCCAATTTG
TGGCTTGCCTTTCCCTCCCTTATGATGTTCTTTGATAAAAACAATTTATTAATGGTTAAGTACTAGGAAGTATGA
GTGTTTTAAAATTAGAGCGTGAGTTGTTTTAAAAAACCATTCCCTACCCTGGAGTCATGAAGATAGTCTTATATA
TCGTCTTCTTAAAGCTTTAGTTTTGCCTTTCATATTTAAATTTTTTTCATGAGGAATTAATTTGGTGT**ATG**CTAG
GAGATGCCTCACTACCGTTTATTGACCAAATCTGGGTTTTATTCCTCCTTTCTGTAGTTGCACCAAAGTCCTGTT
T

FIGURE 138

MLGDASLPFIDQIWVLFLLSVVAPKSC

FIGURE 139

CCCGGC**<u>ATG</u>**GAGGAGGAGTGCCGGGTGCTCTCCATACAGAGCCACGTCATCCGCGGCTACGTGGGCAACCGGGCG
GCCACGTTCCCGCTGCAGGTTTTGGGATTTGAGATTGACGCGGTGAACTCTGTCCAGTTTTCAAACCACACAGGC
TATGCCCACTGGAAGGGCCAAGTGCTGAATTCAGATGAGCTCCAGGAGTTGTACGAAGGCCTGAGGCTGAACAAC
ATGAATAAATATGACTACGTGCTCACAGGTTATACGAGGGACAAGTCGTTCCTGGCCATGGTGGTGGACATTGTG
CAGGAGCTGAAGCAGCAGAACCCCAGGCTGGTGTACGTGTGTGATCCAGTCTTGGGTGACAAGTGGGACGGCGAA
GGCTCGATGTACGTCCCGGAGGACCTCCTTCCCGTCTACAAAGAAAAAGTGGTGCCGCTTGCAGACATTATCACG
CCCAACCAGTTTGAGGCCGAGTTACTGAGTGGCCGGAAGATCCACAGCCAGGAGGAAGCCTTGCGGGTGATGGAC
ATGCTGCACTCTATGGGCCCCGACACCGTGGTCATCACCAGCTCCGACCTGCCCTCCCCGCAGGGCAGCAACTAC
CTGATTGTGCTGGGGAGTCAGAGGAGGAGGAATCCCGCTGGCTCCGTGGTGATGGAACGCATCCGGATGGACATT
CGCAAAGTGGACGCCGTCTTTGTGGGCACTGGGGACCTGTTTGCTGCCATGCTCCTGGCGTGGACACACAAGCAC
CCCAATAACCTCAAGGTGGCCTGTGAGAAGACCGTGTCTACCTTGCACCACGTTCTGCAGAGGACCATCCAGTGT
GCAAAAGCCCAGGCCGGGGAAGGAGTGAGGCCCAGCCCCATGCAGCTGGAGCTGCGGATGGTGCAGAGCAAAAGG
GACATCGAGGACCCAGAGATCGTCGTCCAGGCCACGGTGCTG**<u>TGA</u>**GGGCCCCGCCGCTTG

FIGURE 140

MEEECRVLSIQSHVIRGYVGNRAATFPLQVLGFEIDAVNSVQFSNHTGYAHWKGQVLNSDELQELYEGLRLNNMN
KYDYVLTGYTRDKSFLAMVVDIVQELKQQNPRLVYVCDPVLGDKWDGEGSMYVPEDLLPVYKEKVVPLADIITPN
QFEAELLSGRKIHSQEEALRVMDMLHSMGPDTVVITSSDLPSPQGSNYLIVLGSQRRRNPAGSVVMERIRMDIRK
VDAVFVGTGDLFAAMLLAWTHKHPNNLKVACEKTVSTLHHVLQRTIQCAKAQAGEGVRPSPMQLELRLRMVQSKRDI
EDPEIVVQATVL

FIGURE 141

GGATCGAGGGGACTCTGACCACAGCCTGTGGCTGGGAAGGGAGACAGAGGCGGCGGCGGCTCAGGGGAAACGAGG
CTGCAGTGGTGGTAGTAGGAAG**ATG**TCGGGCGAGGACGAGCAACAGGAGCAAACTATCGCTGAGGACCTGGTCGT
GACCAAGTATAAGATGGGGGGCGACATCGCCAACAGGGTACTTCGGTCCTTGGTGGAAGCATCTAGCTCAGGTGT
GTCGGTACTCAGCCTGTGTGAGAAAGGTGATGCCATGATTATGGAAGAAACAGGGAAAATCTTCAAGAAAGAAAA
GGAAATGAAGAAAGGTATTGCTTTTCCCACCAGCATTTCGGTAAATAACTGTGTATGTCACTTCTCCCCTTTGAA
GAGCGACCAGGATTATATTCTCAAGGAAGGTGACTTGGTAAAAATTGACCTTGGGGTCCATGTGGATGGCTTCAT
CGCTAATGTAGCTCACACTTTTGTGGTTGATGTAGCTCAGGGGACCCAAGTAACAGGGAGGAAAGCAGATGTTAT
TAAGGCAGCTCACCTTTGTGCTGAAGCTGCCCTACGCCTGGTCAAACCTGGAAATCAGAACACACAAGTGACAGA
AGCCTGGAACAAAGTTGCCCACTCATTTAACTGCACGCCAATAGAAGGTATGCTGTCACACCAGTTGAAGCAGCA
TGTCATCGATGGAGAAAAAACCATTATCCAGAATCCCACAGACCAGCAGAAGAAGGACCATGAAAAAGCTGAATT
TGAGGTACATGAAGTATATGCTGTGGATGTTCTCGTCAGCTCAGGAGAGGGCAAGGCCAAGGATGCAGGACAGAG
AACCACTATTTACAAACGAGACCCCTCTAAACAGTATGGACTGAAAATGAAAACTTCACGTGCCTTCTTCAGTGA
GGTGGAAAGGCGTTTTGATGCCATGCCGTTTACTTTAAGAGCATTTGAAGATGAGAAGAAGGCTCGGATGGGTGT
GGTGGAGTGCGCCAAACATGAACTGCTGCAACCATTTAATGTTCTCTATGAGAAGGAGGGTGAATTTGTTGCCCA
GTTTAAATTTACAGTTCTGCTCATGCCCAATGGCCCCATGCGGATAACCAGTGGTCCCTTCGAGCCTGACCTCTA
CAAGTCTGAGATGGAGGTCCAGGATGCAGAGCTAAAGGCCCTCCTCCAGAGTTCTGCAAGTCGAAAAACCCAGAA
AAAGAAAAAAAAAGAAGGCCTCCAAGACTGCAGAGAATCCCACCAGTGGGGAAACATTAGAAGAAAATGAAGCTGG
GGAC**TGA**GGTGCGTCCCATCTCCCCAGCTTGCTGCTCCTGCCTCATCCCCTTCCCACCAAACCCCAGACTCTGTG
AAGTGCAGTTCTTCTCCACCTAGGACCGCCAGCAGAGCGGGGGGATCTCCCTGCCCCCACCCCAGTTCCCCAACC
CACTCCCTTCCAACAACAACCAGCTCCAACTGACTCTGGTCTTGGGAGGTGAGGCTTCCCAACCACGGAAGACTA
CTTTAAACGAAAAAAAGAAATTGAATAATAAAATCAGGAGTCAAAATTCATCGTCTTCAAGGCCCCTCTTTCTAG
CCTTTTCTACTACTCTCTGCTTGGTCAAGGTTTGTGCCCCACTACAGAACAGGGCTAAATTAGCCACCACCACTG
AAAACTCAGCCGAATTTTTTATACCACTCTGACGTCAGCATTTTTT

FIGURE 142

MSGEDEQQEQTIAEDLVVTKYKMGGDIANRVLRSLVEASSSGVSVLSLCEKGDAMIMEETGKIFKKEKEMKKGIA
FPTSISVNNCVCHFSPLKSDQDYILKEGDLVKIDLGVHVDGFIANVAHTFVVDVAQGTQVTGRKADVIKAAHLCA
EAALRLVKPGNQNTQVTEAWNKVAHSFNCTPIEGMLSHQLKQHVIDGEKTIIQNPTDQQKKDHEKAEFEVHEVYA
VDVLVSSGEGKAKDAGQRTTIYKRDPSKQYGLKMKTSRAFFSEVERRFDAMPFTLRAFEDEKKARMGVVECAKHE
LLQPFNVLYEKEGEFVAQFKFTVLLMPNGPMRITSGPFEPDLYKSEMEVQDAELKALLQSSASRKTQKKKKKKAS
KTAENPTSGETLEENEAGD

FIGURE 143

GTAACCGCTACTCCCGGACACCAGACCACCGCCTTCCGTACACAGGGGCCCGCATCCCACCCTCCCGGACCTAAG
AGCCTGGGTCCCCTGTTTCCGGAGGTCCGCTTCCCGGCCCCCAGATTCTGGCATCCCAGCCCTCAGTGTCCAAGA
CCCAGGCAGCCCGGGTCCCCGCCTCCCGGATCCAGGCGTCCGGGATCTGCGCCACCAGAACCTAGCCTCCTGCAG
ACCTCCGCCATCTGGGGGCACTCAACCTCCTGGAGCCAAGGGCCCCACGTCCCACCCAGAGAAACTCTCGTATTC
CCAGCTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACTCCCAGCTTTCGGACATCTGGCACACGGGGCAGAGCAG
AGAAGCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACTTCAGTGCTGTGAACT
CACAACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCCTAGGAACGTCGGGTC
CTGGGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATC**ATG**GTGGCCG
ATCCTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCCACCGCCAACGGGGGCCTGGCGCTGGCCTCCATCG
AGGACCAAGGCGCGGCAGCAGGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGC
TTGTGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCCGGGGGTGCGC
TGGCGTTGGGCCCGGAGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCTGCTGCTGCGTCTGCTGCGGATGATCA
TCTTGCCGCTGGTGGTGTGCAGCTTGATCGGCGGCGCCGCCAGCCTGGACCCCGGCGCGCTCGGCCGTCTGGGCG
CCTGGGCGCTGCTCTTTTTCCTGGTCACCACGCTGCTGGCGTCGGCGCTCGGAGTGGGCTTGGCGCTGGCTCTGC
AGCCGGGCGCCGCCTCCGCCGCCATCAACGCCTCCGTGGGAGCCGCGGGCAGTGCCGAAAATGCCCCCAGCAAGG
AGGTGCTCGATTCGTTCCTGGATCTTGCGAGAAATATCTTCCCTTCCAACCTGGTGTCAGCAGCCTTTCGCTCAT
ACTCTACCACCTATGAAGAGAGGAATATCACCGGAACCAGGGTGAAGGTGCCCGTGGGGCAGGAGGTGGAGGGGA
TGAACATCCTGGGCTTGGTAGTGTTTGCCATCGTCTTTGGTGTGGCGCTGCGGAAGCTGGGGCCTGAAGGGGAGC
TGCTTATCCGCTTCTTCAACTCCTTCAATGAGGCCACCATGGTTCTGGTCTCCTGGATCATGTGGTACGCCCCTG
TGGGCATCATGTTCCTGGTGGCTGGCAAGATCGTGGAGATGGAGGATGTGGGTTTACTCTTTGCCCGCCTTGGCA
AGTACATTCTGTGCTGCCTGCTGGGTCACGCCATCCATGGGCTCCTGGTACTGCCCCTCATCTACTTCCTCTTCA
CCCGCAAAAACCCCTACCGCTTCCTGTGGGGCATCGTGACGCCGCTGGCCACTGCCTTTGGGACCTCTTCCAGTT
CCGCCACGCTGCCGCTGATGATGAAGTGCGTGGAGGAGAATAATGGCGTGGCCAAGCACATCAGCCGTTTCATCC
TGCCCATCGGCGCCACCGTCAACATGGACGGTGCCGCGCTCTTCCAGTGCGTGGCCGCAGTGTTCATTGCACAGC
TCAGCCAGCAGTCCTTGGACTTCGTAAAGATCATCACCATCCTGGTCACGGCCACAGCGTCCAGCGTGGGGGCAG
CGGGCATCCCTGCTGGAGGTGTCCTCACTCTGGCCATCATCCTCGAAGCAGTCAACCTCCCGGTCGACCATATCT
CCTTGATCCTGGCTGTGGACTGGCTAGTCGACCGGTCCTGTACCGTCCTCAATGTAGAAGGTGACGCTCTGGGGG
CAGGACTCCTCCAAAATTATGTGGACCGTACGGAGTCGAGAAGCACAGAGCCTGAGTTGATACAAGTGAAGAGTG
AGCTGCCCCTGGATCCGCTGCCAGTCCCCACTGAGGAAGGAAACCCCCTCCTCAAACACTATCGGGGGCCCGCAG
GGGATGCCACGGTCGCCTCTGAGAAGGAATCAGTCATG**TAA**ACCCCGGGAGGGACCTTCCCTGCCCTGCTGGGGG
TGCTCTTTGGACACTGGATTATGAGGAATGGATAAATGGATGAGCTAGGGCTCTGGGGGTCTGCCTGCACACTCT
GGGGAGCCAGGGGCCCCAGCACCCTCCAGGACAGGAGATCTGGGATGCCTGGCTGCTGGAGTACATGTGTTCACA
AGGGTTACTCCTCAAAACCCCCAGTTCTCACTCATGTCCCCAACTCAAGGCTAGAAAACAGCAAGATGGAGAAAT
AATGTTCTGCTGCGTCCCCACCGTGACCTGCCTGGCCTCCCCTGTCTCAGGGAGCAGGTCACAGGTCACCATGGG
GAATTCTAGCCCCCACTGGGGGGATGTTACAACACCATGCTGGTTATTTTGGCGGCTGTAGTTGTGGGGGGATGT
GTGTGTGCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTCTGTGACCTCCTGTCCCCATGGTACGTC
CCACCCTGTCCCCAGATCCCCTATTCCCTCCACAATAACAGAAACACTCCCAGGGACTCTGGGGAGAGGCTGAGG
ACAAATACCTGCTGTCACTCCAGAGGACATTTTTTTAGCAATAAAATTGAGTGTCAACTATTTAAAAAAAAAAA
AAAAAA

FIGURE 144

MVADPPRDSKGLAAAEPTANGGLALASIEDQGAAAGGYCGSRDQVRRCLRANLLVLLTVVAVVAGVALGLGVSGA
GGALALGPERLSAFVFPGELLLRLLRMIILPLVVCSLIGGAASLDPGALGRLGAWALLFFLVTTLLASALGVGLA
LALQPGAASAAINASVGAAGSAENAPSKEVLDSFLDLARNIFPSNLVSAAFRSYSTTYEERNITGTRVKVPVGQE
VEGMNILGLVVFAIVFGVALRKLGPEGELLIRFFNSFNEATMVLVSWIMWYAPVGIMFLVAGKIVEMEDVGLLFA
RLGKYILCCLLGHAIHGLLVLPLIYFLFTRKNPYRFLWGIVTPLATAFGTSSSSATLPLMMKCVEENNGVAKHIS
RFILPIGATVNMDGAALFQCVAAVFIAQLSQQSLDFVKIITILVTATASSVGAAGIPAGGVLTLAIILEAVNLPV
DHISLILAVDWLVDRSCTVLNVEGDALGAGLLQNYVDRTESRSTEPELIQVKSELPLDPLPVPTEEGNPLLKHYR
GPAGDATVASEKESVM

FIGURE 145

AAAAATCTATGATTCAGCTTTTCATCCTGACACTGGTGAGAAG**ATG**ATTTTGATAGGAAGAATGTCAGCCCAGGT
TCCCATGAACATGACCATCACAGGTTGTATGATGACGTTTTACAGGACTACGCCGGCTGTGCTGTTCTGGCAGTG
GATTAACCAGTCCTTCAATGCCGTCGTCAATTACACCAACAGAAGTGGAGACGCACCCCTCACTGTCAATGAGTT
GGGAACAGCTTACGTTTCTGCAACAACTGGTGCCGTAGCAACAGCTCTAGGACTCAATGCATTGACCAAGCATGT
CTCACCACTGATAGGACGTTTTGTTCCCTTTGCTGCCGTAGCTGCTGCTAATTGCATTAATATTCCATTAATGAG
GCAAAGGGAACTCAAAGTTGGCATTCCCGTCACGGATGAGAATGGGAACCGCTTGGGGGAGTCGGCGAACGCTGC
GAAACAAGCCATCACGCAAGTTGTCGTGTCCAGGATTCTCATGGCAGCCCCTGGCATGGCCATCCCTCCATTCAT
TATGAACACTTTGGAAAAGAAAGCCTTTTTGAAGAGGTTCCCATGGATGAGTGCACCCATTCAAGTTGGGTTAGT
TGGCTTCTGTTTGGTGTTTGCTACACCCCTGTGTTGTGCCCTGTTTCCTCAGAAAAGTTCCATGTCTGTGACAAG
CTTGGAGGCCGAGTTGCAAGCTAAGATCCAAGAGAGCCATCCTGAATTGCGACGCGTGTACTTCAATAAGGGATT
G**TAA**AGCAGGGAGGAAACCTCTGCAGCTCATTCTGCCACTGCAAAGCTGGTGTAGCCATGCTGGTGAGAAAAATC
CTGTTCAACCTGGGTTCTCCCAGTTACGGAAACCTTTTAAAGATCCACATTAGCCTTTTAGAATAAAGCTGCTAC
TTTAACAGAGCACCTGGCGTGGGCCAAGTGCCTGATACTCCCTTACACTGAATCATGTTATGATTTATAGAAATA
CCTTTCCTGTAGCTTTTATAGTCATTGTTTTTCAAAGACGATATACCAGCCCTCACCCAGGTTTAAAAAAGCAC
TGGTAGGCATAGAATAGGTGCTCAGTATATGGTCAGTAAATGTTCTATTGATTATCAATCAGTGAAAAAAGAAAT
CTGTTTAAAATACTGAATTTTCATCTCACTCCCATTGCAAATCAAGGAGATCTCAGCAGTGAACTGGGAAAATAC
AAAAGCTCTGGGCTAATCTATAAAAACTTACCCTGAAATATTAAGGGCAGTTTGCTTCTAGTTTGGGGATTGCGC
TAGCCCAATGAAGGTGATGAAGCTTTTGGATTTGGAGGGTAAAAGCTCCTTCACACCCCTTCCAAAAGTCAGTCA
CAGACCACTGCAACATGCCTTCCCTGCTGGATCATTATATACATTCAGATTGTGAGTGGATTGCCTTGGTTGACT
TTTAATTTATTGTTTTTTGTTCTTATAAAGATGATAATCTTACCTTGCAGTTATTGACTTTATATTCAATTATTT
ACATCAAATAATGAAATAACTGAAATGTACAAATGTCAAATTTTGGAAGTATATTCAATACCAATGCTGTATGAG
TGGGCTGAATCCAGTTCATTGTTTTTTTTTTGGTAAGAAGTGAGACTACAGTTCCAGCTACCTACATGTCTTTTC
TTGTCATCCTTATAGATCTCTTTGGCTTTCAGAAAGATACAGTGATAATGTGTGTATGAATCAGTCACAATGAAT
TTTACTTGAATATTGTATGTTGCATTCCACTTCATTTGAAAATAATGAAACCATGTACCACTGTTTACATCATCT
GTAGTGATTTCATAGATAATATATTTAATATGACAGATTATGTTTCAACTCTGTAGATGTTTAACGTCATAGACA
GTTGGCCCTCTGTATCCGTGAGCTCTATATCTGTGAATTCAACCAAGTTTGGATGGAAAATTTTTTTTTTTTTTT
TTTTTTTTTTGAGACGGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGGCGTAGTCTCGGCTCACTGCAAG
CCCCGCCTCCTGGGTTCACGCCGTTCTCCTGCCTCAGCCTCTCTGAGAAGCTGGGACTACAGGCGCCCGCCACCA
CGCCCGGCTAATTTTTTTGTATTTTTAGTAGAGACGGGGTTTCACTGTGGTCTCGATCTCCTGACCTCGTGATCC
GCCCGCCTTGGCCTCCCAAGGTGCTGGGATTACAAGCGTGAGCCACCGCACCCGGCCTGAAAATATTTTCTAAAA
AGATAAAAAATATACATAACGATGAAAAATAATACAAATTTAAAAACCAATACAGTATAACAACTATTTACATAG
TGCTTACATTGTATTAGGTGTTATAAGCAATCTAGAGATGATTTAGCAAGTATACAGGAGGATGTGCCTAGGTTA
TATGCAAATACTGTGCCATTTTATATCAGGAACTTGAGCATCTGCAGATATTGGTATCGGAGGGCGGTCCTGGAA
CCAAGCATCCACGGATACTGAGGGGTGACATTTCATGAAGTGTAGATCATTGTATTCAGAGATTGTAAATGAAAA
AAATATAGAAACTATTTAGTTTTGGTAGATTTTTTTTCTGACAATGTGACCAGACTGAATTTCCTCATAAAGAAA
AAATGGCGTGCCTTGTG

FIGURE 146

MILIGRMSAQVPMNMTITGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNELGTAYVSATTGAVAT
ALGLNALTKHVSPLIGRFVPFAAVAAANCINIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRILM
AAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFATPLCCALFPQKSSMSVTSLEAELQAKIQESHP
ELRRVYFNKGL

FIGURE 147

ATGCTGCGCTTCCTGGCACCCCGGCTGCTTAGCCTCCAGGGCAGGACCGCCCTCTACTCCTCGGCAGCAGCCCTC
CCAAGCCCCATTCTGAACCCAGACATCCCCTACAACCAGCTGTTCATCAACAATGAATGGCAAGATGCAGTCAGC
AAGAAGACCTTCCCGACGGTCAACCCTACCACCGGGGAGGTCATCGGGCACGTGGCTGAAGGTGACCGGGCTGAT
GTGGATCGGGCCGTGAAAGCAGCCCGGGAAGCCTTCCGCCTGGGGTCCCCATGGCGCCGGATGGATGCCTCTGAG
CGGGGCCGGCTGCTGAACCTCCTGGCAGACCTAGTGGAGCGGGATCGAGTCTACTTGGCCTCACTCGAGACCTTG
GACAATGGGAAGCCTTTCCAAGAGTCTTACGCCTTGGACTTGGATGAGGTCATCAAGGTGTATCGGTACTTTGCT
GGCTGGGCTGACAAGTGGCATGGCAAGACCATCCCCATGCATGGCCAGCATTTCTGCTTCACCCGGCATGAGCCC
GTTGGTGTCTGTGGCCAGATCATCCCGTGGAACTTCCCCTTGGTCATGCAGGGTTGGAAACTTGCCCCGGCACTC
GCCACAGGCAACACTGTGGTTATGAAGGTGGCAGAGCAGACCCCCCTCTCTGCCCTGTATTTGGCCTCCCTCATC
AAGGAGGCAGGCTTTCCCCCTGGGGTGGTGAACATCATCACGGGGTATGGCCCAACAGCAGGTGCGGCCATCGCC
CAGCACATGGATGTTGACAAAGTTGCCTTCACCGGTTCCACCGAGGTGGGCCACCTGATCCAGAAAGCAGCTGGC
GATTCCAACCTCAAGAGAGTCACCCTGGAGCTGGGTGGTAAGAGCCCCAGCATCGTGCTGGCCGATGCTGACATG
GAGCATGCCGTGGAGCAGTGCCACGAAGCCCTGTTCTTCAACATGGGCCAGTGCTGCTGTGCTGGCTCCCGGACC
TTCGTGGAAGAATCCATCTACAATGAGTTTCTCGAGAGAACCGTGGAGAAAGCAAAGCAGAGGAAAGTGGGGAAC
CCCTTTGAGCTGGACACCCAGCAGGGGCCTCAGGTGGACAAGGAGCAGTTTGAACGAGTCCTAGGCTACATCCAG
CTTGGCCAGAAGGAGGGCGCAAAACTCCTCTGTGGCGGAGAGCGTTTCGGGGAGCGTGGTTTCTTCATCAAGCCT
ACTGTCTTTGGTGGCGTGCAGGATGACATGAGAATTGCCAAAGAGGAGATCTTTGGGCCTGTGCAGCCCCTGTTC
AAGTTCAAGAAGATTGAGGAGGTGGTTGAGAGGGCCAACAACACCAGGTATGGCCTGGCTGCGGCTGTGTTCACC
CGGGATCTGGACAAGGCCATGTACTTCACCCAGGCACTCCAGGCCGGGACCGTGTGGGTAAACACCTACAACATC
GTCACCTGCCACACGCCATTTGGAGGGTTTAAGGAATCTGGAAACGGGAGGGAGCTGGGTGAGGATGGGCTTAAG
GCCTACACAGAGGTAAAGACGGTCACCATCAAGGTTCCTCAGAAGAACTCG**TAA**

FIGURE 148

MLRFLAPRLLSLQGRTALYSSAAALPSPILNPDIPYNQLFINNEWQDAVSKKTFPTVNPTTGEVIGHVAEGDRAD
VDRAVKAAREAFRLGSPWRRMDASERGRLLNLLADLVERDRVYLASLETLDNGKPFQESYALDLDEVIKVYRYFA
GWADKWHGKTIPMHGQHFCFTRHEPVGVCGQIIPWNFPLVMQGWKLAPALATGNTVVMKVAEQTPLSALYLASLI
KEAGFPPGVVNIITGYGPTAGAAIAQHMDVDKVAFTGSTEVGHLIQKAAGDSNLKRVTLELGGKSPSIVLADADM
EHAVEQCHEALFFNMGQCCCAGSRTFVEESIYNEFLERTVEKAKQRKVGNPFELDTQQGPQVDKEQFERVLGYIQ
LGQKEGAKLLCGGERFGERGFFIKPTVFGGVQDDMRIAKEEIFGPVQPLFKFKKIEEVVERANNTRYGLAAAVFT
RDLDKAMYFTQALQAGTVWVNTYNIVTCHTPFGGFKESGNGRELGEDGLKAYTEVKTVTIKVPQKNS

FIGURE 149

GCCAGGACTCCACAAGGCTGGTCCCCTGCCCTGGAGCAACTTAAACAGGCCCTCTGGCCAGCCTGGAACCCTGAG
ATGGCCTCCAGCTCAGGCAGCAGTCCTCGCCCGGCCCCTGATGAGAATGAGTTTCCCTTTGGGTGCCCTCCCACC
GTCTGCCAGGACCCAAAGGAGCCCAGGGCTCTCTGCTGTGCAGGCTGTCTCTCTGAGAACCCGAGGAATGGCGAG
GATCAGATCTGCCCCAAATGCAGAGGGGAAGACCTCCAGTCTATAAGCCCAGGAAGCCGTCTTCGAACTCAGGAG
AAGGCTCACCCCGAGGTGGCTGAGGCTGGAATTGGGTGCCCCTTTGCAGGTGTCGGCTGCTCCTTCAAGGGAAGC
CCACAGTCTGTGCAAGAGCATGAGGTCACCTCCCAGACCTCCCACCTAAACCTGCTGTTGGGGTTCATGAAACAG
TGGAAGGCCCGGCTGGGCTGTGGCCTGGAGTCTGGGCCCATGGCCCTGGAGCAGAACCTGTCAGACCTGCAGCTG
CAGGCAGCCGTGGAAGTGGCGGGGGACCTGGAGGTCGATTGCTACCGGGCACCCTGCTCCGAGAGCCAGGAGGAG
CTGGCCCTGCAGCACTTCATGAAGGAGAAGCTTCTGGCTGAGCTGGAGGGGAAGCTGCGTGTGTTTGAGAACATT
GTTGCTGTCCTCAACAAGGAGGTGGAGGCCTCCCACCTGGCCCTGGCCACCTCTATCCACCAGAGCCAGCTGGAC
CGTGAGCGCATCCTGAGCTTGGAGCAGAGGGTGGTGGAGCTTCAGCAGACCCTGGCCCAGAAAGACCAGGCCCTG
GGCAAGCTGGAGCAGAGCTTGCGCCTCATGGAGGAGGCCTCCTTCGATGGCACTTTCCTGTGGAAGATCACCAAT
GTCACCAGGCGGTGCCATGAGTCGGCCTGTGGCAGGACCGTCAGCCTCTTCTCCCCAGCCTTCTACACTGCCAAG
TATGGCTACAAGTTGTGCCTGCGGCTGTACCTGAATGGAGATGGCACTGGAAAGAGAACCCATCTGTCGCTCTTC
ATCGTGATCATGAGAGGGGAGTATGATGCGCTGCTGCCGTGGCCCTTCCGGAACAAGGTCACCTTCATGCTGCTG
GACCAGAACAACCGTGAGCACGCCATTGACGCCTTCCGGCCTGACCTAAGCTCAGCGTCCTTCCAGAGGCCCCAG
AGTGAAACCAACGTGGCCAGTGGATGCCCACTCTTCTTCCCCCTCAGCAAACTGCAGTCACCCAAGCACGCCTAC
GTGAAGGACGACACAATGTTCCTCAAGTGCATTGTGGAGACCAGCACT**TAG**GGTGGGCGGGGCTCCTGAGGGAGC
TCCAACTCAGAAGGGAGCTAGCCAGAGGACTGTGATGCCCTGCCCTTGGCACCCAAGACCTCAGGGCACAAAGAT
GGGTGAAGGCTGGCATGATCCAAGCAAGACTGAGGGGTCGACTTCGGGCTGGCCATCTGGTTAGGATGGCAGGAC
GTGGGCTGGGCCCACAAAGGCAAAGGGTCCAGAAGGAGACAGGCAGAGCTGCTCCCCTCTGCACGGACCATGCGA
CACTGGGAGGCCAGTGAGCCACTCCGGCCCCGAATGTTGAGGTGGACTCTCACCAAATGAGAAGAAAATGGAACC
AGGCTTGGAACCGTAGGACCCAAGCAGAGAAGCTCTCGGGCTAGGAAGATCTCTGCAGGGCCGCCAGGGAGACCT
GGACACAGGCCTGCTCTCTTTTTCTCCAGGGTCAGAAACAGGACCGGGTGGAAGGGATGGGGTGCCAGTTTGAAT
GCAGTCTGTCCAGGCTCGTCATTGGAGGTGAACAAGCAAACCCAGACGGCTCCACTAGGACTTCAAATTGGGGGT
TGGATTTGAAGACTTTTAAGTTTCCTTCCAGCCCAGAAAGTCTCTCATTCTAGCCTCCTGGCCCAGGTGAGTCCT
AGAGCTACAGGGGTTCTGGAAACATTCAGGAGCTTCCTGTCCTCCCAGCTCCTCACTCACCTTCAGTAACCCCCA
CTGGACTGACCTGGTCCACAGGGCACCTGCCACCCTGGGCCTGGCAGCTCAGCTTCCCAACACGCAGGAGCACAC
CCAGCCCCCACATCCTGTGCCTCCATCAGCTAAACACCACGTCACTTCATGCAGGTGAAACCCAGTCACTGTGAG
CTCCCAGGTGCAGCCAGAGGCACCTCAAGAAGAAGAGGGGCATAAACTTTCCTCTTCCTGCCTAGAGGCCCCACC
TTTGGTGCTTTCCAGAATCCCGTAACACCTGATTAACTGAGGCATCCACTTCTTTCAGCAGACTGATCAGGACCT
CCAAGCCACTGAGCAATGTATAACCCCAAAGGGAATTCAAAAAAAAAAAAAAAAA

FIGURE 150

MASSSGSSPRPAPDENEFPFGCPPTVCQDPKEPRALCCAGCLSENPRNGEDQICPKCRGEDLQSISPGSRLRTQE
KAHPEVAEAGIGCPFAGVGCSFKGSPQSVQEHEVTSQTSHLNLLLGFMKQWKARLGCGLESGPMALEQNLSDLQL
QAAVEVAGDLEVDCYRAPCSESQEELALQHFMKEKLLAELEGKLRVFENIVAVLNKEVEASHLALATSIHQSQLD
RERILSLEQRVVELQQTLAQKDQALGKLEQSLRLMEEASFDGTFLWKITNVTRRCHESACGRTVSLFSPAFYTAK
YGYKLCLRLYLNGDGTGKRTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAIDAFRPDLSSASFQRPQ
SETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVETST

FIGURE 151

GAATTCGGCACGAGCGCGCGGCGAATCTCAACGCTGCGCCGTCTGCGGGCGCTTCCGGGCCACCAGTTTCTCTGC
TTTCCACCCTGGCGCCCCCCAGCCCTGGCTCCCCAGCTGCGCTGCCCCGGGCGTCCACGCCCTGCGGGCTTAGCG
GGTTCAGTGGGCTCAATCTGCGCAGCGCCACCTCC**ATG**TTGACCAAGCCTCTACAGGGGCCTCCCGCGCCCCCCG
GGACCCCCACGCCGCCGCCAGGAGGCAAGGATCGGGAAGCGTTCGAGGCCGAGTATCGACTCGGCCCCCTCCTGG
GTAAGGGGGGCTTTGGCACCGTCTTCGCAGGACACCGCCTCACAGATCGACTCCAGGTGGCCATCAAAGTGATTC
CCCGGAATCGTGTGCTGGGCTGGTCCCCCTTGTCAGACTCAGTCACATGCCCACTCGAAGTCGCACTGCTATGGA
AAGTGGGTGCAGGTGGTGGGCACCCTGGCGTGATCCGCCTGCTTGACTGGTTTGAGACACAGGAAGGCTTCATGC
TGGTCCTCGAGCGGCCTTTGCCCGCCCAGGATCTCTTTGACTATATCACAGAGAAGGGCCCACTGGGTGAAGGCC
CAAGCCGCTGCTTCTTTGGCCAAGTAGTGGCAGCCATCCAGCACTGCCATTCCCGTGGAGTTGTCCATCGTGACA
TCAAGGATGAGAACATCCTGATAGACCTACGCCGTGGCTGTGCCAAACTCATTGATTTTGGTTCTGGTGCCCTGC
TTCATGATGAACCCTACACTGACTTTGATGGGACAAGGGTGTACAGCCCCCCAGAGTGGATCTCTCGACACCAGT
ACCATGCACTCCCGGCCACTGTCTGGTCACTGGGCATCCTCCTCTATGACATGGTGTGTGGGGACATTCCCTTTG
AGAGGGACCAGGAGATTCTGGAAGCTGAGCTCCACTTCCCAGCCCATGTCTCCCCAGACTGCTGTGCCCTAATCC
GCCGGTGCCTGGCCCCCAAACCTTCTTCCCGACCCTCACTGGAAGAGATCCTGCTGGACCCCTGGATGCAAACAC
CAGCCGAGGATGTTACCCCTCAACCCCTCCAAAGGAGGCCCTGCCCCTTTGGCCTGGTCCTTGCTACCCTAAGCC
TGGCCTGGCCTGGCCTGGCCCCCAATGGTCAGAAGAGCCATCCCATGGCCATGTCACAGGGA**TAG**ATGGACATTT
GTTGACTTGGTTTTACAGGTCATTACCAGTCATTAAAGTCCAGTATTACTAAGGTAAGGGATTGAGGATCAGGGG
TTAGAAGACATAAACCAAGTTTGCCCAGTTCCCTTCCCAATCCTACAAAGGAGCCTTCCTCCCAGAACCTGTGGT
CCCTGATTTTGGAGGGGGAACTTCTTGCTTCTCATTTTGCTAAGGAAGTTTATTTTGGTGAAGTTGTTCCCATTT
TGAGCCCCGGGACTCTTATTTTGATGATGTGTCACCCCACATTGGCACCTCCTACTACCACCACACAAACTTAGT
TCATATGCTTTTACTTGGGCAAGGGTGCTTTCCTTCCAATACCCCAGTAGCTTTTATTTTAGTAAAGGGACCCTT
TCCCCTAGCCTAGGGTCCCATATTGGGTCAAGCTGCTTACCTGCCTCAGCCCAGGATTTTTTATTTTGGGGGAGG
TAATGCCCTGTTGTTACCCCAAGGCTTCTTTTTTTTTTTTTTTTTTTTTTGGGTGAGGGGACCCTACTTTGTTATC
CCAAGTGCTCTTATTCTGGTGAGAAGAACCTTAATTCCATAATTTGGGAAGGAATGGAAGATGGACACCACCGGA
CACCACCAGACAATAGGATGGGATGGATGGTTTTTTGGGGGATGGGCTAGGGGAAATAAGGCTTGCTGTTTGTTT
TCCTGGGGCGCTCCCTCCAATTTTGCAGATTTTTGCAACCTCCTCCTGAGCCGGGATTGTCCAATTACTAAAATG
TAAATAATCACGTATTGTGGGGAGGGGAGTTCCAAGTGTGCCCTCCTTTTTTTTCCTGCCTGGATTATTTAAAAA
GCCATGTGTGGAAACCCACTATTTAATAAAAGTAATAGAATCAGAAAAAAAAAAAAAAAAAA

FIGURE 152

MLTKPLQGPPAPPGTPTPPPGGKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLS
DSVTCPLEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSRCFFGQVVAA
IQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTRVYSPPEWISRHQYHALPATVWSLG
ILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCALIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQPLQR
RPCPFGLVLATLSLAWPGLAPNGQKSHPMAMSQG

FIGURE 153

AAAATTTGAAGACAAG**ATG**GGCACCTACTCTACAATTCTGATAAAAACAGAGGTCATCGAATGTGGGAACTACTG
TGGAGTACGCATCATTCACTCTTTGATTGCAGAGTTCTCACTGGAAGAATTGAAGAAAAGCTATCACCTGAATAA
AAGTCAAATTATGTTGGATATGCTAACTGAGAATTTGTTCTTCGATACTGGTATGGGAAAAAGTAAATTTTTGCA
AGATATGCACACACTCCTACTCACAAGACACCGCGATGAACATGAAGGTGAAACAGGAAATTGGTTTTCCCCATT
TATTGAAGCATTACATAAAGATGAAGGAAATGAAGCAGTTGAAGCTGTATTGCTTGAAAGTATCCATCGGTTCAA
CCCAAATGCATTCATTTGCCAAGCGTTGGCAAGACATTTCTACATTAAAAAGAAGGACTTTGGCAATGCTCTAAA
CTGGGCAAAACAAGCAAAAAATCATAGAACCTGACAATTCTTATATCTCAGATACACTGGGTCAAGTCTACAAAAG
TAAAATAAGATGGTGGATAGAGGAAAACGGAGGAAACGGGAACATTTCAGTTGATGATCTAATTGCTCTTTTGGA
TTTAGCAGAACATGCCTCAAGTGCATTCAAAGAATCTCAACAGCAAAGTGAAGATAGAGAGTATGAAGTGAAGGA
AAGATTGTATCCGAAGTCAAAAAGGCGGTATGATACTTACAATATAGCTGGTTATCAAGGAGAGATAGAAGTTGG
GCTTTACACAATCCAAATTCTCCAGCTCATTCCTTTTTTTGATAATAAAAATGAGCTATCTAAAAGATATATGGT
CAATTTTGTATCAGGAAGTAGTGATATTCCAGGGGATCCAAACAATGAATATAAATTAGCCCTCAAAAACTATAT
TCCTTATTTAACTAAATTGAAATTTTCTTTGAAAAAGTCCTTTGATTTTTTTGATGAATACTTTGTCCTGCTAAA
ACCCAGGAACAATATTAAGCAAAATGAAGAGGCCAAAACTCGGAGAAAGGTGGCTGGATATTTTAAGAAATATGT
AGATATATTTTGTCTCTTAGAAGAATCACAAAACAACACAGGTCTTGGATCAAAGTTCAGTGAGCCACTTCAAGT
AGAGAGATGCAGGAGAAACCTAGTAGCTTTAAAAGCAGACAAGTTTTCTGGGCTCTTGGAATATCTTATCAAAAG
TCAAGAGGATGCTATAAGCACTATGAAATGTATAGTGAACGAATATACTTTTCTCTTAGAACAATGCACTGTCAA
AATCCAGTCAAAAGAAAAGCTAAATTTCATCTTGGCCAACATTATTCTCTCCTGTATCCAACCTACCTCCAGATT
AGTAAAGCCAGTTGAAAAACTAAAAGATCAGCTTCGAGAAGTCTTGCAACCAATAGGACTGACTTATCAGTTTTC
AGAACCGTATTTTCTAGCTTCCCTCTTATTCTGGCCAGAAAATCAACAACTAGATCAACATTCTGAACAAATGAA
AGAGTATGCTCAAGCACTAAAAAATTCTTTCAAGGGGCAATATAAACATATGCATCGTACAAAGCAACCAATTGC
ATATTTCTTTCTTGGAAAAGGTAAAAGACTGGAAAGACTTGTTCACAAAGGAAAAATTGACCAGTGCTTTAAGAA
GACACCAGATATTAATTCCTTGTGGCAGAGTGGAGATGTGTGGAAGGAGGAAAAAGTCCAAGAACTTTTGCTTCG
TTTACAAGGTCGAGCTGAAAACAATTGTTTATATATAGAATATGGAATCAATGAAAAAATCACAATACCCATCAC
TCCCGCTTTTTTAGGTCAACTTAGAAGTGGCAGAAGCATAGAGAAGGTGTCTTTTTACCTGGGATTTCCCATTGG
AGGCCCACTTGCTTATGACATTGAAATTGTT**TAA**GAGCCTGATATTCTTCCTCCAAGAATTTGATCTCAGTACCC
ATTTAATTTTTTTGGACTCAAGATCTATGCTTTAAACCGGCAAGGTTATAGATACAGCCTCTAGCTCTTCAGATC
TGTACATGCAGTATTTAATTTCCTCTTAAACATGTTATGAGTTCTACAAGGACAATAGTGAAAAAGGAAGGAGTG
AGATATATGAAAAGTAGCAAATATGTTCCTTGGTTTGGTTAACATCATTGATGACAAAATAATAAGGAGCTATGA
CTGGAGTCAGGAGAAGTTAGTGTAATAAGCTGGCTACACAGAACCCCACTACTTACCAGGCATGGATTGAAGAAG
ATTGTCTACTCAAATGGCATTTAGACATTAGAATGTCTGGGAAAATATTTCTCAAAGACAGCAAAAACCTCTCAA
ACTGAGGAGCAACATTTATTCTTACTAAGCAGATCATCAATGTATCATGTGCTTGGCACTCAAGGATCTTCCAAA
ACAGAGGACCAACCAGTCTTCTGAAGGTCATGCCCACAGAAGTCATCGGACCTTACCAAAGTAGGTTGGAGAATT
AGATTGCCTTTTCATGCAGTGAGATTCAGTTAAGCAAAAATGAAATTTGTCTCTATAGCTAATTAGCTTATCAAC
TCCCCTCCAAACAAACAATTAAAAAAAAAACATACAGACACTCAAATTCCACAAGCTAATGAACAAAAGGGACTC
TTGTGAGAAGACTAATGAGTCCCTCATCCAGAAGATGCCAATGTACTGGCAGATTAACATACAACCTATGTTTTG
AACAAAAACAACCAGCGATACGTAATCAAAATGTAATTTTCCCCTAATAAAATTATGGATATGGGCAGTCATCAA
TGGCTGCCAAAACCATTAAGTGGAAAGCTGATTAAAAAACAAAAATTTCTAATGGATTTATCAAACTGTCCCAAA
TCCTGATAAATATTAACATCACAGAGGAAGACCAGACATTATGGGCCTGGAAGTACTATAGGAGTGCACACATCA
CCCGTGACATGGTCTTGCCAAATAATTAAACCTGAATTTGATCAGGTCTCTGGATCTTATTTGCAATTCAAAAGA
AATTTTAAAAAAATCCTACTAACACCACCACAAATATGCAATCAGCAATATCCAGAAAGGGGAAATTCACAGGAC
AAAAACCTGGTTTTCTTTTTTGGTTTCTTCAACCAAAAAAGAAAGAAATTGCAAAGGACCAAAAAAATGTTGGGG
AATCTATACATTATAAGGGACTTAACAACTAAAGGGCAACATATAGACTTTAGATCCTAATTTGAGCAAAATCTA
AAATCAATTATTAGGCAATCAGAAAAATTTGAACACAGACTAGATATTTGAGGATATTAAGGTACTATATTATTG
AAGATTCCATGGTTATGTTTTTTAAAGAGTTCATGCCTTTTAGAGATACATACTAAAGTATTTGTAAATAAATGA
CATGATCTAGAAAAAAAAAAAAAAAA

FIGURE 154

MGTYSTILIKTEVIECGNYCGVRIIHSLIAEFSLEELKKSYHLNKSQIMLDMLTENLFFDTGMGKSKFLQDMHTL
LLTRHRDEHEGETGNWFSPFIEALHKDEGNEAVEAVLLESIHRFNPNAFICQALARHFYIKKKDFGNALNWAKQA
KIIEPDNSYISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASSAFKESQQQSEDREYEVKERLYPK
SKRRYDTYNIAGYQGEIEVGLYTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLALKNYIPYLTK
LKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTRRKVAGYFKKYVDIFCLLEESQNNTGLGSKFSEPLQVERCRR
NLVALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLEQCTVKIQSKEKLNFILANIILSCIQPTSRLVKPVE
KLKDQLREVLQPIGLTYQFSEPYFLASLLFWPENQQLDQHSEQMKEYAQALKNSFKGQYKHMHRTKQPIAYFFLG
KGKRLERLVHKGKIDQCFKKTPDINSLWQSGDVWKEEKVQELLLRLQGRAENNCLYIEYGINEKITIPITPAFLG
QLRSGRSIEKVSFYLGFPIGGPLAYDIEIV

FIGURE 155

CGCCCCTGCTCTCGCGCCGGCGTCGGCTGCGTCTCCGGCGTTTGAATTGCGCTTCCGCCATCTTTCCAGCCTCAG
TCGGACGGGCGCGGAGGCGCTTCTGGAAGGAACGCCGCG**ATG**GCTGCGCAGGGAGAGCCCCAGGTCCAGTTCAAA
CTTGTATTGGTTGGTGATGGTGGTACTGGAAAAACGACCTTCGTGAAACGTCATTTGACTGGTGAATTTGAGAAG
AAGTATGTAGCCACCTTGGGTGTTGAGGTTCATCCCCTAGTGTTCCACACCAACAGAGGACCTATTAAGTTCAAT
GTATGGGACACAGCCGGCCAGGAGAAATTCGGTGGACTGAGAGATGGCTATTATATCCAAGCCCAGTGTGCCATC
ATAATGTTTGATGTAACATCGAGAGTTACTTACAAGAATGTGCCTAACTGGCATAGAGATCTGGTACGAGTGTGT
GAAAACATCCCCATTGTGTTGTGTGGCAACAAAGTGGATATTAAGGACAGGAAAGTGAAGGCGAAATCCATTGTC
TTCCACCGAAAGAAGAATCTTCAGTACTACGACATTTCTGCCAAAAGTAACTACAACTTTGAAAAGCCCTTCCTC
TGGCTTGCTAGGAAGCTCATTGGAGACCCTAACTTGGAATTTGTTGCCATGCCTGCTCTCGCCCCACCAGAAGTT
GTCATGGACCCAGCTTTGGCAGCACAGTATGAGCACGACTTAGAGGTTGCTCAGACAACTGCTCTCCCGGATGAG
GATGATGACCTG**TGA**GAATGAAGCTGGAGCCCAGCGTCAGAAGTCTAGTTTTATAGGCAGCTGTCCTGTGATGTC
AGCGGTGCAGCGTGTGTGCCACCTCATTATTATCTAGCTAAGCGGAACATGTGCTTTATCTGTGGGATGCTGAAG
GAGATGAGTGGGCTTCGGAGTGAATGTGGCAGTTTAAAAAATAACTTCATTGTTTGGACCTGCATATTTAGCTGT
TTGGACGCAGTTGATTCCTTGAGTTTCATATATAAGACTGCTGCAGTCACATCACAATATTCAGTGGTGAAATCT
TGTTTGTTACTGTCATTCCCATTCCTTTTCTTTAGAATCAGAATAAAGTTGTATTTCAAATATCTAAGCAAGTGA
ACTCATCCCTTGTTTATAAATAGCATTTGGAAACCACTAAAGTAGGGAAGTTTTATGCCATGTTAATATTTGAAT
TGCCTTGCTTTTATCACTTAATTTGAAATCTATTGGGTTAATTTCTCCCTATGTTTATTTTTGTACATTTGAGCC
ATGTCACACAAACTGATGATGACAGGTCAGCAGTATTCTATTTGGTTAGAAGGGTTACATGGTGTAAATATTAGT
GCAGTTAAGCTAAAGCAGTGTTTGCTCCACCTTCATATTGGCTAGGTAGGGTCACCTAGGGAAGCACTTGCTCAA
AATCTGTGACCTGTCAGAATAAAAATGTGGTTTGTACATATCAAATAGATATTTTAAGGGTAATATTTTCTTTTA
TGGCAAAAGTAATCATGTTTTAATGTAGAACCTCAAACAGGATGGAACATCAGTGGATGGCAGGAGGTTGGGAAT
TCTTGCTGTTAAAAATAATTACAAATTTTGCACTTTTTGTTTGAATGTTAGATGCTTAGTGTGAAGTTGATACGC
AAGCCG

FIGURE 156

MAAQGEPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGPIKFNVWDTAGQEKFGGL
RDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDIS
AKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTTALPDEDDDL

FIGURE 157

TTAATTTTCTTTTA**ATG**TTTTGTAACCTTACATGTGAT**TAA**AGTGTTGTCCAGACTTTTTATTTTGGACCAGTCT
CTCGTGGAAGTTGCACAAATAGCTTGGAGGGTTCCTGTGTATCTTTTGCCAGCTCTCCCCAGTGATGGTGTCTTA
CATAACCACAGCCTGGGTGACAGAGTGAGCCCCATCTC

FIGURE 158

MFCNLTCD

FIGURE 159

GCAGAGGAGGCGGCGGAACACCCCGGGTTGGTCGGGTTTCCAAGGGCTGACCCGAGCTCCAGCACTTTTTCCGCG
CCTGATTTTTCAGAGCTCTTCAGAAACCAGGCTGCTTTCAGGAACATTGCTGTGGATTCCCAGGGCCTATTCCAC
TAGAAGCAAG**ATG**GCTGAACTCAATACTCATGTGAATGTCAAGGAAAAGATCTATGCAGTTAGATCAGTTGTTCC
CAACAAAAGCAATAATGAAATAGTCCTGGTGCTCCAACAGTTTGATTTTAATGTGGATAAAGCCGTGCAAGCCTT
TGTGGATGGCAGTGCAATTCAAGTTCTAAAAGAATGGAATATGACAGGAAAAAAGAAGAACAATAAAAGAAAAAG
AAGCAAGTCCAAGCAGCATCAAGGCAACAAAGATGCTAAAGACAAGGTGGAGAGGCCTGAGGCAGGGCCCCTGCA
GCCGCAGCCACCACAGATTCAAAACGGCCCCATGAATGGCTGCGAGAAGGACAGCTCGTCCACAGATTCTGCTAA
CGAAAAACCAGCCCTTATCCCTCGTGAGAAAAAGATCTCGATACTTGAGGAACCTTCAAAGGCACTTCGTGGGGT
CACAGAAGGCAACAGACTACTGCAACAGAAACTATCCTTAGATGGGAACCCCAAACCTATACATGGAACAACAGA
GAGGTCAGATGGCCTACAGTGGTCAGCTGAGCAGCCTTGTAACCCAAGCAAGCCTAAGGCAAAAACATCTCCTGT
TAAGTCCAATACCCCTGCAGCTCATCTTGAAATAAAGCCAGATGAGTTGGCAAAGAAAAGAGGCCCAAATATTGA
GAAATCAGTGAAGGATTTGCAACGCTGCACCGTTTCTCTAACTAGATATCGCGTCATGATTAAGGAAGAAGTGGA
TAGTTCCGTGAAGAAGATCAAAGCTGCCTTTGCTGAATTACACAACTGCATCATTGACAAAGAAGTTTCATTAAT
GGCAGAAATGGATAAAGTTAAAGAAGAAGCCATGGAAATCCTGACTGCTCGTCAGAAGAAAGCAGAAGAACTAAA
GAGACTCACTAACCTTGCCAGTCAGATGGCAGAGATGCAGCTGGCCGAACTCAGGGCAGAAATTAAGCACTTTGT
CAGCGAGCGTAAATATGACGAGGAGCTCGGGAAAGCTGCCCGGTTTTCCTGTGACATCGAACAGCTGAAGGCCCA
AATCATGCTCTGCGGAGAAATTACACATCCAAAGAACAACTATTCCTCAAGAACTCCCTGCAGCTCCCTGCTGCC
TCTGCTGAATGCGCACGCAGCAACCTCTGGGAAACAGAGTAACTTTTCCCGAAAATCATCCACTCACAATAAGCC
CTCTGAAGGCAAAGCGGCAAACCCCAAAATGGTGAGCAGTCTCCCCAGCACCGCCGACCCCTCTCACCAGACCAT
GCCGGCCAACAAGCAGAATGGATCTTCTAACCAAAGACGGAGATTTAATCCACAGTATCATAACAACAGGCTAAA
TGGGCCTGCCAAGTCGCAGGGCAGTGGGAATGAAGCCGAGCCACTGGGAAAGGGCAACAGCCGCCACGAACACAG
AAGACAGCCGCACAACGGCTTCCGGCCCAAAAACAAAGGCGGTGCCAAAAATCAAGAGGCTTCCTTGGGGATGAA
GACCCCCGAGGCCCCGGCCCATTCTGAAAAGCCCCGGCGAAGGCAGCACGCTGCAGACACCTCGGAGGCCAGGCC
CTTCCGGGGTAGTGTCGGTAGGGTTTCACAGTGCAATCTCTGCCCCACGAGAATAGAAGTTTCCACAGATGCAGC
AGTTCTCTCAGTCCCGGCTGTGACGTTGGTGGCC**TGA**GCTAGGAGGAAAAAGAGCAGTTTTCACTCAGTTTTGGT
TCCCTGCCCCGAGGTGCTGACCCAATTCGCTGCCAAAAGAGTGTCAATCAGAATATACAAATCCCGTATGGTTGTG
TCATCCTCTCTTAATCATTTTTACTAATTCTAATAATCAGCTCTAGCTTGCTTCATAATTTTCATGGCTTTGCTT
GATCTGTTGATGCTTTCTCTCATCAAGACTTTGCAGCATTTTAGCCAGGCAGTATTTACTCATTATTAGGAAAAT
CAAGATGTGGCTGAAGATCAGAGGCTCAGTTAGCAACCTGTGTTGTAGCAGTGATGTCAGTCCATAGATTGTCTT
TAGAGAGTTAATGTTACAAAAAAGAATTCTTAATAATCAGACAAACATGATCTGCTGAGGACACATGCGCTTTTG
TAGAATTTAACATCTGGTGTTTTTCTGAAAAAATATATATACATATATTGCTTTATTTGAAACAAATTAAAATAT
GCTGCATTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 160

MAELNTHVNVKEKIYAVRSVVPNKSNNEIVLVLQQFDFNVDKAVQAFVDGSAIQVLKEWNMTGKKKNNKRKRSKS
KQHQGNKDAKDKVERPEAGPLQPQPPQIQNGPMNGCEKDSSSTDSANEKPALIPREKKISILEEPSKALRGVTEG
NRLLQQKLSLDGNPKPIHGTTERSDGLQWSAEQPCNPSKPKAKTSPVKSNTPAAHLEIKPDELAKKRGPNIEKSV
KDLQRCTVSLTRYRVMIKEEVDSSVKKIKAAFAELHNCIIDKEVSLMAEMDKVKEEAMEILTARQKKAEELKRLT
NLASQMAEMQLAELRAEIKHFVSERKYDEELGKAARFSCDIEQLKAQIMLCGEITHPKNNYSSRTPCSSLLPLLN
AHAATSGKQSNFSRKSSTHNKPSEGKAANPKMVSSLPSTADPSHQTMPANKQNGSSNQRRRFNPQYHNNRLNGPA
KSQGSGNEAEPLGKGNSRHEHRRQPHNGFRPKNKGGAKNQEASLGMKTPEAPAHSEKPRRRQHAADTSEARPFRG
SVGRVSQCNLCPTRIEVSTDAAVLSVPAVTLVA

FIGURE 161

GGGGGAGTGAAAGCGAAAGCCCGGGCGACTAGCCGGGAGACCAGAGATCTAGCGACTGAAGCAGC**ATG**GCCAAGC
CGTGTGGGGTGCGCCTGAGCGGGGAAGCCCGCAAACAGGTGGAGGTCTTCAGGCAGAATCTTTTCCAGGAGGCTG
AGGAATTCCTCTACAGATTCTTGCCACAGAAAATCATATACCTGAATCAGCTCTTGCAAGAGGACTCCCTCAATG
TGGCTGACTTGACTTCCCTCCGGGCCCCACTGGACATCCCCATCCCAGACCCTCCACCCAAGGATGATGAGATGG
AAACAGATAAGCAGGAGAAGAAAGAAGTCCCTAAGTGTGGATTTCTCCCTGGGAATGAGAAAGTCCTGTCCCTGC
TTGCCCTGGTTAAGCCAGAAGTCTGGACTCTCAAAGAGAAATGCATTCTGGTGATTACATGGATCCAACACCTGA
TCCCCAAGATTGAAGATGGAAATGATTTTGGGGTAGCAATCCAGGAGAAGGTGCTGGAGAGGGTGAATGCCGTCA
AGACCAAAGTGGAAGCTTTCCAGACAACCATTTCCAAGTACTTCTCAGAACGTGGGGATGCTGTGGCCAAGGCCT
CCAAGGAGACTCATGTAATGGATTACCGGGCCTTGGTGCATGAGCGAGATGAGGCAGCCTATGGGGAGCTCAGGG
CCATGGTGCTGGACCTGAGGGCCTTCTATGCTGAGCTTTATCATATCATCAGCAGCAACCTGGAGAAAATTGTCA
CCCCAAAGGGTGAAGAAAAGCCATCTATGTAC**TGA**ACCCGGGACTAGAAGGAAAATAAATGATCTATATGTTGTG
TGG

FIGURE 162

MAKPCGVRLSGEARKQVEVFRQNLFQEAEEFLYRFLPQKIIYLNQLLQEDSLNVADLTSLRAPLDIPIPDPPPKD
DEMETDKQEKKEVPKCGFLPGNEKVLSLLALVKPEVWTLKEKCILVITWIQHLIPKIEDGNDFGVAIQEKVLERV
NAVKTKVEAFQTTISKYFSERGDAVAKASKETHVMDYRALVHERDEAAYGELRAMVLDLRAFYAELYHIISSNLE
KIVTPKGEEKPSMY

FIGURE 163

CACGCTTGCCGCCGCCCCGCAGAA**ATG**CTTCGGTTACCCACAGTCTTTCGCCAGATGAGACCGGTGTCCAGGGTA
CTGGCTCCTCATCTCACTCGGGCTTATGCCAAAGATGTAAAATTTGGTGCAGATGCCCGAGCCTTAATGCTTCAA
GGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGGAAGAACAGTGATTATTGAGCAGGGT
TGGGGAAGTCCCAAAGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATTGACTTAAAAGATAAATACAAGAAC
ATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACACAAATGAAGAAGCTGGGGATGGCACTACCACTGCTACT
GTACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGTGCTAATCCAGTGGAAATCAGGAGA
GGTGTGATGTTAGCTGTTGATGCTGTAATTGCTGAACTTAAAAAGCAGTCTAAACCTGTGACCACCCCTGAAGAA
ATTGCACAGGTTGCTACGATTTCTGCAAACGGAGACAAAGAAATTGGCAATATCATCTCTGATGCAATGAAAAAA
GTTGGAAGAAAGGGTGTCATCACAGTAAAGGATGGAAAAACACTGAATGATGAATTAGAAATTATTGAAGGCATG
AAGTTTGATCGAGGCTATATTTCTCCATACTTTATTAATACATCAAAAGGTCAGAAATGTGAATTCCAGGATGCC
TATGTTCTGTTGAGTGAAAAGAAAATTTCTAGTATCCAGTCCATTGTACCTGCTCTTGAAATTGCCAATGCTCAC
CGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCTAAGTACACTCGTCTTGAATAGGCTAAAG
GTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGGTTTGGTGACAATAGAAAGAACCAGCTTAAAGATATGGCT
ATTGCTACTGGTGGTGCAGTGTTTGGAGAAGAGGGATTGACCCTGAATCTTGAAGACGTTCAGCCTCATGACTTA
GGAAAAGTTGGAGAGGTCATTGTGACCAAAGACGATGCCATGCTCTTAAAAGGAAAAGGTGACAAGGCTCAAATT
GAAAAACGTATTCAAGAAATCATTGAGCAGTTAGATGTCACAACTAGTGAATATGAAAAGGAAAAACTGAATGAA
CGGCTTGCAAAACTTTCAGATGGAGTGGCTGTGCTGAAGGTTGGTGGGACAAGTGATGTTGAAGTGAATGAAAAG
AAAGACAGAGTTACAGATGCCCTTAATGCTACAAGAGCTGCTGTTGAAGAAGGCATTGTTTTGGGAGGGGGTTGT
GCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCAGCTAATGAAGATCAAAAAATTGGTATAGAAATT
ATTAAAAGAACACTCAAAATTCCAGCAATGACCATTGCTAAGAATGCAGGTGTTGAAGGATCTTTGATAGTTGAG
AAAATTATGCAAAGTTCCTCAGAAGTTGGTTATGATGCTATGGCTGGAGATTTTGTGAATATGGTGGAAAAAGGA
ATCATTGACCCAACAAAGGTTGTGAGAACTGCTTTATTGGATGCTGCTGGTGTGGCCTCTCTGTTAACTACAGCA
GAAGTTGTAGTCACAGAAATTCCTAAAGAAGAGAAGGACCCTGGAATGGGTGCAATGGGTGGAATGGGAGGTGGT
ATGGGAGGTGGCATGTTC**TAA**CTCCTAGACTAGTGCTTTACCTTTATTAATGAACTGTGACAGGAAGCCCAAGGC
AGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCTGAAAATCACTATAA
CCATCAGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCATTGTCCATGCCTACAGATAATTT
ATTTTGTATTTTTGAATAAAAAACATTTGTACATTCCTGATACTGGGTACAAGAGCCATGTACCAGTGTACTGCT
TTCAACTTAAATCACTGAGGCATTTTTACTACTATTCTGTTAAAATCAGGATTTTAGTGCTTGCCACCACCAGAT
GAGAAGTTAAGCAGCCTTTCTGTGGAGAGTGAGAATAATTGTGTACAAAGTAGAGAAGTATCCAATTATGTGACA
ACCTTTGTGTAATAAAAATTTGTTTAA

FIGURE 164

MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQGWGSPKVTK
DGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEIRRGVMLAVDA
VIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDELEIIEGMKFDRGYIS
PYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDGEALSTLVLNRLKVGLQVVAV
KAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIVTKDDAMLLKGKGDKAQIEKRIQEII
EQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLRCIPA
LDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLIVEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVV
RTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMGGGMGGGMF

FIGURE 165

TACATGGCGAGCAAAAAAACAACGCTGAGAGAATCTTTTCTCTAATGCCAGAGAAAAATGAACATTCCTATTGCA
CAATGATCCGAGGAATGGTGAAGCTGATGTATACACATTTAATGCATTGATTGAAGCAACAGTATGTGCGATAAA
TGAGAAATTTGAGGAAAAATGGAGTAAAATACTGGAGCTGCTAAGACACATGGTTGCACAGAAGGTGAAACCAAA
TCTTCAGACTTTTAATACCATTCTGAAATGTCTCCGAAGATTTCATGTGTTTGCAAGATCGCCAGCCTTACAGGT
TTTACGTGAAATGAAAGCCATTGGAATAGAACCCTCGCTTGCAACATATCACCATATTATTCGCCTGTTTGATCA
ACCTGGAGACCCTTTAAAGAGATCATCCTTCATCATTTATGATATAATGAATGAATTAATGGGAAAGAGATTTTC
TCCAAAGGACCCGG**ATG**ATGGCATATAAGTTTTTTCAGTCAGCCATGAGCATATGCTCATCTCTCAGAGATCTAG
AACTTGCCTACCAAGTACATGGCCTTTTAAAAACCGGAGACAACTGGAAATTCATTGGACCTGATCAACATCGTA
ATTTCTATTATTCCAAGTTCTTCGATTTGATTTGTCTAATGGAACAAATTGATGTTACCTTGAAGTGGTATGAGG
ACCTGATACCTTCAGCCTACTTTCCCCACTCCCAAACAATGATACATCTTCTCCAAGCATTGGATGTGGCCAATC
GGCTAGAAGTGATTCCTAAAATTTGGAAAGATAGTAAAGAATATGGTCATACTTTCCGCAGTGACCTGAGAGAAG
AGATCCTGATGCTCATGGCAAGGGACAAGCACCCACCAGAGCTTCAGGTGGCATTTGCTGACTGTGCTGCTGATA
TCAAATCTGCGTATGAAAGCCAACCCATCAGACAGACTGCTCAGGATTGGCCAGCCACCTCTCTCAACTGTATAG
CTATCCTCTTTTTAAGGGCTGGGAGAACTCAGGAAGCCTGGAAAATGTTGGGGCTTTTCAGGAAGCATAATAAGA
TTCCTAGAAGTGAGTTGCTGAATGAGCTTATGGACAGTGCAAAAGTGTCTAACAGCCCTTCCCAGGCCATTGAAG
TAGTAGAGCTGGCAAGTGCCTTCAGCTTACCTATTTGTGAGGGCCTCACCCAGAGAGTAATGAGTGATTTTGCAA
TCAACCAGGAACAAAAGGAAGCCCTAAGTAATCTAACTGCATTGACCAGTGACAGTGATACTGACAGCAGCAGTG
ACAGCGACAGTGACACCAGTGAAGGCAAA**TGA**AAGTGGAGATTCAGGAGCAGCAATGGTCTCACCATAGCTGCTG
GAATCACACCTGAGAACTGAGATATACCAATATTTAACATTGTTACAAAGAAGAAAAGATACAGATTTGGTGAAT
TTGTTACTGTGAGGTACAGTCAGTACACAGCTGACTTATGTAGATTTAAGCTGCTAATATGCTACTTAACCATCT
ATTAATGCACCATTAAAGGCTTAGCATTTAAGTAGCAACATTGCGGTTTTCAGACACATGGTGAGGTCCATGGCT
CTTGTCATCAGGATAAGCCTGCACACCTAGAGTGTCGGTGAGCTGACCTCACGATGCTGTCCTCGTGCGATTGCC
CTCTCCTGCTGCTGGACTTCTGCCTTTGTTGGCCTGATGTGCTGCTGTGATGCTGGTCCTTCATCTTAGGTGTTC
ATGCAGTTCTAACACAGTTGGGGTTGGGTCAATAGTTTCCCAATTTCAGGATATTTCGATGTCAGAAATAACGCA
TCTTAGGAATGACTAAACAAGATAATGGCAGTTTAGGCTGCACAACTGGTAAAATGACTGTAGATAAATGTTGTA
ATTAGTGTACACGTTTGTATTTTTGTTAATATAGCCGCTGCCATAGTTTTCTAACTTGAACAGCC

FIGURE 166

MMAYKFFQSAMSICSSLRDLELAYQVHGLLKTGDNWKFIGPDQHRNFYYSKFFDLICLMEQIDVTLKWYEDLIPS
AYFPHSQTMIHLLQALDVANRLEVIPKIWKDSKEYGHTFRSDLREEILMLMARDKHPPELQVAFADCAADIKSAY
ESQPIRQTAQDWPATSLNCIAILFLRAGRTQEAWKMLGLFRKHNKIPRSELLNELMDSAKVSNSPSQAIEVVELA
SAFSLPICEGLTQRVMSDFAINQEQKEALSNLTALTSDSDTDSSSDSDSDTSEGK

FIGURE 167

ATGGAAGATTCGATGGACATGGACATGAGCCCCCTGAGGCCCCAGAACTATCTTTTCGGTTGTGAACTAAAGGCC
GACAAAGATTATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTATCTTTAAGAACGGTCAGTTTAGGG
GCTGGTGCAAAGGATGAGTTGCACATTGTTGAAGCAGAGGCAATGAATTACGAAGGCAGTCCAATTAAAGTAACA
CTGGCAACTTTGAAAATGTCTGTACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACCAGTGGTCTTA
AGGTTGAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTGTGGAGGAAGATGCAGAGTCA
GAAGATGAAGAGGAGGAGGATGTGAAACTCTTAAGTATATCTGGAAAGCGGTCTGCCCCTGGAGGTGGTAGCAAG
GTTCCACAGAAAAAAGTAAAACTTGCTGCTGATGAAGATGATGACGATGATGATGAAGAGGATGATGATGAAGAT
GATGATGATGATGATTTTGATGATGAGGAAGCTGAAGAAAAAGCGCCAGTGAAGAAATCTATACGAGATACTCCA
GCCAAAAATGCACAAAAGTCAAATCAGAATGGAAAAGACTCAAAACCATCATCAACACCAAGATCAAAAGGACAA
GAATCCTTCAAGAAACAGGAAAAAACTCCTAAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAAGCAAAA
ATGCAAGCAAGTATAGAAAAAGGTGGTTCTCTTCCCAAAGTGGAAGCCAAATTCATCAATTATGTGAAGAATTGC
TTCCGGATGACTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTT**TAA**

FIGURE 168

MEDSMDMDMSPLRPQNYLFGCELKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIKVT
LATLKMSVQPTVSLGGFEITPPVVLRLKCGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGKRSAPGGGSK
VPQKKVKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKKSIRDTPAKNAQKSNQNGKDSKPSSTPRSKGQ
ESFKKQEKTPKTPKGPSSVEDIKAKMQASIEKGGSLPKVEAKFINYVKNCFRMTDQEAIQDLWQWRKSL

FIGURE 169

AATGACAGGTTGCTCAGAGACTGCTGATTTCCATCCCTATATAAAGAGAGTCCCTGGCATACAGGGACTGCTCTG
CTCCAGGCATCTGCCACA**ATG**TGGGTGCTTACACCTGCTGCTTTTGCTGGGAAGCTCTTGAGTGTGTTCAGGCAA
CCTCTGAGCTCTCTGTGGAGGAGCCTGGTCCCGCTGTTCTGCTGGCTGAGGGCAACCTTCTGGCTGCTAGCTACC
AAGAGGAGAAAGCAGCAGCTGGTCCTGAGAGGGCCAGATGAGACCAAAGAGGAGGAAGAGGACCCTCCTCTGCCC
ACCACCCCAACCAGCGTCAACTATCACTTCACTCGCCAGTGCAACTACAAATGCGGCTTCTGTTTCCACACAGCC
AAAACATCCTTTGTGCTGCCCCTTGAGGAAGCAAAGAGAGGATTGCTTTTGCTTAAGGAAGCTGGTATGGAGAAG
ATCAACTTTTCAGGTGGAGAGCCATTTCTTCAAGACCGGGGAGAATACCTGGGCAAGTTGGTGAGGTTCTGCAAA
GTAGAGTTGCGGCTGCCCAGCGTGAGCATCGTGAGCAATGGAAGCCTGATCCGGGAGAGGTGGTTCCAGAATTAT
GGTGAGTATTTGGACATTCTCGCTATCTCCTGTGACAGCTTTGACGAGGAAGTCAATGTCCTTATTGGCCGTGGC
CAAGGAAAGAAGAACCATGTGGAAAACCTTCAAAAGCTGAGGAGGTGGTGTAGGGATTATAGAGTCGCTTTCAAG
ATAAATTCTGTCATTAATCGTTTCAACGTGGAAGAGGACATGACGGAACAGATCAAAGCACTAAACCCTGTCCGC
TGGAAAGTGTTCCAGTGCCTCTTAATTGAGGGTGAGAATTGTGGAGAAGATGCTCTAAGAGAAGCAGAAAGATTT
GTTATTGGTGATGAAGAATTTGAAAGATTCTTGGAGCGCCACAAAGAAGTGTCCTGCTTGGTGCCTGAATCTAAC
CAGAAGATGAAAGACTCCTACCTTATTCTGGATGAATATATGCGCTTTCTGAACTGTAGAAAGGGACGGAAGGAC
CCTTCCAAGTCCATCCTGGATGTTGGTGTAGAAGAAGCTATAAAATTCAGTGGATTTGATGAAAAGATGTTTCTG
AAGCGAGGAGGAAAATACATATGGAGTAAGGCTGATCTGAAGCTGGATTGG**TAG**AGCGGAAAGTGGAACGAGACT
TCAACACACCAGTGGGAAAACTCCTAGAGTAACTGCCATTGTCTGCAATACTATCCCGTTGGTATTTCCCAGTGG
CTGAAAACCTGATTTTCTGCTGCACGTGGCATCTGATTACCTGTGGTCACTGAACACACGAATAACTTGGATAGC
AAATCCTGAGACAATGGAAAACCATTAACTTTACTTCATTGGCTTATAACCTTGTTGTTATTGAAACAGCACTTC
TGTTTTTGAGTTTGTTTTAGCTAAAAAGAAGGAATACACACAGGAATAATGACCCCAAAAATGCTTAGATAAGGC
CCCTATACACAGGACCTGACATTTAGCTCAATGATGCGTTTGTAAGAAATAAGCTCTAGTGATATCTGTGGGGGC
AATATTTAATTTGGATTTGATTTTTTAAAACAATGTTTACTGCGATTTCTATATTTCCATTTTGAAACTATTTCT
TGTTCCAGGTTTGTTCATTTGACAGAGTCAGTATTTTTTGCCAAATATCCAGATAACCAGTTTTCACATCTGAGA
CATTACAAAGTATCTGCCTCAATTATTTCTGCTGGTTATAATGCTTTTTTTTTTTTTGCCTTTATGCCATTGCAG
TCTTGTACTTTTTACTGTGATGTACAGAAATAGTCAACAGATGTTTCCAAGAACATATGATATGATAATCCTACC
AATTTTCAAGAAGTCTCTAGAAAGAGATAACACATGGAAAGACGGTGTGGTGCAGCCCAGCCCACGGTGGCTGTT
CCATGAATGCTGGCTACCTATGTGTGTGGTACCTGTTGTGTCCCTTTCTCTTCAAAGATCCTGAGCAAAACAAAG
ATACGCTTTCCATTTGATGATGGAGTTGACATGGAGGCAGTGCTTGCATTGCTTTGTTCGCCTATCATCTGGCCA
CATGAGGCTGTCAAGCAAAAGAATAGGAGTGTAGTTGAGTAGCTGGTTGGCCCTACATCTCTGAGAAGTGACGTT
ACACTGGGTTGGCATAAGATATCCTAAAATCACGCTGGAACCTTGGGCAAGGAAGAATGTGAGCAAGAGTAGAGA
GAGTGCCTGGATTTCATGTCAGTGAAGCCATGTCACCATATCATATTTTTGAATGAACTCTGAGTCAGTTGAAAT
AGGGTACCATCTAGGTCAGTTTAAGAAGAGTCAGCTCAGAGAAAGCAAGCATAAGGGAAAATGTCACGTAAACTA
GATCAGGGAACAAAATCCTCTCCTTGTGGAAATATCCCATGCAGTTTGTTGATACAACTTAGTATCTTATTGCCT
AAAAAAAAATTTCTTATCATTGTTTCAAAAAAGCAAAATCATGGAAAATTTTTGTTGTCCAGGCAAATAAAAGGT
CATTTTAATTTAGCTGCAATTTCAGTGTTCCTCACTAGGTGGCATTTAAATGTCGCCTGATGTCATTAAGCACCA
TCCAAAAAGTCTGCTTCATAATCTATTTTCAAGACTTGGTGATTCTGAAAGTTTTGGTTTTTGTGACTTTGTTTC
TCAGGAAAAAAAATATTCCTACTTAAATTTTAAGTCTATAATTCAATTTAAATATGTGTGTGTCTCATCCAGGAT
AGGATAGGTTGTCTTCTATTTTCCATTTTACCTATTTACTTTTTTTGTAAGAAAAGAGAAAAATGAATTCTAAAG
ATGTTCCCCATGGGTTTTGATTGTGTCTAAGCTATGATGACCTTCATATAATCAGCATAAACATAAAACAAATTT
TTTACTTAACATGAGTGCACTTTACTAATCCTCATGGCACAGT

FIGURE 170

MWVLTPAAFAGKLLSVFRQPLSSLWRSLVPLFCWLRATFWLLATKRRKQQLVLRGPDETKEEEEDPPLPTTPTSV
NYHFTRQCNYKCGFCFHTAKTSFVLPLEEAKRGLLLLKEAGMEKINFSGGEPFLQDRGEYLGKLVRFCKVELRLP
SVSIVSNGSLIRERWFQNYGEYLDILAISCDSFDEEVNVLIGRGQGKKNHVENLQKLRRWCRDYRVAFKINSVIN
RFNVEEDMTEQIKALNPVRWKVFQCLLIEGENCGEDALREAERFVIGDEEFERFLERHKEVSCLVPESNQKMKDS
YLILDEYMRFLNCRKGRKDPSKSILDVGVEEAIKFSGFDEKMFLKRGGKYIWSKADLKLDW

FIGURE 171

CTGAGGCCCACGCAGGGCCTAGGGTGGGAAG**ATG**GCAGGTGGGGGCGGCGACCTGAGCACCAGGAGGCTGAATGA
ATGTATTTCACCAGTAGCAAATGAGATGAACCATCTTCCTGCACACAGCCACGATTTGCAAAGGATGTTCACGGA
AGACCAGGGTGTAGATGACAGGCTGCTCTATGACATTGTATTCAAGCACTTCAAAAGAAATAAGGTGGAGATTTC
AAATGCAATAAAAAAGACATTTCCATTCCTCGAGGGCCTCCGTGATCGTGATCTCATCACAAATAAAATGTTTGA
AGATTCTCAAGATTCTTGTAGAAACCTGGTCCCTGTACAGAGAGTGGTGTACAATGTTCTTAGTGAACTGGAGAA
GACATTTAACCTGCCAGTTCTGGAAGCACTGTTCAGCGATGTCAACATGCAGGAATACCCCGATTTAATTCACAT
TTATAAAGGCTTTGAAAATGTAATCCATGACAAATTGCCTCTCCAAGAAAGTGAAGAAGAAGAGAGGGAGGAGAG
GTCTGGCCTCCAACTAAGTCTTGAACAAGGAACTGGTGAAAACTCTTTTCGAAGCCTGACTTGGCCACCTTCGGG
TTCCCCATCTCATGCTGGTACAACCCCACCTGAAAATGGACTCTCAGAGCACCCCTGTGAAACAGAACAGATAAA
TGCAAAGAGAAAAGATACAACCAGTGACAAAGATGATTCGCTAGGAAGCCAACAAACAAATGAACAATGTGCTCA
AAAGGCTGAGCCAACAGAGTCCTGCGAACAAATTGCTGTCCAAGTGAATAATGGGGATGCTGGAAGGGAGATGCC
CTGCCCGTTGCCCTGTGATGAAGAAAGCCCAGAGGCAGAGCTACACAACCATGGAATCCAAATTAATTCCTGTTC
TGTGCGACTGGTGGATATAAAAAAGGAAAAGCCATTTTCTAATTCAAAAGTTGAGTGCCAAGCCCAAGCAAGAAC
TCATCATAACCAGGCATCTGACATAATAGTCATCAGCAGTGAGGACTCTGAAGGATCCACTGACGTTGATGAGCC
CTTAGAAGTCTTCATCTCAGCACCGAGAAGTGAGCCTGTGATCAATAATGACAACCCTTTAGAATCAAATGATGA
AAAGGAGGGCCAAGAAGCCACTTGCTCACGACCCCAGATTGTACCAGAGCCCATGGATTTCAGAAAATTATCTAC
ATTCAGAGAAAGTTTTAAGAAAAGAGTGATAGGACAAGACCACGACTTTTCAGAATCCAGTGAGGAGGAGGCGCC
CGCAGAAGCCTCAAGCGGGGCACTGAGAAGCAAGCATGGTGAGAAGGCTCCTATGACTTCTAGAAGTACATCTAC
TTGGAGAATACCCAGCAGGAAGAGACGTTTCAGCAGTAGTGACTTTTCAGACCTGAGTAATGGAGAAGAGCTTCA
GGAAACCTGCAGCTCATCCCTAAGAAGAGGGTCAGGTAAAGAAGAT**TAG**GATGCCAAGACTTGGCCTGCAGAATG
TCAGGAATGTGAATTAAAAGCTGCTGTTTCCAGACGCTTTTTATTCTGAGCACCTTCACTACCTTGTATCCAGTT
CATCTGGGAACTCCTTTTTGCATTTTAGAAAATGGAAAGAGGCAGGAAATTATGATAAACTCATGTTTAACAGAA
AGAGTTTCACTGACTAAATGTATGTAATTATATTTTGTTGTTGTAGAAGAAATAAATAGCAAATTTGTGGTATTC
TTTTTTTTAAACCTGCTCTCATTCCTATTAACACTAAGATCTTAGATTTTTATAGTGATAAATGGGTTGACATCA
TTGTCGTTTGTAATTGTAAAGCCTCAAAAGACAACTGTTCCTACTATGTAATTATAGACAGAAATAAAAACTTCA
GATC

FIGURE 172

MAGGGGDLSTRRLNECISPVANEMNHLPAHSHDLQRMFTEDQGVDDRLLYDIVFKHFKRNKVEISNAIKKTFPFL
EGLRDRDLITNKMFEDSQDSCRNLVPVQRVVYNVLSELEKTFNLPVLEALFSDVNMQEYPDLIHIYKGFENVIHD
KLPLQESEEEEREERSGLQLSLEQGTGENSFRSLTWPPSGSPSHAGTTPPENGLSEHPCETEQINAKRKDTTSDK
DDSLGSQQTNEQCAQKAEPTESCEQIAVQVNNGDAGREMPCPLPCDEESPEAELHNHGIQINSCSVRLVDIKKEK
PFSNSKVECQAQARTHHNQASDIIVISSEDSEGSTDVDEPLEVFISAPRSEPVINNDNPLESNDEKEGQEATCSR
PQIVPEPMDFRKLSTFRESFKKRVIGQDHDFSESSEEEAPAEASSGALRSKHGEKAPMTSRSTSTWRIPSRKRRF
SSSDFSDLSNGEELQETCSSSLRRGSGKED

FIGURE 173

GGTCAGGATCTGGGAAGGTGACGGATGAGTAGCCTGATGAGGCTGAAGCTGCCACCATTCAGCTTTTCAGCAGCA
GACACTCCACCCCAAAGCCTGCAGAAGGGATTTTGTGAAGAGGGTCACCAGGCTGAGCCTCGGCCAGAACCCGTC
TACAGAGGACCCTCAGCCAGAGCAGAAAGCTCCTGAGCCAGCTCCCTTGG**<u>ATG</u>**GACTCCCAGAGGCCTGAGCCCA
GANNNNNNNNNNNNNNNNNNNNNNNACTGCGGTGGATGGAGCTGGACTCCGAAGAGGCCCTGGGAACCAGGACAG
AGGGGCCTAGTGTTGTCCAGGGCTGGGGGCACCTGCTCCAGGCCGTGTGGAGGGGCCCTGCAGGCCTGGTGACGC
AGCTGCTGCGGCAAGGTGCCAGCGTGGAGGAGAGGACATTGAGGTGCTGCTGGGCCACGGGGCAGACCCAGGCAT
CAGGGACAGGCATGGCCGCTCTGCGCTGCACAGGGCTGCCGCCCGAGGACACCTGCTTGCCGTCCAGTTGCTGGT
CACCCAGGGGGCCGAGGTGGATGCGCGGGACACCCTGGGCCTCACACCCCTGCATCACGCCTCTCGGGAAGGCCA
CGTGGAGGTTGCCGGCTGCCTGCTGGACAGGGTGTGCCCAGGTGGATGCTACCGGCTGGCTCCGAAAGACCCCCC
TACACCTGGCTGCAGAGCGAGGGCATGGGCCTACCGTGGGGCTTCTGCTGAGCCGAGGGGCCAGCCCCACTCTGC
GGACGCAGTGGGCCGAGGTGGCCCAGATGCCTGAGGGGGACCTGCCCCAGGCGCTGCTGAACTTGGAGGGGGGGA
AAGGAGTG**<u>TGA</u>**GGGC

FIGURE 174

MDSQRPEPRXXXXXXXXXLRWMELDSEEALGTRTEGPSVVQGWGHLLQAVWRGPAGLVTQLLRQGASVEERTLRCC
WATGQTQASGTGMAALRCTGLPPEDTCLPSSCWSPRGPRWMRGTPWASHPCITPLGKATWRLPAACWTGCAQVDA
TGWLRKTPLHLAAERGHGPTVGLLLSRGASPTLRTQWAEVAQMPEGDLPQALLNLEGGKGV

FIGURE 175

GGCACGAGGGCCAGGAACGCCAGCCGTTCACGCGTTCGGTCCTCCTTGGCTGACTCACCGCCCTCGCCGCCGCAC
C**ATG**GACGCCCCCAGGCAGGTGGTCAACTTTGGGCCTGGTCCCGCCAAGCTGCCGCACTCAGTGTTGTTAGAGAT
ACAAAAGGAATTATTAGACTACAAAGGAGTTGGCATTAGTGTTCTTGAAATGAGTCACAGGTCATCAGATTTTGC
CAAGATTATTAACAATACAGAGAATCTTGTGCGGGAATTGCTAGCTGTTCCAGACAACTATAAGGTGATTTTTCT
GCAAGGAGGTGGGTGCGGCCAGTTCAGTGCTGTCCCCTTAAACCTCATTGGCTTGAAAGCAGGAAGGTGTGCGGA
CTATGTGGTGACAGGAGCTTGGTCAGCTAAGGCCGCAGAAGAAGCCAAGAAGTTTGGGACTATAAATATCGTTCA
CCCTAAACTTGGGAGTTATACAAAAATTCCAGATCCAAGCACCTGGAACCTCAACCCAGATGCCTCCTACGTGTA
TTATTGCGCAAATGAGACGGTGCATGGTGTGGAGTTTGACTTTATACCCGATGTCAAGGGAGCAGTACTGGTTTG
TGACATGTCCTCAAACTTCCTGTCCAAGCCAGTGGATGTTTCCAAGTTTGGTGTGATTTTTGCTGGTGCCCAGAA
GAATGTTGGCTCTGCTGGGGTCACCGTGGTGATTGTCCGTGATGACCTGCTGGGGTTTGCCCTCCGAGAGTGCCC
CTCGGTCCTGGAATACAAGGTGCAGGCTGGAAACAGCTCCTTGTACAACACGCCTCCATGTTTCAGCATCTACGT
CATGGGCTTGGTTCTGGAGTGGATTAAAAACAATGGAGGTGCCGCGGCCATGGAGAAGCTTAGCTCCATCAAATC
TCAAACAATTTATGAGATTATTGATAATTCTCAAGGATTCTACGTTTGTCCAGTGGAGCCCCAAAATAGAAGCAA
GATGAATATTCCATTCCGCATTGGCAATGCCAAAGGAGATGATGCTTTAGAAAAAAGATTTCTTGATAAAGCTCT
TGAACTCAATATGTTGTCCTTGAAAGGGCATAGGTCTGTGGGAGGCATCCGGGCCTCTCTGTATAATGCTGTCAC
AATTGAAGACGTTCAGAAGCTGGCCGCCTTCATGAAAAAATTTTTGGAGATGCATCAGCTA**TGA**ACACATCCTAA
CCAGGATATACTCTGTTCTTGAACAACATACAAAGTTTAAAGTAACTTGGGGATGGCTACAAAAAGTTAACACAG
TATTTTTCTCAAATGAACATGTTTATTGCAGATTCTTCTTTTTTGAAAGAACAACAGCAAAACATCCACAACTCT
GTAAAGCTGGTGGGACCTAATGTCACCTTAATTCTGACTTGAACTGGAAGCATTTTAAGAAATCTTGTTGCTTTT
CTAACAAATTCCCGCGTATTTTGCCTTTGCTGCTACTTTTTCTAGTTAGATTTCAAACTTGCCTGTGGACTTAAT
AATGCAAGTTGCGATTAATTATTTCTGGAGTCATGGGAACACACAGCACAGAGGGTAGGGGGGCCCTCTAGGTGC
TGAATCTACACATCTGTGGGGTCTCCTGGGTTCAGCGGCTGTTGATTCAAGGTCAACATTGACCATTGGAGGAGT
GGTTTAAGAGTGCCAGGCGAAGGGCAAACTGTAGATCGATCTTTATGCTGTTATTACAGGAGAAGTGACATACTT
TATATATGTTTATATTAGCAAGGTCTGTTTTTAATACCATATACTTTATATTTCTATACATTTATATTTCTAATA
ATACAGTTATCACTGATATATGTAGACACTTTTAGAATTTATTAAATCCTTGACCTTGTGCATTATAGCATTCCA
TTAGCAAGAGTTGTACCCCCTCCCCAGTCTTCGCCTTCCTCTTTTTAAGCTGTTTTATGAAAAAGACCTAGAAGT
TCTTGATTCATTTTTACCATTCTTTCCATAGGTAGAAGAGAAAGTTGATTGGTTGGTTGTTTTTCAATTATGCCA
TTAAACTAAACATTTCTGTTAAATTACCCTATCCTTTGTTCTCTACTGTTTTCTTTGTAATGTATGACTACGAGA
GTGATACTTTGCTGAAAAGTCTTTCCCCTATTGTTTATCTATTGTCAGTATTTTATGTTGAATATGTAAAGAACA
TTAAAGTCCTAAAACATCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 176

MDAPRQVVNFGPGPAKLPHSVLLEIQKELLDYKGVGISVLEMSHRSSDFAKIINNTENLVRELLAVPDNYKVIFL
QGGGCGQFSAVPLNLIGLKAGRCADYVVTGAWSAKAAEEAKKFGTINIVHPKLGSYTKIPDPSTWNLNPDASYVY
YCANETVHGVEFDFIPDVKGAVLVCDMSSNFLSKPVDVSKFGVIFAGAQKNVGSAGVTVVIVRDDLLGFALRECP
SVLEYKVQAGNSSLYNTPPCFSIYVMGLVLEWIKNNGGAAAMEKLSSIKSQTIYEIIDNSQGFYVCPVEPQNRSK
MNIPFRIGNAKGDDALEKRFLDKALELNMLSLKGHRSVGGIRASLYNAVTIEDVQKLAAFMKKFLEMHQL

FIGURE 177

GGCGTCTGCCAGGAGCTACGGCCGGAAG**ATG**GCGGCGGCCGCAGAGTTGTCGCTACTGGAGAAGTCCCTGGGACT
GAGTAAGGGGAATAAATACAGTGCTCAGGGCGAGCGACAGATTCCAGTTCTTCAGACAAACAATGGTCCAAGTCT
AACAGGATTGACTACTATAGCAGCTCATCTAGTCAAGCAAGCCAACAAAGAATATTTGCTGGGGAGTACTGCAGA
AGAAAAAGCAATCGTTCAGCAGTGGTTAGAATACAGGGTCACTCAAGTAGATGGGCACTCCAGTAAAAATGACAT
CCACACACTGTTGAAGGATCTTAATTCATATCTTGAAGATAAAGTCTACCTTACAGGGTATAACTTTACATTAGC
AGATATACTATTGTACTATGGACTTCATCGCTTTATAGTTGACCTGACAGTTCAAGAAAAGGAGAAATATCTTAA
TGTGTCTCGCTGGTTTTGTCACATTCAGCATTATCCAGGCATCAGGCAACATCTGTCTAGTGTTGTCTTCATCAA
GAACAGACTATATACTAATTCCCAC**TAG**AAGCTGTCCATGCCATACAGAAGATCTATTAAAAATGTTTTAAATGG
AAAATGTACTCTAGACCACAGGACTAATGTAAATTAATATACAGTCATTCATTATTTGTTGAAGTTGATAGAATT
TTTGAAGTGTAAACTTGTGTCTGAATGTTTTATTTGTTCTTTAGCTGAAGTTTTGCAATTTTTATGTCAAAATTC
AATTGCTATTAAACAAGTTGAGATCCAGTTATAAATTAACCTTGTTTTTAGTAGATGACATTTATTTCAATAAAA
GTTGCAAATCGGGAA

FIGURE 178

MAAAAELSLLEKSLGLSKGNKYSAQGERQIPVLQTNNGPSLTGLTTIAAHLVKQANKEYLLGSTAEEKAIVQQWL
EYRVTQVDGHSSKNDIHTLLKDLNSYLEDKVYLTGYNFTLADILLYYGLHRFIVDLTVQEKEKYLNVSRWFCHIQ
HYPGIRQHLSSVVFIKNRLYTNSH

FIGURE 179

GGCACGAGCCCAGAAACAAAGACTTCACGGACAAAGTCCCTTGGAACCAGAGAGAAGCCGGG**ATG**GAAACTCCAA
ACACCACAGAGGACTATGACACGACCACAGAGTTTGACTATGGGGATGCAACTCCGTGCCAGAAGGTGAACGAGA
GGGCCTTTGGGGCCCAACTGCTGCCCCCTCTGTACTCCTTGGTATTTGTCATTGGCCTGGTTGGAAACATCCTGG
TGGTCCTGGTCCTTGTGCAATACAAGAGGCTAAAAAACATGACCAGCATCTACCTCCTGAACCTGGCCATTTCTG
ACCTGCTCTTCCTGTTCACGCTTCCCTTCTGGATCGACTACAAGTTGAAGGATGACTGGGTTTTTGGTGATGCCA
TGTGTAAGATCCTCTCTGGGTTTTATTACACAGGCTTGTACAGCGAGATCTTTTTCATCATCCTGCTGACGATTG
ACAGGTACCTGGCCATCGTCCACGCCGTGTTTGCCTTGCGGGCACGGACCGTCACTTTTGGTGTCATCACCAGCA
TCATCATTTGGGCCCTGGCCATCTTGGCTTCCATGCCAGGCTTATACTTTTCCAAGACCCAATGGGAATTCACTC
ACCACACCTGCAGCCTTCACTTTCCTCACGAAAGCCTACGAGAGTGGAAGCTGTTTCAGGCTCTGAAACTGAACC
TCTTTGGGCTGGTATTGCCTTTGTTGGTCATGATCATCTGCTACACAGGGATTATAAAGATTCTGCTAAGACGAC
CAAATGAGAAGAAATCCAAAGCTGTCCGTTTGATTTTTGTCATCATGATCATCTTTTTTCTCTTTTGGACCCCCT
ACAATTTGACTATACTTATTTCTGTTTTCCAAGACTTCCTGTTCACCCATGAGTGTGAGCAGAGCAGACATTTGG
ACCTGGCTGTGCAAGTGACGGAGGTGATCGCCTACACGCACTGCTGTGTCAACCCAGTGATCTACGCCTTCGTTG
GTGAGAGGTTCCGGAAGTACCTGCGGCAGTTGTTCCACAGGCGTGTGGCTGTGCACCTGGTTAAATGGCTCCCCT
TCCTCTCCGTGGACAGGCTGGAGAGGGTCAGCTCCACATCTCCCTCCACAGGGGAGCATGAACTCTCTGCTGGGT
TC**TGA**CTCAGACCATAGGAGGCCAACCCAAAATAAGCAGGCGTGACCTGCCAGGCACACTGAGCCAGCAGCCTGG
CTCTCCCAGCCAGGTTCTGACTCTTGGCACAGCATGGAGTCACAGCCACTTGGGATAGAGAGGGAATGTAATGGT
GGCCTGGGGCTTCTGAGGCTTCTGGGGCTTCAGTCTTTTCCATGAACTTCTCCCCTGGTAGAAAGAAGATGAATG
AGCAAAACCAAATATTCCAGAGACTGGGACTAAGTGTACCAGAGAAGGGCTTGGACTCAAGCAAGATTTCAGATT
TGTGACCATTAGCATTTGTCAACAAAGTCACCCACTTCCCACTATTGCTTGCACAAACCAATTAAACCCAGTAGT
GGTGACTGTGGGCTCCATTCAAAGTGAGCTCCTAAGCCATGGGAGACACTGATGTATGAGGAATTTCTGTTCTTC
CATCACCTCCCCCCCCCCGCCACCCTCCCACTGCCAAGAACTTGGAAATAGTGATTTCCACAGTGACTCCACTCT
GAGTCCCAGAGCCAATCAGTAGCCAGCATCTGCCTCCCCTTCACTCCCACCGCAGGATTTGGGCTCTTGGAATCC
TGGGGAACATAGAACTCATGACGGAAGAGTTGAGACCTAACGAGAAATAGAAATGGGGGAACTACTGCTGGCAGT
GGAACTAAGAAAGCCCTTAGGAAGAATTTTTATATCCACTAAAATCAAACAATTCAGGGAGTGGGCTAAGCACGG
GCCATATGAATAACATGGTGTGCTTCTTAAAATAGCCATAAAGGGGAGGGACTCATCATTTCCATTTACCCTTCT
TTTCTGACTATTTTTCAGAATCTCTCTTCTTTTCAAGTTGGGTGATATGTTGGTAGATTCTAATGGCTTTATTGC
AGCGATTAATAACAGGCAAAAGGAAGCAGGGTTGGTTTCCCTTCTTTTTGTTCTTCATCTAAGCCTTCTGGTTTT
ATGGGTCAGAGTTCCGACTGCCATCTTGGACTTGTCAGCAAAAAAAAAAAAAAAAA

FIGURE 180

METPNTTEDYDTTTEFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYKRLKNMTSIYLLN
LAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFG
VITSIIIWALAILASMPGLYFSKTQWEFTHHTCSLHFPHESLREWKLFQALKLNLFGLVLPLLVMIICYTGIIKI
LLRRPNEKKSKAVRLIFVIMIIFFLFWTPYNLTILISVFQDFLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVI
YAFVGERFRKYLRQLFHRRVAVHLVKWLPFLSVDRLERVSSTSPSTGEHELSAGF

FIGURE 181A

AGAGCGAGCAGGGGAGAGCGAGACCAGTTTTAAGGGGAGGACCGGTGCGAGTGAGGCAGCCCCGAGGCTCTGCTC
GCCCACCACCCAATCCTCGCCTCCCTTCTGCTCCACCTTCTCTCTCTGCCCTCACCTCTCCCCCGAAAACCCCCT
ATTTAGCCAAAGGAAGGAGGTCAGGGGAACGCTCTCCCCTCCCCTTCCAAAAAACAAAAACAGAAAAACCCTTTT
CCAGGCCGGGGAAAGCAGGAGGGAGAGGGGCCGCCGGGCTGGCC**ATG**GAGCTGCTGTGCCACGAGGTGGACCCGG
TCCGCAGGGCCGTGCGGGACCGCAACCTGCTCCGAGACGACCGCGTCCTGCAGAACCTGCTCACCATCGAGGAGC
GCTACCTTCCGCAGTGCTCCTACTTCAAGTGCGTGCAGAAGGACATCCAACCCTACATGCGCAGAATGGTGGCCA
CCTGGATGCTGGAGGTCTGTGAGGAACAGAAGTGCGAAGAAGAGGTCTTCCCTCTGGCCATGAATTACCTGGACC
GTTTCTTGGCTGGGGTCCCGACTCCGAAGTCCCATCTGCAACTCCTGGGTGCTGTCTGCATGTTCCTGGCCTCCA
AACTCAAAGAGACCAGCCCGCTGACCGCGGAGAAGCTGTGCATTTACACCGACAACTCCATCAAGCCTCAGGAGC
TGCTGGAGTGGGAACTGGTGGTGCTGGGGAAGTTGAAGTGGAACCTGGCAGCTGTCACTCCTCATGACTTCATTG
AGCACATCTTGCGCAAGCTGCCCCAGCAGCGGGAGAAGCTGTCTCTGATCCGCAAGCATGCTCAGACCTTCATTG
CTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACCCACCGTCGATGATCGCAACTGGAAGTGTGGGAGCAGCCA
TCTGTGGGCTCCAGCAGGATGAGGAAGTGAGCTCGCTCACTTGTGATGCCCTGACTGAGCTGCTGGCTAAGATCA
CCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGGAGCAGATTGAGGCGGTGCTCCTCAATAGCCTGCAGCAGT
ACCGTCAGGACCAACGTGACGGATCCAAGTCGGAGGATGAACTGGACCAAGCCAGCACCCCTACAGACGTGCGGG
ATATCGACCTG**TGA**GGATGCCAGTTGGGCCGAAAGAGAGAGACGCGTCCATAATCTGGTCTCTTCTTCTTTCTGG
TTGTTTTTGTTCTTTGTGTTTTAGGGTGAAACTTAAAAAAAAAATTCTGCCCCCACCTAGATCATATTTAAAGAT
CTTTTAGAAGTGAGAGAAAAAGGTCCTACGAAAACGGAATAATAAAAAGCATTTGGTGCCTATTTGAAGTACAGC
ATAAGGGAATCCCTTGTATATGCGAACAGTTATTGTTTGATTATGTAAAAGTAATAGTAAAATGCTTACAGGAAA
ACCTGCAGAGTAGTTAGAGAATATGTATGCCTGCAATATGGGAACAAATTAGAGGAGACTTTTTTTTTCATGTT
ATGAGCTAGCACATACACCCCCTTGTAGTATAATTTCAAGGAACTGTGTACGCCATTTATGGCATGATTAGATTG
CAAAGCAATGAACTCAAGAAGGAATTGAAATAAGGAGGGACATGATGGGGAAGGAGTACAAAACAATCTCTCAAC
ATGATTGAACCATTTGGGATGGAGAAGCACCTTTGCTCTCAGCCACCTGTTACTAAGTCAGGAGTGTAGTTGGAT
CTCTACATTAATGTCCTCTTGCTGTCTACAGTAGCTGCTACCTAAAAAAAGATGTTTTATTTTGCCAGTTGGACA
CAGGTGATTGGCTCCTGGGTTTCATGTTCTGTGACATCCTGCTTCTTCTTCCAAATGCAGTTCATTGCAGACACC
ACCATATTGCTATCTAATGGGGAAATGTAGCTATGGGCCATAACCAAAACTCACATGAAACGGAGGCAGATGGAG
ACCAAGGGTGGGATCCAGAATGGAGTCTTTTCTGTTATTGTATTTAAAAGGGTAATGTGGCCTTGGCATTTCTTC
TTAGAAAAAAACTAATTTTTGGTGCTGATTGGCATGTCTGGTTCACAGTTTAGCATTGTTATAAACCATTCCATT
CGAAAAGCACTTTGAAAAATTGTTCCCGAGCGATAGATGGGATGGTTTATGCAAGTCATGCTGAATACTCCTCCC
CTCTTCTCTTTTGCCCCCTCCCTTCCTGCCCCCAGTCTGGGTTACTCTTCGCTTCTGGTATCTGGCGTTCTTTGG
TACACAGTTCTGGTGTTCCTACCAGGACTCAAGAGACACCCCTTCCTGCTGACATTCCCATCACAACATTCCTCA
GACAAGCCTGTAAACTAAAATCTGTTACCATTCTGATGGCACAGAAGGATCTTAATTCCCATCTCTATACTTCTC
CTTTGGACATGGAAAGAAAAGTTATTGCTGGTGCAAAGATAGATGGCTGAACATCAGGGTGTGGCATTTTGTTCC
CTTTTCCGTTTTTTTTTTTTTTTATTGTTGTTGTTAATTTTATTGCAAAGTTGTATTCAGCGTACTTGAATTTTTC
TTCCTCTCCACTTCTTAGAGGCATTCAGTTAGCAAAGAGGTTGGAGCAACAACTTTTTTTTTTTTTTTTGCACAA
TTGTAATTGACAGGTAATGAAGCTATTTGTTAAAATATTTGCCTTTTTAAGTAAAAAAGAAAAATCAGAACAGGG
CTATTTGAAGAATTATTTTATACACAGATTCTGCCTTGTTTCATAGTATGAGGGTTGAAGACGGAAAACAATCTA
AGGGTCTCTCATTTTTTTAATTTTGTTTTGTTCAGTTTGGTTTTTTTTTTTTTTTTGCGCTGCTAAGAAGCTAAAG
TCATCCATCCTTATTCACGTTGACAGTACCTAGCTGTAATGTTTCACAGAGTGTGCTGCTATTTTATAAACATTT
TTATAATATATTATTTTACTGCTTAAATTCCAAGTCCTGAAGTAGATGGTTGAGATATGAGTTCTTCGTACTGGA
AAAGCCCTTCCGTAGTTTGTTTTCTTCTGGTAGCATATTCATGGTTGTTTTTTTTTTTCTTTTTTGGTTTTTTGG
TTTTTTTTTTTTCCTCTGATCACATTCTTCAAAGACGGAGTATTCTTTACCTCAGGTTTACTGGACAAAATCAAT
AACTACAAAAGGCAATGATTCACGCTTTTGTTTTCATAATACCTCACAACCGTACAGTTTCTGCTTGGGAGCCCA
TTCGCATGAGGAATACAGAAGCAGTGTGAGCAGGGCTGACTCCCTCTCAGGTGGAAGGCAGGGCGGTCTCACTCC
CAGGGACCTTTTTGGTCATGGAGGCCATCGGGCTCCCAGTTAGACCCTGGTATCCTCATCATGATGGAAAAAATA
CATTGAACCAAGGGATCCTCCCTCCCCTTCAAGGCAGACGTTCAGTACAAACATTTATGCGGTAGGCTCAGATGT
CGTAATTTGCACTTAGGTACCAGGTGTCAGGAAACAGACTAAAAAGAATTCCACCAGGCTGTTTGGAGATCCTCA
TCTTGGAGCTTTTTCAAAAGCGGGGCTTCATCTGCAAAGGGCCCTTTCATCTTGAAGTTTTTCCCCTCCGTCTTT

FIGURE 181B

CCCCTCCCCTGGCATGGACACCTTGTGTTTAGGATCATCTCTGCAGGTTTCCTAGGTCTGAATCTGCGAGTAGAT
GAACCTGCAGCAAGCAGCGTTTATGGTGCTTCCTTCTCCCTCCTCTGTCTCAAACTGCGCAGGCAAGCACTATGC
AAGCCCAGGCCCTCTGCTGAGCGGTACTAAACGGTCGGGTTTTCAATCACACTGAATTGGCAGGATAAGAAAAAT
AGGTCAGATAAGTATGGGATGATAGTTGAAGGGAGGTGAAGAGGCTGCTTCTCTACAGAGGTGAAATTCCAGATG
AGTCAGTCTCTTGGGAAGTGTGTTTAGAAGGGTTCAGGACTTTGTGAGTTAGCATGACCCTAAAATTCTAGGGGA
TTTCTGGTGGGACAATGGGTGGTGAATTTTGAAGTTTTGGAGAGGGAAGTGGAGCAGCCAGCAAGTAAGCTAGCC
AGAGTTTTCTCAAGAGCCAGCTTTGCTCAGCACACTCTCCTGGGCCCCAAGGAGTCCCACGGAATGGGGAAAGTG
GGAACCCTGGAGTTCTTGGGAATCTTGGAGCCTAAAGAGAAACCGAGGTGCAAATTCATTTCATGGTGACTGACC
CTTGAGCTTAAACAGAAGCAGCAAATGAAAGAACCGGACAAATAAGGAAGGGCACAAGCCTACCCGACTCTATTT
ACAGTCTGTAACTTTCCACTCTTCCTGTAGTCCCGAGGCCCCTGGGTCCTTCTAGCTTTTCTCTTTCCCATCCTT
GGGGCCTTGTGTGATGATGGGTGTGGGGCTGCCGATGGGAAAGTCGGGGGTTGTTAGGCTTTTCTGCCTGCTCCT
GCTTAAACACAAGAAGGAATCCTGGATTTTGCCCTCTCCTTAGCTCTTAGTCTCTTTGGTAGGAGTTTTGTTCCA
GAGGAGCTCTCCCCCTTGGATTTGAACTTGCTCTTTTTGTTGTTGTTGTTCTTTCTCTTCTTTTTCTTACCTCCC
ACTAAAGGGGTTCCAAATTATCCTGGTCTTTTTCTACCTTGTTGTGTTTCTATCTCGTCTTTACTTCCATCTGTT
TGTTTTTTTCTCCATCAGTGGGGGCCGAGTTGTTCCCCCAGCCTGCCAAATTTTGATCCTTCCCCTCTTTTGGCC
AAATCCTAGGGGGAAGAAATCCTAGTATGCCAAAAATATATGCTAAGCATAATTAAACTCCATGCGGGTCCATAA
CAGCCAAGAAGCCTGCAGGAGAAAGCCAAGGGCAGTTCCCTCCGCAGAACACCCCATGCGTGCTGAGAGGCGAGC
TCCTTGAAGAAGGGGCTGTTCTTCCAGGAGGCCTTATTTTGAACTGCCTCAGGACCCCACTGGAGAGCACAGCAT
GCCTTACTACTGGGTCATCCTTGGTCTATGTGCTCTGTACTGGAGGCTCTGTTCTGCCTCTTATCAGCCAGGTCA
GGGGCACACATGGCTTAAGTGACAAAGCCAGAGGAGAAGACAACCCTGACAGCATCACGCTGCATCCCATTGCTA
GCAGGATTGGCAACTCTTCAGACGGAGCTGCGCTTCCCTGCAGTCTAGCACCTCTAGGGCCTCTCCAGACTGTGC
CCTGGGAGCTCTGGGACTGAAAGGTTAAGAACATAAGGCAGGATCAGATGACTCTCTCCAAGAGGGCAGGGGAAT
TTTCTCTCCATGGGCCACAGGGGACAGGGCTGGGAGAAGAAATAGACTTGCACCTTATGTCATGTAAATAATTGA
TTTTCTAGTTCAAGAAGATAATATTGGTAGTGTGGGAATTGGAGGTAGGAAGGGGAGGAAGTCTGAGTAAGCCAG
TTGGCTTCTAAGCCAAAAGGATTCCTCTTTGTTTATCTCTGAGACAGTCCAACCTTGAGAATAGCTTTAAAAGGG
AAATTAATGCTGAGATGATAAAGTCCCCTTAAGCCAACAAACCCTCTGTAGCTATAGAATGAGTGCAGGTTTCTA
TTGGTGTGGACTCAGAGCAATTTACAAGAGCTGTTCATGCAGCCATCCATTTGTGCAAAATAGGGTAAGAAGATT
CAAGAGGATATTTATTACTTCCTCATACCACATGGCTTTTGATGATTCTGGATTCTAAACAACCCAGAATGGTCA
TTTCAGGCACAACGATACTACATTCGTGTGTGTCTGCTTTTAAACTTGGCTGGGCTATCAGACCCTATTCTCGGC
TCAGGTTTTGAGAAGCCATCAGCAAATGTGTACGTGCATGCTGTAGCTGCAGCCTGCATCCCTTCGCCTGCAGCC
TACTTTGGGGAAATAAAGTGCCTTACTGACTGTAGCCATTACAGTATCCAATGTCTTTTGACAGGTGCCTGTCCT
TGAAAAACAAAGTTTCTATTTTTATTTTTAATTGGTTTAGTTCTTAACTGCTGGCCAACTCTTACATCCCCAGCA
AATCATCGGGCCATTGGATTTTTTCCATTATGTTCATCACCCTTATATCATGTACCTCAGATCTCTCTCTCTCTC
CTCTCTCTCAGTTATATAGTTTCTTGTCTTGGACTTTTTTTTTCTTTTCTTTTTCTTTTTTTTTTTGCTTTAAAA
CAAGTGTGATGCCATATCAAGTCCATGTTATTCTCTCACAGTGTACTCTATAAGAGGTGTGGGTGTCTGTTTGGT
CAGGATGTTAGAAAGTGCTGATAAGTAGCATGATCAGTGTATGCGAAAAGGTTTTTAGGAAGTATGGCAAAAATG
TTGTATTGGCTATGATGGTGACATGATATAGTCAGCTGCCTTTTAAGAGGTCTTATCTGTTCAGTGTTAAGTGAT
TTAAAAAAATAATAACCTGTTTTCTGACTAGTTTAAAGATGGATTTGAAAATGGTTTTGAATGCAATTAGGTTAT
GCTATTTGGACAATAAACTCACCTTGACCT

FIGURE 182

MELLCHEVDPVRRAVRDRNLLRDDRVLQNLLTIEERYLPQCSYFKCVQKDIQPYMRRMVATWMLEVCEEQKCEEE
VFPLAMNYLDRFLAGVPTPKSHLQLLGAVCMFLASKLKETSPLTAEKLCIYTDNSIKPQELLEWELVVLGKLKWN
LAAVTPHDFIEHILRKLPQQREKLSLIRKHAQTFIALCATDFKFAMYPPSMIATGSVGAAICGLQQDEEVSSLTC
DALTELLAKITNTDVDCLKACQEQIEAVLLNSLQQYRQDQRDGSKSEDELDQASTPTDVRDIDL

FIGURE 183

ATGGCCGCGCTTGCACCGCTGCCCCCGCTCCCCGCACAGTTCAAGAGCATACAGCATCATCTGAGGACGGCTCAG
GAGCATGACAAGCGAGACCCTGTGGTGGCTTATTACTGTCGTTTATACGCAATGCAGACTGGAATGAAGATCGAT
AGTAAAACTCCTGAATGTCGCAAATTTTTATCAAAGTTAATGGATCAGTTAGAAGCTCTAAAGAAGCAGTTGGGT
GATAATGAAGCTATTACTCAAGAAATAGTGGGCTGTGCCCATTTGGAGAATTATGCTTTGAAAATGTTTTTGTAT
GCAGACAATGAAGATCGTGCTGGACGATTTCACAAAAACATGATCAAGTCCTTCTATACTGCAAGTCTTTTGATA
GATGTCATAACAGTATTGGAGAACTCACTGATGAAATGTGAACACAGGAAGTATGCCAGATGGAAGGCAACATAC
ATCCATAATGTTAAGAATGGGGAGACTCCTCAAGCAGGCCCTGTTGGAATTGAAGAAGATAATGATATTGAAGAA
AATGAAGATGCTGGAGCAGCCTCTCTGCCCACTCAGCCAACTCAGCCATCATCATCTTCAACTTATGACCCAAGC
AACATGCCATCAGGCAACTATACTGGAATACAGATTCCTCCGGGTGCACACGCTCCAGCTAATACACCAGCAGAA
GTGCCTCACAGCACAGGTGTAGCAAGTAATACTATCCAACCTACTCCACAGACTATACCTGCCATTGATCCCGCA
CTTTTCAATACAATTTCCCAGGGGGATGTTCGTCTAACCCCAGAAGACTTTGCTAGAGCTCAGAAGTACTGCAAA
TATGCTGGCAGTGCTTTGCAGTATGAAGATGTAAGCACTGCTGTCCAGAATCTACAAAAGGCTCTCAAGTTACTG
ACGACAGGCAGAGAA**TGA**

FIGURE 184

MAALAPLPPLPAQFKSIQHHLRTAQEHDKRDPVVAYYCRLYAMQTGMKIDSKTPECRKFLSKLMDQLEALKKQLG
DNEAITQEIVGCAHLENYALKMFLYADNEDRAGRFHKNMIKSFYTASLLIDVITVLENSLMKCEHRKYARWKATY
IHNVKNGETPQAGPVGIEEDNDIEENEDAGAASLPTQPTQPSSSSTYDPSNMPSGNYTGIQIPPGAHAPANTPAE
VPHSTGVASNTIQPTPQTIPAIDPALFNTISQGDVRLTPEDFARAQKYCKYAGSALQYEDVSTAVQNLQKALKLL
TTGRE

FIGURE 185

ACGTGTATCGCTGCCGTCAAG**ATG**GAGGGGCCTTTGTCCGTGTTCGGTGACCGCAGCACTGGGGAAACGATCCGC
TCCCAAAACGTTATGGCTGCAGCTTCGATTGCCAATATTGTAAAAAGTTCTCTTGGTCCAGTTGGCTTGGATAAA
ATGTTGGTGGATGATATTGGTGATGTAACCATTACTAACGATGGTGCAACCATCCTGAAGTTACTGGAGGTAGAA
CATCCTGCAGCTAAAGTTCTTTGTGAGCTGGCTGATCTGCAAGACAAAGAAGTTGGAGATGGAACTACTTCAGTG
GTTATTATTGCAGCAGAACTCCTAAAAAATGCAGATGAATTAGTCAAACAGAAAATTCATCCCACATCAGTTATT
AGTGGCTATCGACTTGCTTGCAAGGAAGCAGTGCGTTATATCAATGAAAACCTAATTGTTAACACAGATGAACTG
GGAAGAGATTGCCTGATTAATGCTGCTAAGACATCCATGTCTTCCAAAATCATTGGGATAAATGGTGATTTCTTT
GCTAACATGGTAGTAGATGCTGTACTTGCTATTAAATACACAGACATAAGAGGCCAGCCACGCTATCCAGTCAAC
TCTGTTAATATTTTGAAAGCCCATGGGAGAAGTCAAATGGAGAGTATGCTCATCAGTGGCTATGCACTCAACTGT
GTGGTGGGATCCCAGGGCATGCCCAAGAGAATCGTAAATGCAAAAATTGCTTGCCTTGACTTCAGCCTGCAAAAA
ACAAAAATGAAGCTTGGTGTACAGGTGGTCATTACAGACCCTGAAAAACTGGACCAAATTAGACAGAGAGAATCA
GATATCACCAAGGAGAGAATTCAGAAGATCCTGGCAACTGGTGCCAATGTTATTCTAACCACTGGTGGAATTGAT
GATATGTGTCTGAAGTATTTTGTGGAGGCTGGTGCTATGGCAGTTAGAAGAGTTTTAAAAAGGGACCTTAAACGC
ATTGCCAAAGCTTCTGGAGCAACTATTCTGTCAACCCTGGCCAATTTGGAAGGTGAAGAAACTTTTGAAGCTGCA
ATGTTGGGACAGGCAGAAGAAGTGGTACAGGAGAGAATTTGTGATGATGAGCTGATCTTAATCAAAAATACTAAG
GCTCGTACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTTCATGTGTGATGAGATGGAGCGCTCTTTACAT
GATGCACTTTGTGTAGTGAAGAGAGTTTTGGAGTCAAAATCTGTGGTTCCCGGTGGGGGTGCTGTAGAAGCAGCC
CTTTCCATATACCTTGAAAACTATGCAACCAGCATGGGGTCTCGGGAACAGCTTGCGATTGCAGAGTTTGCAAGA
TCACTTCTTGTTATTCCCAATACACTAGCAGTTAATGCTGCCCAGGACTCCACAGATCTGGTTGCAAAATTAAGA
GCTTTTCATAATGAGGCCCAGGTTAACCCAGAACGTAAAAATCTAAAATGGATTGGTCTTGATTTGAGCAATGGT
AAACCTCGAGACAACAAACAAGCAGGGGTGTTTGAACCAACCATAGTTAAAGTTAAGAGTTTGAAATTTGCAACA
GAAGCTGCAATCACCATTCTTCGAATTGATGATCTTATTAAATTACATCCAGAAATCCTTCGGATTAAACATGGA
AGTTATGAAGATGCTGTTCACTCTGGAGCCCTTAATGAT**TGA**TCTGATGTTCCTTTTATTTATAACAATGTTAAA
TGCAATGTCTTGTACCTTGAGTTGAGTATTACACATTAAAGTAAAGTACAAGCTGTAAACTTGGGTTTTTGTGAT
GTAGGAAATGGTTTCCATCTGTACTTTGGTCCTCTGATTTCAGATATTGCAACCTAGTACTTTATTAGTTTAAAA
AGAAATTGAGGTTGTTCAAAGTTTAAGCAATTCATTCTCTCTGAACACACATTGCTATTCCCATCCCACCCCCAA
TGCACAGGGCTGCAACACCACGACTTCTGCCCATTCTCTCCAGTGTGTGTAACAGGGTCACAAGAATTC

FIGURE 186

MEGPLSVFGDRSTGETIRSQNVMAAASIANIVKSSLGPVGLDKMLVDDIGDVTITNDGATILKLLEVEHPAAKVL
CELADLQDKEVGDGTTSVVIIAAELLKNADELVKQKIHPTSVISGYRLACKEAVRYINENLIVNTDELGRDCLIN
AAKTSMSSKIIGINGDFFANMVVDAVLAIKYTDIRGQPRYPVNSVNILKAHGRSQMESMLISGYALNCVVGSQGM
PKRIVNAKIACLDFSLQKTKMKLGVQVVITDPEKLDQIRQRESDITKERIQKILATGANVILTTGGIDDMCLKYF
VEAGAMAVRRVLKRDLKRIAKASGATILSTLANLEGEETFEAAMLGQAEEVVQERICDDELILIKNTKARTSASI
ILRGANDFMCDEMERSLHDALCVVKRVLESKSVVPGGGAVEAALSIYLENYATSMGSREQLAIAEFARSLLVIPN
TLAVNAAQDSTDLVAKLRAFHNEAQVNPERKNLKWIGLDLSNGKPRDNKQAGVFEPTIVKVKSLKFATEAAITIL
RIDDLIKLHPEILRIKHGSYEDAVHSGALND

FIGURE 187

GCTTCGGGTGCC**ATG**GGGACTCCTCCCGGCCTGCAGACCGACTGCGAGGCGCTGCTCAGCCGCTTCCAGGAGACG
GACAGTGTACGCTTCGAGGACTTCACGGAGCTCTGGAGAAACATGAAGTTCGGGACTATCTTCTGTGGCAGAATG
AGAAATTTAGAAAAGAACATGTTTACAAAAGAAGCTTTAGCTTTGGCTTGGCGATATTTTTTACCTCCATACACC
TTCCAGATCAGAGTTGGTGCTTTGTATCTGCTATATGGATTATATAATACCCAACTGTGTCAACCAAAACAAAAG
ATCAGAGTTGCCCTGAAGGATTGGGATGAAGTTTTAAAATTTCAGCAAGATTTAGTAAATGCACAGCATTTTGAT
GCAGCTTATATTTTTAGGAAGCTACGACTAGACAGAGCATTTCACTTTACAGCAATGCCCAAATTGCTGTCATAT
AGGATGAAGAAAAAAATTCACCGAGCTGAAGTTACAGAAGAATTTAAGGACCCAAGTGATCGTGTGATGAAACTT
ATCACTTCTGATGTATTAGAGGAAATGCTGAATGTTCATGATCATTATCAGAACATGAAACATGTAATTTCAGTT
GATAAGTCCAAGCCAGATAAAGCCCTCAGCTTGATAAAGGATGATTTTTTTGACAATATTAAGAACATAGTTTTG
GAGCATCAGCAGTGGCACAAAGACAGAAAGAATCCATCCTTAAAGTCAAAAACTAATGATGGAGAAGAAAAAATG
GAAGGAAATTCACAAGAAACGGAGAGATGTGAAAGGGCAGAATCATTAGCGAAAATAAAATCAAAGGCCTTTTCA
GTTGTCATACAGGCATCCAAATCAAGAAGGCATCGTCAAGTCAAACTCGACTCTTCTGACTCTGATTCTGCATCT
GGTCAAGGGCAAGTCAAAGCAACTAGGAAAAAAGAGAAGAAAGAAAGATTGAAACCAGCAGGAAGGAAGATGTCT
CTCAGAAACAAAGGCAATGTGCAGAATATACACAAGGAAGATAAACCTTTAAGTCTGAGTATGCCTGTAATTACA
GAAGAAGAAGAGAATGAAAGTTTGAGTGGAACAGAGTTCACTGCATCCAAGAAGAGGAGAAAACAC**TGA**ACAAAG
AGCCTGGTGTAGTTTTTAATTTTGAGTTTTCTGACAGAAGAAAAGATTGATATTTTGTGTATTGAACAGGAAGAC
TGCCAGTATTAAAAAAATCCTTCTGGGAATCTGTAGGTTATTTCTTGGAAATTGCAATACGTAGTTCTAGAATAA
AAGTACAAAAAATTAGAATAAGAATTC

FIGURE 188

MGTPPGLQTDCEALLSRFQETDSVRFEDFTELWRNMKFGTIFCGRMRNLEKNMFTKEALALAWRYFLPPYTFQIR
VGALYLLYGLYNTQLCQPKQKIRVALKDWDEVLKFQQDLVNAQHFDAAYIFRKLRLDRAFHFTAMPKLLSYRMKK
KIHRAEVTEEFKDPSDRVMKLITSDVLEEMLNVHDHYQNMKHVISVDKSKPDKALSLIKDDFFDNIKNIVLEHQQ
WHKDRKNPSLKSKTNDGEEKMEGNSQETERCERAESLAKIKSKAFSVVIQASKSRRHRQVKLDSSDSDSASGQGQ
VKATRKKEKKERLKPAGRKMSLRNKGNVQNIHKEDKPLSLSMPVITEEEENESLSGTEFTASKKRRKH

FIGURE 189

GCGCGCAGCTGGTTCCCGCTCTGCAGCGCAACGCCTGAGGCAGTGGGCGCGCTCAGTCCCGGGACCAGGCGTTCT
CTCCTCTCGCCTCTGGGCCTGGGACCCGCAAAGCGGCG**ATG**GAGCGGAGGTCGCGGAGGAAGTCGCGGCGCAACG
GGCGCTCGACCGCGGGCAAGGCCGCCGCGACCCAGCCCGCGAAGTCTCCGGGCGCACAGCTCTGGCTCTTTCCCA
GCGCCGCGGGCCTCCACCGCGCGCTGCTCCGGAGGGTGGAGGTGACGCGCCAACTCTGCTGCTCGCCGGGGCGCC
TCGCGGTCTTGGAACGCGGCGGGGCGGGCGTCCAGGTTCACCAGCTGCTCGCCGGGAGCGGCGGCGCCCGGACGC
CGAAATGCATTAAATTAGGAAAAAACATGAAGATACATTCCGTGGACCAAGGAGCAGAGCACATGCTGATTCTCT
CATCAGATGGAAAACCATTTGAGTATGACAACTATAGCATGAAACATCTAAGGTTTGAAAGCATTTTACAAGAAA
AAAAAATAATTCAGATCACATGTGGAGATTACCATTCTCTTGCACTCTCAAAAGGCGGTGAGCTTTTTGCCTGGG
GACAGAACCTGCATGGGCAGCTTGGAGTTGGAAGGAAATTTCCCTCAACCACCACACCACAGATTGTGGAGCACC
TCGCAGGAGTACCCTTGGCTCAGATTTCTGCCGGAGAAGCCCACAGCATGGCCTTATCCATGTCTGGCAACATTT
ATTCATGGGGAAAAAATGAATGTGGACAACTAGGCCTGGGCCACACTGAGAGTAAAGATGATCCATCCCTTATTG
AAGGACTAGACAATCAGAAAGTTGAATTTGTCGCTTGTGGTGGCTCTCACAGTGCCCTACTCACACAGGATGGGC
TGCTGTTTACTTTCGGTGCTGGAAAACATGGGCAACTTGGTCATAATTCAACACAGAATGAGCTAAGACCCTGTT
TGGTGGCTGAGCTTGTTGGGTATAGAGTGACTCAGATAGCATGTGGAAGGTGGCACACACTTGCCTATGTTTCTG
ATTTGGGAAAGGTCTTTTCCTTTGGTTCTGGAAAAGATGGACAACTGGGAAATGGTGGAACACGTGACCAGCTGA
TGCCGCTTCCAGTGAAAGTATCATCAAGTGAAGAACTCAAACTTGAAAGCCATACCTCAGAAAAGGAGTTAATAA
TGATTGCTGGAGGGAATCAAAGCATTTTGCTCTGGATAAAGAAAGAGAATTCATATGTTAATCTGAAGAGGACAA
TTCCTACTCTGAATGAAGGGACTGTAAAGAGATGGATTGCTGATGTGGAGACTAAACGGTGGCAGAGCACAAAAA
GGGAAATCCAAGAGATATTTTCATCTCCTGCTTGTCTAACTGGAAGTTTTTAAGGAAAAGAAGAACTACAGAAA
TGATGCCTGTTTATTTGGACTTAAATAAAGCAAGAAACATCTTCAGGGAGTTAACCCAAAAGGACTGGATTACTA
ACATGATAACCACCTGCCTCAAAGATAATCTGCTCAAAAGACTTCCATTTCATTCTCCACCCCAAGAAGCTTTAG
AAATTTTCTTCCTTCTCCCAGAATGTCCTGTGATGCATATTTCCAACAACTGGGAGAGCCTTGTGGTTCCATTTG
CAAAGGTTGTTTGTAAAATGAGTGACCAGTCTTCACTGGTTCTGGAAGAGTATTGGGCAACTCTGCAAGAATCCA
CTTTCAGCAAACTGGTCCAGATGTTTAAAACAGCCGTCATATGCCAGTTGGATTACTGGGATGAAAGTGCTGAGG
AGAATGGTAATGTTCAAGCTCTCCTAGAAATGTTGAAGAAGCTGCACAGGGTAAACCAGGTGAAATGTCAACTAC
CTGAAAGTATTTTCCAAGTAGACGAACTCTTGCACCGTCTCAATTTTTTTGTAGAAGTATGCAGAAGGTACTTGT
GGAAAATGACTGTGGACGCTTCAGAAAATGTACAATGCTGCGTCATATTCAGTCACTTTCCATTTATCTTTAATA
ATCTGTCGAAAATTAAACTACTACATACAGACACACTTTTAAAAATAGAGAGTAAAAAACATAAAGCTTATCTTA
GGTCGGCAGCAATTGAGGAAGAAAGAGAGTCTGAATTCGCTTTGAGGCCCACGTTTGATCTAACAGTCAGAAGGA
ATCACTTGATTGAGGATGTTTTGAATCAGCTAAGTCAATTTGAGAATGAAGACCTGAGGAAAGAGTTATGGGTTT
CATTTAGTGGAGAAATTGGGTATGACCTCGGAGGAGTCAAGAAAGAGTTCTTCTACTGTCTGTTTGCAGAGATGA
TCCAGCCGGAATATGGGATGTTCATGTATCCTGAAGGGGCTTCCTGCATGTGGTTTCCTGTCAAGCCTAAATTTG
AGAAGAAAAGATACTTCTTTTTTGGGGTTCTATGTGGACTTTCCCTGTTCAATTGCAATGTTGCCAACCTCCCTT
TCCCACTGGCACTGTTTAAGAAACTTTTGGACCAAATGCCATCATTGGAAGACTTGAAAGAACTCAGTCCTGATT
TGGGAAAGAATTTGCAAACACTTCTGGATGATGAAGGTGATAACTTTGAGGAAGTATTTTACATCCATTTTAATG
TGCACTGGGACAGAAACGACACAAACTTAATTCCTAATGGAAGTAGCATAACTGTCAACCAGACTAACAAGAGAG
ACTATGTTTCTAAGTATATCAATTACATTTTCAACGACTCTGTAAAGGCGGTTTATGAAGAATTTCGGAGAGGAT
TTTATAAAATGTGCGACGAAGACATTATCAAATTATTCCACCCCGAAGAACTGAAGGATGTGATTGTTGGAAATA
CAGATTATGATTGGAAAACATTTGAAAAGAATGCACGTTATGAACCAGGATATAACAGTTCACATCCCACCATAG
TGATGTTTTGGAAGGCTTTCCACAAATTGACTCTGGAAGAAAAGAAAAAATTCCTTGTATTTCTTACAGGAACTG
ACAGACTACAAATGAAAGATTTAAATAATATGAAAATAACATTTTGCTGTCCTGAAAGTTGGAATGAAAGAGACC
CTATAAGAGCACTGACATGTTTCAGTGTCCTCTTCCTCCCTAAATATTCTACAATGGAAACAGTTGAAGAAGCGC
TTCAAGAAGCCATCAACAACAACAGAGGATTTGGC**TGA**CCAGCTTGCTTGTCCAACAGCCTTATTTTGTTGTTGT
TATCGTTGTTGTTGTTGTTGTTGTTGTTGTTTCTCTACTTTGTTTTGTTTTAGGCTTTTAGCAGCCTGAAGCCAT
GGTTTTTCATTTCTGTCTCTAGTGATAAGCAGGAAAGAGGGATGAAGAAGAGGGTTTACTGGCCGGTTAGAACCC
GTGACTGTATTCTCTCCCTTGGATACCCCTATGCCTACATCATATTCCTTACCTCTTTTGGGAAATATTTTTCAA
AAATAAAATAACCGAAAAACTAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 190

MERRSRRKSRRNGRSTAGKAAATQPAKSPGAQLWLFPSAAGLHRALLRRVEVTRQLCCSPGRLAVLERGGAGVQV
HQLLAGSGGARTPKCIKLGKNMKIHSVDQGAEHMLILSSDGKPFEYDNYSMKHLRFESILQEKKIIQITCGDYHS
LALSKGGELFAWGQNLHGQLGVGRKFPSTTTPQIVEHLAGVPLAQISAGEAHSMALSMSGNIYSWGKNECGQLGL
GHTESKDDPSLIEGLDNQKVEFVACGGSHSALLTQDGLLFTFGAGKHGQLGHNSTQNELRPCLVAELVGYRVTQI
ACGRWHTLAYVSDLGKVFSFGSGKDGQLGNGGTRDQLMPLPVKVSSSEELKLESHTSEKELIMIAGGNQSILLWI
KKENSYVNLKRTIPTLNEGTVKRWIADVETKRWQSTKREIQEIFSSPACLTGSFLRKRRTTEMMPVYLDLNKARN
IFRELTQKDWITNMITTCLKDNLLKRLPFHSPPQEALEIFFLLPECPVMHISNNWESLVVPFAKVVCKMSDQSSL
VLEEYWATLQESTFSKLVQMFKTAVICQLDYWDESAEENGNVQALLEMLKKLHRVNQVKCQLPESIFQVDELLHR
LNFFVEVCRRYLWKMTVDASENVQCCVIFSHFPFIFNNLSKIKLLHTDTLLKIESKKHKAYLRSAAIEEERESEF
ALRPTFDLTVRRNHLIEDVLNQLSQFENEDLRKELWVSFSGEIGYDLGGVKKEFFYCLFAEMIQPEYGMFMYPEG
ASCMWFPVKPKFEKKRYFFFGVLCGLSLFNCNVANLPFPLALFKKLLDQMPSLEDLKELSPDLGKNLQTLLDDEG
DNFEEVFYIHFNVHWDRNDTNLIPNGSSITVNQTNKRDYVSKYINYIFNDSVKAVYEEFRRGFYKMCDEDIIKLF
HPEELKDVIVGNTDYDWKTFEKNARYEPGYNSSHPTIVMFWKAFHKLTLEEKKKFLVFLTGTDRLQMKDLNNMKI
TFCCPESWNERDPIRALTCFSVLFLPKYSTMETVEEALQEAINNNRGFG

FIGURE 191

CAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAG
GTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCAGCGAGGTCGGCAGCGGCACAGC
GAGGTCGGCAGCGGCAGCGAGGTCGGCAGCGGCGCGCGCTGTGCTCTTCCGCGGACTCTGAATC**ATG**GCGACCAC
GGCCACGATGGCGACCTCGGGCTCGGCGCGAAAGCGGCTGCTCAAAGAGGAAGACATGACTAAAGTGGAATTCGA
GACCAGCGAGGAGGTGGATGTGACCCCCACGTTCGACACCATGGGCCTGCGGGAGGACCTGCTGCGGGGCATCTA
CGCTTACGGTTTTGAAAAACCATCAGCAATCCAGCAACGAGCAATCAAGCAGATCATCAAAGGGAGAGATGTCAT
CGCACAGTCTCAGTCCGGCACAGGAAAAACAGCCACCTTCAGTATCTCAGTCCTCCAGTGTTTGGATATTCAGGT
TCGTGAAACTCAAGCTTTGATCTTGGCTCCCACAAGAGAGTTGGCTGTGCAGATCCAGAAGGGGCTGCTTGCTCT
CGGTGACTACATGAATGTCCAGTGCCATGCCTGCATTGGAGGCACCAATGTTGGCGAGGACATCAGGAAGCTGGA
TTACGGACAGCATGTTGTCGCGGGCACTCCAGGGCGTGTTTTTGATATGATTCGTCGCAGAAGCCTAAGGACACG
TGCTATCAAAATGTTGGTTTTGGATGAAGCTGATGAAATGTTGAATAAAGGTTTCAAAGAGCAGATTTACGATGT
ATACAGGTACCTGCCTCCAGCCACACAGGTGGTTCTCATCAGTGCCACGCTGCCACACGAGATTCTGGAGATGAC
CAACAAGTTCATGACCGACCCAATCCGCATCTTGGTGAAACGTGATGAATTGACTCTGGAAGGCATCAAGCAATT
TTTCGTGGCAGTGGAGAGGGAAGAGTGGAAATTTGACACTCTGTGTGACCTCTACGACACACTGACCATCACTCA
GGCGGTCATCTTCTGCAACACCAAAAGAAAGGTGGACTGGCTGACGGAGAAAATGAGGGAAGCCAACTTCACTGT
ATCCTCAATGCATGGAGACATGCCCCAGAAAGAGCGGGAGTCCATCATGAAGGAGTTCCGGTCGGGCGCCAGCCG
AGTGCTTATTTCTACAGATGTCTGGGCCAGGGGGTTGGATGTCCCTCAGGTGTCCCTCATCATTAACTATGATCT
CCCTAATAACAGAGAATTGTACATACACAGAATTGGGAGATCAGGTCGATACGGCCGGAAGGGTGTGGCCATTAA
CTTTGTAAAGAATGACGACATCCGCATCCTCAGAGATATCGAGCAGTACTATTCCACTCAGATTGATGAGATGCC
GATGAACGTTGCTGATCTTATC**TGA**AGCAGCAGATCAGTGGGATGAGGGAGACTGTTCACCTGCTGTGTACTCCT
GTTTGGAAGTATTTAGATCCAGATTCTACTTAATGGGGTTTATATGGACTTTCTTCTCATAAATGGCCTGCCGTC
TCCCTTCCTTTGAAGAGGATATGGGGATTCTGCTCTCTTTTCTTATTTACATGTAAATAATACATTGTTCTAAGT
CTTTTTCATTAAAAATTTAAAACTTTTCCCAT

FIGURE 192

MATTATMATSGSARKRLLKEEDMTKVEFETSEEVDVTPTFDTMGLREDLLRGIYAYGFEKPSAIQQRAIKQIIKG
RDVIAQSQSGTGKTATFSISVLQCLDIQVRETQALILAPTRELAVQIQKGLLALGDYMNVQCHACIGGTNVGEDI
RKLDYGQHVVAGTPGRVFDMIRRRSLRTRAIKMLVLDEADEMLNKGFKEQIYDVYRYLPPATQVVLISATLPHEI
LEMTNKFMTDPIRILVKRDELTLEGIKQFFVAVEREEWKFDTLCDLYDTLTITQAVIFCNTKRKVDWLTEKMREA
NFTVSSMHGDMPQKERESIMKEFRSGASRVLISTDVWARGLDVPQVSLIINYDLPNNRELYIHRIGRSGRYGRKG
VAINFVKNDDIRILRDIEQYYSTQIDEMPMNVADLI

FIGURE 193

CGCGGACGGCGGAAGGTGGACTCGCGAATGTTAGGCCTGTGGGTGCCATAGCGACCGGGAGGTTGGGCTGGCCAG
ATTCAGCTGCCGGGACCGGACCAGGTGCTTAGGAGAACATGCAGTAGAACTTTTCATCAAACAAATGGAACACGT
CACAGAATTTTGCTAACATGGACAACTCTGCACAGAAAAATGAACGCACTGGCAAACATCCCAGACGTGCCAGTG
AAGTACAGAAAGAATGATATCCCAGGACCTGGGTTCTACAATGTTATTCACCAGTCACCGGTGTCCAACAGTGTC
TCATTGTCCAAGAAAGGAACTTGCATGTTTCCCTCAATGTGCGCCCGATTGGACACCATCATTTCTAAATACCCT
GCAGCGAATGCATACACTATCCCATCGGATTTTATTTCCAAGAGAGACTTTAGTAATTCGTGTTCCAGCATGTTC
CAGTTGCCAAGCTTTATGAAAGCTCTCAAGTTTGAAACTCCTGCACCAAACTATTACAATGCCTCTGTCTCTTGC
TGCAAGCAGAGAAACAACGTCTGTACTCGAGCCGGGTTTATGTCAAAAACCCAAAGAGGATCTTTCGCTTTTGCT
GATAAAGGACCTCCCCCAGGGCATTATGATATCAACGAATCCCTTGTGAAGCAGTCGCCAAATACATTAATGTCT
TGTTTTAAATCAAAAACCAACCGTGGATTAAAACTGACGTCAACAGGCCCGGGACCTGGTTATTACAACCCCAGT
GATTGCACAAAAGTTCCAAAAAAGACTCTTTTCCCGAAAAACCCCATCCTGAACTTCTCTGCTCAGCCTTCGCCT
CTGCCTCCGAAGCCACCTTTCCCAGGTCCTGGTCAGTATGAGATCGTGGACTACTTAGGCCCCCGCAAGCATTTC
ATCTCTAGTGCATCATTCGTGTCCAATACCAGCCGGTGGACAGCGGCGCCGCCTCAGCCAGGCCTGCCTGGCCCA
GCTACGTACAAGCCAGAGCTTCCAGGAAAGCAGTCCTTCCTCTACAACGAGGACAAGAAATGGATCCCGGTTCTG
TAGGGATGTCACACAAGGTCAAGGAGAACTCCAGCCACCAGCCCACCCTGCCCAGCGTCCCCAGGACATTCCTCA
GGAGGAGACCGATCATGAGTGTGGCAGCTGACAACTTGGGGGGTGGCTCTACCACTCTGGCCTGGCATCCTAGCC
GGACTGCTGCCATTGCCTTTGTCTTGAGCTGGAGACATTGCTCCCTGGAGACTTCACCCCAGCCCCACAGACTCC
AGTGGCTTCCTGAGCAGAAGGGAGGAGTGGACAGAGCCCCCTGGCTGCTTCCCCACGCACCCATCCAGGCTGCCT
TCCGGCACGACTCCCTGCCGCAGACTGAAGGGACTCCTGAAGCGCAGACTTCAAGGAGGATCAGTCCACCCTGAA
GGTGGCCAAGCCTGGAAGCCCCACCCTTCCCTGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCCTCAC
TCCTGCCTTTCTCATTTGTCCCTTTCTGACCTCACTCACTTACGGTATGTCTACTGGGCGAAAGCTACCTGCAGG
CAGGTGATGCTTTTTCCACCAGTCCACAGCTTCCTTTCTAAAGTGACCACCTGTTTGGAAAGACCTCTCTTTACT
CCTTTTAGACCTTTTTCTCTTTGGAGTGGGAGATCATCTTGGAATGGCAGTGGCCGGGCCCGGGGGCTGCGCTTT
TCCCTGACTTTCTCTGCTGGCGGGACTGAATTTTCTCAAGGCTTACAGGCCCTTCCATGGAGTCCACATGGCCTG
TCTAGGCCTGATAGCTTTCGTCTCTCTATGTGGAGGGAAAAAGAAATGTGCCCTAGTGGTTTTGGTGGAGGCTGC
ACAGATTCGCGGTGGGTGGGGAGCTGCCAGGCTCCTTTTCTGATCTCCCAGCAGGCTTTGACTGACGCTGTTTAG
TCTTTCTGTACATTAACCCCGCCAGATACCGAGAGGTTACAAAGCCTCCAAGGCCTGTACAACTGTGGCCTCTCC
AGAGAAGTGGTTCTCAGCCTTGACTGCACACTGTAATCACCTGGGGACTTTAAAAAGTACTGAGGCCTGGGGCCC
ACCCACAAATGCTGATTTAACTCCTCCAGGGTGGGGTCTGGGCAGTGGGGAGGCAGGAGCCACCCAGGTGATTCC
AATGATAGGTGTAGGTTGAGAAGCGCCACCTTCCAGCTTCCTAACTGGCTCTGGGAGGGGAGCTGGGTGGGAAGT
TCAGGAGGTGGGAACTTTGTACACGCAGAGCACCTGGAGCACCTACAGCATGGCTGTGGTTCCACACTCCTCTGT
CATTTAACCTTCACACATCACCTCGTTCTGACATCAAGGGTGCGTCACAGCCACAGTGAGGCCTCGCCTGGGCAG
AGCAACTCTGGGTGCCCCACTGGGTCCCTCCCACAGGGGCAGGCAAGCCTAATGGGAACCCGAGGCAAAAGGAAA
CATCAGTAATACGAATCCTGTCTTTAAAACTGTGATGTTTTGTTCACCATGGATTTTTTTTTGGGGGGGGGGCC
TTAATTTTAAAAATATTGCATTAAACTTATTTATCTTGCTTATTGAGCTTTTGGGTACCCCTTAATTTTTGTGCC
TTAGGCTAGAGACTCACCTGCCCATAGCCTTGACTCTAGGTAGGGGCTTGGGAATTAGGACCACAGACTGTCAGC
GCTGGGAGGTTCTTAGAGGGATCATGGTTTTCACACCTTTTTAAAAAAAGTTTTACTCAGACAGATGT

FIGURE 194

RTAEGGLANVRPVGAIARPGGWAGQIQLPGPDQVLRRTCSRTFHQTNGTRHRILLTWTTLHRKMNALANIPDVPV
KYRKNDIPGPGFYNVIHQSPVSNSVSLSKKGTCMFPSMCARLDTIISKYPAANAYTIPSDFISKRDFSNSCSSMF
QLPSFMKALKFETPAPNYYNASVSCCKQRNNVCTRAGFMSKTQRGSFAFADKGPPPGHYDINESLVKQSPNTLMS
CFKSKTNRGLKLTSTGPGPGYYNPSDCTKVPKKTLFPKNPILNFSAQPSPLPPKPPFPGPGQYEIVDYLGPRKHF
ISSASFVSNTSRWTAAPPQPGLPGPATYKPELPGKQSFLYNEDKKWIPVL

FIGURE 195

CGGCTGAGAGGCAGCGAACTCATCTTTGCCAGTACAGGAGCTTGTGCCGTGGCCCACAGCCCACAGCCCACAGCC
ATGGGCTGGGACCTGACGGTGAAGATGCTGGCGGGCAACGAATTCCAGGTGTCCCTGAGCAGCTCCATGTCGGTG
TCAGAGCTGAAGGCGCAGATCACCCAGAAGATTGGCGTGCACGCCTTCCAGCAGCGTCTGGCTGTCCACCCGAGC
GGTGTGGCGCTGCAGGACAGGGTCCCCCTTGCCAGCCAGGGCCTGGGCCCTGGCAGCACGGTCCTGCTGGTGGTG
GACAAATGCGACGAACCTCTGAGCATCCTGGTGAGGAATAACAAGGGCCGCAGCAGCACCTACGAGGTCCGGCTG
ACGCAGACCGTGGCCCACCTGAAGCAGCAAGTGAGCGGGCTGGAGGGTGTGCAGGACGACCTGTTCTGGCTGACC
TTCGAGGGGAAGCCCCTGGAGGACCAGCTCCCGCTGGGGGAGTACGGCCTCAAGCCCCTGAGCACCGTGTTCATG
AATCTGCGCCTGCGGGGAGGCGGCACAGAGCCTGGCGGGCGGAGC**TAA**GGGCCTCCACCAGCATCCGAGCAGGAT
CAAGGGCCGGAAATAAAGGCTGTTGTAAGAGAAT

FIGURE 196

MGWDLTVKMLAGNEFQVSLSSSMSVSELKAQITQKIGVHAFQQRLAVHPSGVALQDRVPLASQGLGPGSTVLLVV
DKCDEPLSILVRNNKGRSSTYEVRLTQTVAHLKQQVSGLEGVQDDLFWLTFEGKPLEDQLPLGEYGLKPLSTVFM
NLRLRGGGTEPGGRS

FIGURE 197

CCAGTTAGAGCTCGGGTCTCCTCGCCACAGCTCCGAGTCTTTCGTTCTGGGAGGCCCAGGCGGCTTCGCGTTCTG
AGAATAAACAGAACCTCTGTTGCTCTGCGACTTGCAGGCACTGGGAGATTCGTAGCTAAGACGCCAGGGCATCCC
GGAAGCTGGGAA**ATG**GGACTGTTGACATTCAGGGATGTGGCCGTAGAATTCTCTTTGGAGGAGTGGGAACACCTG
GAACCAGCTCAGAAGAATTTGTATCAGGATGTGATGTTAGAAAACTACAGAAACCTGGTCTCTCTGGGTCTTGTT
GTCTCTAAGCCGGACCTGATCACCTTTTTGGAACAAAGGAAAGAGCCTTGGAATGTGAAGAGTGAGGAGACAGTA
GCCATCCAGCCAGATGTGTTTTCGCATTATAACAAGGACCTGTTGACAGAGCACTGCACAGAAGCTTCATTCCAA
AAAGTGATATCGAGGAGACATGGGAGCTGTGATCTTGAGAATTTACATTTAAGAAAAAGGTGGAAAAGGGAGGAG
TGTGAAGGGCACAATGGATGTTATGATGAAAAGACTTTTAAATATGATCAATTTGATGAATCCTCTGTTGAAAGT
TTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTTTGATCAATATAGGAAGGTCTTTACTCAT
TCATCATTGCTTAATCAACAAGAGGAAATAGATATTTGGGGAAAACATCACATATATGATAAAACTTCAGTGTTA
TTTAGGCAGGTCTCTACTCTAAATAGTTACCGAAATGTTTTTATTGGAGAGAAAAATTATCATTGCAATAATTCT
GAAAAAACCTTGAACCAAAGCTCAAGCCCTAAAAATCATCAGGAAAATTATTTTCTAGAAAAACAATACAAATGT
AAAGAATTTGAGGAAGTCTTTCTTCAGAGTATGCATGGGCAAGAGAAACAAGAACAGTCTTACAAATGTAATAAA
TGTGTAGAAGTTTGTACCCAGTCATTAAAACATATTCAACATCAGACCATCCATATCAGAGAAAACTCATATAGC
TATAACAAATATGATAAAGATCTTAGTCAGTCATCAAATCTTAGAAAGCAGATAATCCATAATGAAGAGAAACCA
TACAAATGTGAAAAATGTGGGGATAGCTTAAACCATAGTTTGCACCTTACTCAACATCAGATCATTCCTACCGAA
GAGAAACCCTATAAATGGAAAGAATGTGGCAAGGTCTTTAACCTTAACTGTAGTTTATACCTTACTAAACAGCAG
CAAATTGATACTGGAGAAAACCTTTACAAATGTAAAGCATGTAGCAAATCTTTTACTCGTTCCTCCAATCTTATT
GTGCATCAGAGAATTCACACTGGAGAGAAACCATACAAATGTAAAGAATGTGGCAAAGCCTTTCGCTGTAGTTCA
TACCTTACTAAACATAAGCGAATTCATACTGGAGAGAAACCTTATAAATGTAAAGAATGTGGAAAAGCTTTTAAC
CGTAGTTCATGCCTTACTCAACATCAGACAACTCATACAGGAGAAAAACTTTACAAATGTAAAGTATGTAGCAAA
TCTTATGCTCGTTCTTCAAATCTTATTATGCATCAGAGAGTTCATACTGGAGAGAAGCCTTATAAATGTAAAGAA
TGTGGCAAAGTCTTTAGCCGTAGTTCTTGCCTTACTCAACATCGGAAAATTCATACTGGAGAAAATCTTTACAAA
TGCAAAGTATGTGCTAAACCTTTTACTTGTTTCTCAAATCTTATTGTGCATGAGAGAATTCATACTGGAGAGAAA
CCCTATAAATGTAAAGAATGTGGCAAAGCCTTTCCTTATAGTTCACACCTTATTCGACATTATCGAATTCATACT
GGAGAAAAACCATACAAATGTAAAGCATGTAGCAAATCTTTTAGTGACTCCTCAGGTCTTTCTGTGCATCGGCGA
ACTCATACTGGAGAGAAACCCTATACATGTAAAGAATGTGGCAAAGCCTTTAGTTATAGTTCAGATGTTATTCAG
CATCGGAGAATTCATACTGGCCAGAGACCCTACAAATGTGAAGAATGTGGCAAAGCCTTCAACTATAGGTCATAC
CTCACTACACATCAGAGAAGTCATACTGGAGAGAGACCCTACAAATGTGAAGAATGTGGCAAAGCCTTCAACTCT
AGGTCATACCTCACTACACATCGGAGAAGACATACTGGAGAGAGACCCTACAAATGTGATGAATGTGGTAAAGCC
TTCAGCTATAGGTCATACCTCACTACACATCGGAGAAGTCATAGTGGAGAGAGACCCTACAAATGTGAAGAATGT
GGCAAAGCCTTTAACTCTAGGTCATACCTCATTGCACATCAGAGAAGTCATACTAGAGAAAAACTT**TAA**AAATGT
AAAACATGGAGCAGATTTTTTACTTGTTACCCATGTCTTATTGTGCATCAGATAATTTATATGGGAGTGAAACCC
TACAAATGTTAAGAATGTGGCATAACCTTTAACTATTTTCAAGCCTTACACAATAGCAGAGAATATAAACTGAAA
AAATCCATACAAATATTAAAAATGTGGCAAATTATTTTAAACTGTGCTCAACCCTTACTCAAGATAATCCATACT
AGAGAAACACTATAGATGTAAAAATGTGAAAAGTTTTATTCAAAATATCAAACTTATGAGTC

FIGURE 198

MGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLENYRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQP
DVFSHYNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEGHNGCYDEKTFKYDQFDESSVESLFHQ
QILSSCAKSYNFDQYRKVFTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIGEKNYHCNNSEKTL
NQSSSPKNHQENYFLEKQYKCKEFEEVFLQSMHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIPTEEKPYKWKECGKVFNLNCSLYLTKQQQIDT
GENLYKCKACSKSFTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTGEKPYKCKECGKAFNRSSC
LTQHQTTHTGEKLYKCKVCSKSYARSSNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLYKCKVC
AKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLIRHYRIHTGEKPYKCKACSKSFSDSSGLSVHRRTHTG
EKPYTCKECGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQRSHTGERPYKCEECGKAFNSRSYL
TTHRRRHTGERPYKCDECGKAFSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTREKL

FIGURE 199

GCAGTGTCACTCTTTTCAGAAATATGTCCATGGTGGTTTACTCAATTTGCTTCTTTTTTATTCATAGATTTGCAT
ATGTAATGCATTGCGCTATACCATTAAGACAGCTA**TGA**TGTCACTGCAGTTACAGTGTCACTAGGTGATAGAAAT
TGTCCAGCTCCATTACAACCTTATGGAACCACTGGTGCATACGTGGTTCATTGTGGTCCATTGTTGACTGAAACA
ATGTTATGAGGTGCGTAACTATATATCCAAAGCAAAAGCTAAATGAAATAAATGAAACTAATTGTGTTGGTGTCC
TAAACACACAGAGGAGAATTACTTCAAGTATTTTTAAAACACAGTCACTTGTCTATGCATTTTTAGTGGATATGC
CCTAAAGTATGAAACTAAATTNNNNNNNNNNNNNNNNNNNNNNNNNAAATTAATTTACAAATAGTATTAATATTG
AATAATAATATATGTTAATATTGTTACTCTGAATCTATTATATACATTTTGGAGGATAAATAACATGCAATTTTG
TTAATATTAGGAATCAAGAAACTATATATATAAAATCAAAGCTGCTAAATAAAATTATAAATTGTGTTTATAATT
ACAAATTTGAATTGGAAATATCATTATAAAATCATAATGTATTTCCTTTACAGAAGCACATTTTCTAGCCCTGTT
ATTTGAAAATCAGTAATGAGCACCCTTAGAATGCAGATTATAGTCTCTAAATGCAATTTTCTGCTAAAA

FIGURE 200

SVTLFRNMSMVVYSICFFFIHRFAYVMHCAIPLRQL

FIGURE 201

GGGCAGAAAGGGCACGCTCTTGTGGGTGACTACAGGTTAGGAGACCGTTGAACCTGGAGGGGCCCTAGGATGGAC
CCCGTGGAAAGATTCAGAGACTGCGCCCTCTCCCTGGCGCCGCCTTCCCCTACACGCGGCGGGTATATTCTGTTG
CAGTTGGCCCAGGACCTGTTTCCAAGACTCTGCCCCCTCGCACTTCCGTCCCTCCTGGTTTTGTAAAGTG**ATG**CT
CATAGGAACCCCCACCCCGCGTGACACTACTCCCAGCTCCTGGCTGACTTCTAGTCTTCTGGTTGAAGCTGCGCC
TTTAGATGACACGACCCTACCCACCCCTGTTTCCAGCGGATGCCCGGGCCTGGAGCCCACAGAATTCTTCCAGTC
CCTGGGTGGGGACGGAGAAAGGAACGTTCAGATTGAGATGGCCCATGGCACCACCACGCTCGCCTTCAAGTTCCA
GCATGGAGTGATTGCAGCAGTGGATTCTCGGGCCTCAGCTGGGTCCTACATTAGTGCCTTACGGGTGAACAAGGT
GATTGAGATTAACCCTTACCTGCTTGGCACCATGTCTGGCTGTGCAGCAGACTGTCAGTACTGGGAGCGCCTGCT
GGCCAAGGAATGCAGGCTGTACTATCTGCGAAATGGAGAACGTATTTCAGTGTCGGCAGCCTCCAAGCTGCTGTC
CAACATGATGTGCCAGTACCGGGGCATGGGCCTCTCTATGGGCAGTATGATCTGTGGCTGGGATAAGAAGGGTCC
TGGACTCTACTACGTGGATGAACATGGGACTCGGCTCTCAGGAAATATGTTCTCCACGGGTAGTGGGAACACTTA
TGCCTACGGTGTCATGGACAGTGGCTATCGGCCTAATCTTAGCCCTGAAGAGGCCTATGACCTTGGCCGCAGGGC
TATTGCTTATGCCACTCACAGAGACAGCTATTCTGGAGGCGTTGTCAATATGTACCACATGAAGGAAGATGGTTG
GGTGAAAGTAGAAAGTACAGATGTCAGTGACCTGCTGCACCAGTACCGGGAAGCCAATCAA**TAA**TGGTGGTGGTG
GCAGCTGGGCAGGTCTCCTCTGGGAGGTCTTGGCCGACTCAGGGACCTAAGCCACGTTAAGTCCAAGGAGAAGAA
GAGGCCTAGCCTGAGCCAAAGAGAGAGTACGGGCTCAGCAGCCAGAGGAGGCCGGTGAAGTGCATCTTCTGCGTG
TTCTC

FIGURE 202

MLIGTPTPRDTTPSSWLTSSLLVEAAPLDDTTLPTPVSSGCPGLEPTEFFQSLGGDGERNVQIEMAHGTTTLAFK
FQHGVIAAVDSRASAGSYISALRVNKVIEINPYLLGTMSGCAADCQYWERLLAKECRLYYLRNGERISVSAASKL
LSNMMCQYRGMGLSMGSMICGWDKKGPGLYYVDEHGTRLSGNMFSTGSGNTYAYGVMDSGYRPNLSPEEAYDLGR
RAIAYATHRDSYSGGVVNMYHMKEDGWVKVESTDVSDLLHQYREANQ

FIGURE 203

CCCGAATTTTCCGGCTCGAATGCCCGGCAGCCGTGGCGGCTAGAGCGTTCCTCCCCAGCTCGAATGCCCGGCGGC
GAGGCGGCTAGAGCGTCGCCTCCTCCCGGGGAACCGCGTGTGACCTTCCAGCCCGCGGACCG**ATG**CTGCCGGCGG
CCGCTCGCCCCCTGTGGGGGCCTTGCCTTGGGCTTCGGGCCGCTGCGTTCCGCCTTGCCAGGCGACAGGTGCCAT
GTGTCTGTACCGTGCGACATATGAGGAGCAGCGGCCATCAGAGGTGTGAGGCCCTCGCTGGTGCACCCCTGGATA
ACGCCCCCAAGGAGTACCCCCCCAAGATACAGCAGCTGGTCCAGGACATCGCCAGCCTCACTCTCTTGGAAATCT
CAGACCTCAACGAGCTCCTGAAGAAAACGTTGAAGATCCAGGATGTCGGGCTTGTGCCGATGGGTGGTGTGATGT
CTGGGGCTGTCCCTGCTGCAGCAGCCCAGGAGGCGGTGGAAGAAGATATCCCCATAGCGAAAGAACGGACACATT
TCACCGTCCGCCTGACCGAGGCGAAGCCCGTGGACAAAGTGAAGCTGATCAAGGAAATCAAGAACTACATCCAAG
GCATCAACCTCGTCCAGGCAAAGAAGCTGGTGGAGTCCCTGCCCCAGGAAATCAAAGCCAATGTCGCCAAAGCTG
AGGCGGAGAAGATCAAGGCGGCCCTGGAGGCGGTGGGCGGCACCGTGGTTCTGGAG**TAG**CCTCCAGCTCGGAGGA
CTTGTGTTCAGGGGTCCTGGGCCCCGGCGAGGTCCCGCCCTCCCGTGGTCACTGGCTCCGCCCCCAGCACCAGGC
GCCCAGTGGAGCCGTTTGGGAGAATTGCCTGCGCCACGCAGCGGGCCGGACAGGCCGCACAGACCTACTGTGGCG
GGAGGGAGGGGCGGCTGCTGCCTGGTGACGGCACCCGGAAGCCCACCAGGACGCGCCACCGGTCAATGTGCCTCT
GGTGGCTGCTGAGAAAAATACACTGTGCAGCTC

FIGURE 204

MLPAAARPLWGPCLGLRAAAFRLARRQVPCVCTVRHMRSSGHQRCEALAGAPLDNAPKEYPPKIQQLVQDIASLT
LLEISDLNELLKKTLKIQDVGLVPMGGVMSGAVPAAAAQEAVEEDIPIAKERTHFTVRLTEAKPVDKVKLIKEIK
NYIQGINLVQAKKLVESLPQEIKANVAKAEAEKIKAALEAVGGTVVLE

FIGURE 205

GGCACCGATTCGGGGCCTGCCCGGACTTCGCCGCACGCTGCAGAACCTCGCCCAGCGCCCACC**ATG**CCCCGGCAG
CTCAGCGCGGCGGCCGCGCTCTTCGCGTCCCTGGCCGTAATTTTGCACGATGGCAGTCAAATGAGAGCAAAAGCA
TTTCCAGAAACCAGAGATTATTCTCAACCTACTGCAGCAGCAACAGTACAGGACATAAAAAAACCTGTCCAGCAA
CCAGCTAAGCAAGCACCTCACCAAACTTTAGCAGCAAGATTCATGGATGGTCATATCACCTTTCAAACAGCGGCC
ACAGTAAAAATTCCAACAACTACCCCAGCAACTACAAAAAACACTGCAACCACCAGCCCAATTACCTACACCCTG
GTCACAACCCAGGCCACACCCAACAACTCACACACAGCTCCTCCAGTTACTGAAGTTACAGTCGGCCCTAGCTTA
GCCCCTTATTCACTGCCACCCACCATCACCCCACCAGCTCATACAGCTGGAACCAGTTCATCAACCGTCAGCCAC
ACAACTGGGAACACCACTCAACCCAGTAACCAGACCACCCTTCCAGCAACTTTATCGATAGCACTGCACAAAAGC
ACAACCGGTCAGAAGCCTGATCAACCCACCCATGCCCCAGGAACAACGGCAGCTGCCCACAATACCACCCGCACA
GCTGCACCTGCCTCCACGGTTCCTGGGCCCACCCTTGCACCTCAGCCATCGTCAGTCAAGACTGGAATTTATCAG
GTTCTAAACGGAAGCAGACTCTGTATAAAAGCAGAGATGGGGATACAGCTGATTGTTCAAGACAAGGAGTCGGTT
TTTTCACCTCGGAGATACTTCAACATCGACCCCAACGCAACGCAAGCCTCTGGGAACTGTGGCACCCGAAAATCC
AACCTTCTGTTGAATTTTCAGGGCGGATTTGTGAATCTCACATTTACCAAGGATGAAGAATCATATTATATCAGT
GAAGTGGGAGCCTATTTGACCGTCTCAGATCCAGAGACAGTTTACCAAGGAATCAAACATGCGGTGGTGATGTTC
CAGACAGCAGTCGGGCATTCCTTCAAGTGCGTGAGTGAACAGAGCCTCCAGTTGTCAGCCCACCTGCAGGTGAAA
ACAACCGATGTCCAACTTCAAGCCTTTGATTTTGAAGATGACCACTTTGGAAATGTGGATGAGTGCTCGTCTGAC
TACACAATTGTGCTTCCTGTGATTGGGGCCATCGTGGTTGGTCTCTGCCTTATGGGTATGGGTGTCTATAAAATC
CGCCTAAGGTGTCAATCATCTGGATACCAGAGAATC**TAA**TTGTTGCCCGGGGGGAATGAAAATAATGGAATTTAG
AGAACTCTTTCATCCCTTCCAGGATGGATGTTGGGAAATTCCCTCAGAGTGTGGGTCCTTCAAACAATGTAAACC
ACCATCTTCTATTCAAATGAAGTGAGTCATGTGTGATTTAAGTTCAGGCAGCACATCAATTTCTAAATACTTTTT
GTTTATTTTATGAAAGATATAGTGAGCTGTTTATTTTCTAGTTTCCTTTAGAATATTTTAGCCACTCAAAGTCAA
CATTTGAGATATGTTGAATTAACATAATATATGTAAAGTAGAATAAGCCTTCAAATTATAAACCAAGGGTCAATT
GTAACTAATACTACTGTGTGTGCATTGAAGATTTTATTTTACCCTTGATCTTAACAAAGCCTTTGCTTTGTTATC
AAATGGACTTTCAGTGCTTTTACTATCTGTGTTTTATGGTTTCATGTAACATACATATTCCTGGTGTAGCACTTA
ACTCCTTTTCCACTTTAAATTTGTTTTTGTTTTTTGAGACGGAGTTTCACTCTTGTCACCCAGGCTGGAGTACAG
TGGCACGATCTCGGCTTATGGCAACCTCCGCCTCCCGGGTTCAAGTGATTCTCCTGCTTCAGCTTCCCGAGTAGC
TGGGATTACAGGCACACACTACCACGCCTGGCTAATTTTTGTATTTTTATTATAGACGGGTTTCACCATGTTGGC
CAGACTGGTCTTGAACTCTTGACCTCAGGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATG
AGCCATTGCGCCCGGCCTTAAATGTTTTTTTTAATCATCAAAAAGAACAACATATCTCAGGTTGTCTAAGTGTTT
TTATGTAAAACCAACAAAAAGAACAAATCAGCTTATATTTTTTATCTTGATGACTCCTGCTCCAGAATTGCTAGA
CTAAGAATTAGGTGGCTACAGATGGTAGAACTAAACAATAAGCAAGAGACAATAATAATGGCCCTTAATTATTAA
CAAAGTGCCAGAGTCTAGGCTAAGCACTTTATCTATATCTCATTTCATTCTCACAACTTATAAGTGAATGAGTAA
ACTGAGACTTAAGGGAACTGAATCACTTAAATGTCACCTGGCTAACTGATGGCAGAGCCAGAGCTTGAATTCATG
TTGGTCTGACATCAAGGTCTTTGGTCTTCTCCCTACACCAAGTTACCTACAAGAACAATGACACCACACTCTGCC
TGAAGGCTCACACCTCATACCAGCATACGCTCACCTTACAGGGAAATGGGTTTATCCAGGATCATGAGACATTAG
GGTAGATGAAAGGAGAGCTTTGCAGATAACAAAATAGCCTATCCTTAATAAATCCTCCACTCTCTGGAAGGAGAC
TGAGGGGCTTTGTAAAACATTAGTCAGTTGCTCATTTTTATGGGATTGCTTAGCTGGGCTGTAAAGATGAAGGCA
TCAAATAAACTCAAAGTATTTTTAAATTTTTTTGATAATAGAGAAACTTCGCTAACCAACTGTTCTTTCTTGAGT
GTATAGCCCCATCTTGTGGTAACTTGCTGCTTCTGCACTTCATATCCATATTTCCTATTGTTCACTTTATTCTGT
AGAGCAGCCTGCCAAGAATTTTATTTCTGCTGTTTTTTTTGCTGCTAAAGAAAGGAACTAAGTCAGGATGTTAAC
AGAAAAGTCCACATAACCCTAGAATTCTTAGTCAAGGAATAATTCAAGTCAGCCTAGAGACCATGTTGACTTTCC
TCATGTGTTTCCTTATGACTCAGTAAGTTGGCAAGGTCCTGACTTTAGTCTTAATAAAACATTGAATTGTAGTAA
AGGTTTTTGCAATAAAAACTTACTTTGG

FIGURE 206

MPRQLSAAAALFASLAVILHDGSQMRAKAFPETRDYSQPTAAATVQDIKKPVQQPAKQAPHQTLAARFMDGHITF
QTAATVKIPTTTPATTKNTATTSPITYTLVTTQATPNNSHTAPPVTEVTVGPSLAPYSLPPTITPPAHTAGTSSS
TVSHTTGNTTQPSNQTTLPATLSIALHKSTTGQKPDQPTHAPGTTAAAHNTTRTAAPASTVPGPTLAPQPSSVKT
GIYQVLNGSRLCIKAEMGIQLIVQDKESVFSPRRYFNIDPNATQASGNCGTRKSNLLLNFQGGFVNLTFTKDEES
YYISEVGAYLTVSDPETVYQGIKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTTDVQLQAFDFEDDHFGNVDE
CSSDYTIVLPVIGAIVVGLCLMGMGVYKIRLRCQSSGYQRI

FIGURE 207

ATGGCATTGGTTTTTCCATTTTTGCAAATCTCTTTAGTCTGGCTGACGGAAGACGGCTGGACCCACATGCCTCGT
GCCTTCTGGAGATCCTCCCAGGCTCCTGCGGACTGAGTGACGAGGCAGATAGTGTCTATATTACTGTTGAACCAC
ACAGACCTGAAAGGGCCTCGGGGACCCCCAGCCATGCTGACCACACCCCAAGAGCTGGGGCCCAGATGGAAAGAC
AGGGAAGGCTGGCTTTGATGGGTGGAGCTCAAACCAGA**TAG**AGGACAAGGGGGCCTGGCCACCCGCACAGACACT
CCCAGACACAGAGAACAGGCAGGGGGCTTCCAGACCCCTTCCCAAGCAGTTCTCTGGGTTTGTTGGACACAGGAA
GAGGAAGCTGCTCACCTTTGTCCCTAAGCCCAGGGCCTGTGCCCTGTGTGGCTGGTCTGGAACAGCCTTGCTGCC
CTTGCCTGGGGTTGGAACCAGGGCCTCTGGGGTCCTGCGGACCTTTGTTCTCGCACCAGCCTTGGGCCTGCGCTG
GGCAGTGGCCCCCCGCTCGGTTGCCGCGCCTCCCTCCTAACATTGCCAGAGTGAAACACTCCTAGTCTCTCGGCT
TTGCTTGTATTTCTTTACTGCCATGTCTTTCTTGTTGTTCCGTATTTGAAGACCCATGTGATAAATTTCTTCAAA
GCTAGGAAGGAGTTTTGTCTCTCTGCGTGAGATATTGGCTGCTTGCTGGAACCTGGGGCCCAGGTTTGGCCTCAG
CCTCATTTCCAGATGCCTTGGTGCCCACATCTCTCTTCTCCTACTTGGCTCTCCCCTTTTTATTTCTTTATAAAA
ATGAAGGTGGTGAACTAAGCAGCCTCAGGCTTTAGAAGTGAGTCCCTGGCATCGGTGAGGCCACCCACACAGCCA
TTCCCTGTACATCAGGAGGGTGGTCTCACTCTGTACCTATCACCCAGGTTCTCGGGACCGGAAGTCAGGTGGGAG
ACTGGGCTCCCCGAAGCCAGAGCGGCAGAGAGGCCAGAACTCCAAAGCCCCTGCAGCCCCGGCTGACAGGAAGCG
CCAGCTGTCACCCCAGTCCAAGAGCTCCAGCAAGGTCACGAGCGTGCCCGGCAAAGCCTCGGATCCCGGCGCCGC
CAGCACCAAATCAGGGAAGGCCAGCACGCTGTCTCGGCGGGAGGAGCTGCTGAAACAGCTGAAGGCCGTGGAGGA
TGCTATTGCACGCAAGCGGGCCAAGATCCCCGGGAAAGCATAGGCCGTGCCCCGACCGGACTGGACGCATTTTTA
TACATAGGGTAAGCGCAGCCATTTTGGATTTTGCAGTTAATGTCTTATTTTGGCTGTGATTCTTTTTAAAAAGTA
AAAAAGAAAAAAAAGTTTCTCAGCTGGAAAAGAAGCCACACAGGAAATGACAACGACGCTGAATCCCAGCCTCCC
TCCCCAGAGCAGAAGTCCCGCAGGACAGACAGACACAGACAGCGCTAGTGACCAGCACGGTTCTCATGTAAATTA
CAAGCCCCAGCCGCCAGCCCCGCCTTCTCTTCCTCCTCCTCCGTCTTCTTCCCTGGCCCTGGTCAGGCCTGTGGA
GCCCCAGCTCTGGGTCCCTAGCCCGGGTCCAGGCAGCCAGGCTCCCTCCTGAGCTGAGAAACGGAACCTCGCGAA
CCACTGGTGGCACATCCTTCTCCTCCCCCGCCCCTGATCACCCGCCCCCGGATCAGAAATATATCTATATTCTCG
ACTAAAGTCTCATCAGGAAATATTTCCTGTCTTTTATTTTAAGCATCAAATTGTTTTAGTTGATTTAAAAAGGAA
AAAATACAGAAAAGACCAAAAAAAGGCCAAGGGTGTTGTTGGGGCGTCTGTCTAATGTGGTGGGTCTTTTTTTGA
GGGGTCTCCTAAAATAAAATATTTTGATAAGCAAAAAAATCTATGTCGGTGCGGAGAAAGAGGTAATGAAATG

FIGURE 208

GIGFSIFANLFSLADGRRLDPHASCLLEILPGSCGLSDEADSVYITVEPHRPERASGTPSHADHTPRAGAQMERQ
GRLALMGGAQTR

FIGURE 209

CGGTCCGGACAGCCGCGCGCTGAGGGTCTCGGGGCGGGCGCCGCGGGACCTCTCCGGGCCATGGCAGCCCCTGTC
AAAGGGAACAGGAAGCAGTCCACGGAGGGTGACGCCCTAGACCCACCTGCATCCCCCAAACCTGCTGGCAAGCAG
AACGGAATCCAGAACCCCATCTCGCTGGAGGACTCCCCCGAGGCAGGCGGGGAGCGGGAGGAGGAGCAGGAGCGG
GAGGAGGAGCAGGCCTTCCTGGTCAGCCTCTACAAGTTCATGAAGGAGCGACACACGCCCATCGAGAGGGTGCCC
CATCTCGGCTTCAAGCAGATTAACCTGTGGAAGATCTACAAAGCAGTGGAGAAGCTGGGGGCCTATGAGCTGGTG
ACCGGGCGCCGCCTCTGGAAGAACGTGTACGACGAGCTGGGGGGCAGCCCAGGCAGCACCAGCGCGGCCACGTGC
ACGCGCCGCCACTACGAGAGGCTGGTCCTGCCATACGTGCGGCACCTGAAGGGGGAGGATGACAAGCCGCTGCCC
ACCTCCAAGCCCAGGAAACAGTACAAGATGGCTAAGGAGAACAGGGGGGATGATGGGGCCACCGAGAGGCCGAAG
AAGGCCAAGGAGGAGCGGCGCATGGACCAGATGATGCCAGGAAAGACCAAAGCAGATGCTGCTGACCCAGCACCA
CTTCCCAGCCAGGAGCCCCCCAGGAACAGCACAGAACAGCAGGGCCTGGCCTCTGGGTCTTCTGTGTCCTTTGTG
GGTGCCAGCGGCTGTCCTGAGGCCTACAAGCGGCTCCTATCCAGCTTCTACTGCAAGGGGACACACGGCATCATG
TCACCACTGGCCAAAAAGAAGCTCCTGGCCCAGGTGAGCAAGGTGGAGGCCTTGCAGTGCCAGGAGGAGGGCTGC
CGCCATGGGGCAGAGCCCCAGGCGTCCCCAGCTGTTCACCTCCCAGAGAGTCCCCAGAGCCCCAAAGGGCTGACT
GAGAACTCCAGGCACCGGCTGACCCCTCAGGAGGGATTGCAGGCCCCAGGTGGCAGCCTCAGAGAGGAGGCGCAG
GCAGGCCCCTGCCCGGCAGCCCCCATCTTCAAGGGCTGCTTCTACACCCACCCCACCGAGGTGCTGAAGCCTGTC
AGCCAGCACCCCAGGGACTTCTTCTCTAGACTTAAAGATGGGGTGCTATTGGGGCCTCCTGGCAAAGAGGGGCTG
TCAGTGAAAGAGCCCCAGCTGGTGTGGGGCGGAGACGCTAACCGCCCTTCTGCGTTCCATAAAGGTGGCTCCAGA
AAGGGCATCCTCTACCCCAAGCCCAAAGCCTGCTGGGTGTCCCCCATGGCCAAGGTCCCAGCCGAGAGCCCCACG
CTCCCGCCCACCTTCCCCAGTAGCCCAGGCCTGGGCAGCAAGCGCAGCCTGGAGGAAGAGGGTGCTGCCCACAGT
GGGAAGAGACTGCGGGCCGTGTCTCCCTTTCTTAAGGAGGCGGATGCCAAGAAGTGTGGGGCCAAACCTGCAGGG
TCCGGCCTGGTCTCCTGCCTTCTGGGCCCAGCCCTGGGGCCTGTGCCCCCAGAGGCCTACAGGGGCACCATGCTG
CACTGCCCGCTGAACTTCACTGGCACCCCGGGCCCCTTGAAGGGCCAGGCTGCACTCCCCTTCAGCCCCCTGGTC
ATCCCGGCCTTCCCGGCCCACTTCCTGGCCACCGCAGGCCCCTCGCCCATGGCCGCTGGCCTGATGCACTTCCCC
CCAACGTCCTTCGACAGTGCCCTCCGCCACAGACTTTGCCCGGCCTCATCTGCCTGGCACGCACCACCAGTCACA
ACCTATGCAGCGCCCCACTTCTTCCACCTCAACACCAAGCTG**TAG**GCCAGCCCATGGTGTTGTGTACACTGTGGA
GTCGACAGGGGCCTACAACAGGCAGGTACTGCTGCCAGGGGGCTCTGAACTAGTGCCTGCTACCCAGGACACCCG
GGCCATGCCCCTGGCTGGGCAGCCTGGCACAAGTGAAGAAGAAGGCAGTGGGAAAACTGGGTTTATCTCAAGGCA
GCAGCCTGAGCCCAGGAGCAGAGGACCCAGTTGTTATAAGGCGCTGGGAGAGGATGGGCAGCTCCCACTGCCCCA
GAGCGGASSTCGAAGCACCCAGGTTGCCCACGGAAAATCCAATAAAAAGACACCAGTGTGAATCCAAAAAAAA

FIGURE 210

RSGQPRAEGLGAGAAGPLRAMAAPVKGNRKQSTEGDALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQER
EEEQAFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYELVTGRRLWKNVYDELGGSPGSTSAATC
TRRHYERLVLPYVRHLKGEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQMMPGKTKADAADPAP
LPSQEPPRNSTEQQGLASGSSVSFVGASGCPEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEGC
RHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGGSLREEAQAGPCPAAPIFKGCFYTHPTEVLKPV
SQHPRDFFSRLKDGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYPKPKACWVSPMAKVPAESPT
LPPTFPSSPGLGSKRSLEEEGAAHSGKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEAYRGTML
HCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAGPSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVT
TYAAPHFFHLNTKL

FIGURE 211

AAGCTTGCACGAGGCCTTCCCGGCGGCTGATTCGAGGGCTTGTTTGGTCAGAAGGGGGGCGTCAGAGAAGCTGCC
CCTTAGCCAACC**ATG**CCGTCTGAGGGTCGCTGCTGGGAGACCTTGAAGGCCCTACGCAGTTCCGACAAAGGTCGC
CTTTGCTACTACCGCGACTGGCTGCTGCGGCGCGAGGATGTTTTAGAAGAATGTATGTCTCTTCCCAAGCTATCT
TCTTATTCTGGATGGGTGGTAGAGCACGTCCTACCCCATATGCAGGAGAACCAACCTCTGTCTGAGACTTCGCCA
TCCTCTACGTCAGCTTCAGCCCTAGATCAACCCTCATTTGTTCCCAAATCTCCTGACGCAAGCTCTGCCTTTTCC
CCAGCCTCCCCTGCAACACCAAATGGAACCAAGGGCAAAGATGAGTCCCAGCACACAGAATCTATGGTACTTCAG
TCCTCACGGGGGATCAAAGTGGAAGGCTGCGTCCGAATGTACGAACTGGTACACAGAATGAAAGGAACAGAGGGC
CTGAGGCTATGGCAGGAGGAGCAGGAGAGGAAGGTGCAAGCCCTCTCGGAGATGGCATCTGAACAACTGAAGCGG
TTTGATGAATGGAAGGAACTGAAGCAGCATAAAGAATTCCAGGACTTGCGGGAAGTAATGGAGAAGAGCTCCAGA
GAAGCCTTGGGACACCAAGAGAAGTTAAAAGCTGAGCACCGTCACAGAGCAAAGATTCTCAACCTGAAGCTGCGG
GAAGCAGAGCAGCAGCGCGTGAAGCAAGCAGAACAGGAGCGGCTTCGGAAGGAAGAAGGCCAGATCCGCCTGCGG
GCCCTCTATGCTCTGCAGGAGGAGATGCTGCAGCTCAGCCAGCAGCTGGATGCCTCTGAGCAGCACAAAGCCCTG
CTTAAGGTCGACCTGGCTGCCTTCCAGACCCGAGGCAACCAGCTGTGCAGCCTCATCTCAGGGATCATCCGGGCC
TCTTCAGAGAGCAGCTATCCCACAGCAGAGAGTCAAGCTGAGGCTGAGCGAGCTCTGCGGGAAATGCGGGACCTC
CTGATGAACTTGGGGCAGGAGATCACCAGAGCCTGCGAAGACAAGAGGAGGCAGGATGAAGAAGAGGCCCAGGTA
AAGCTGCAAGAGGCACAGATGCAGCAGGGACCAGAGGCCCACAAAGAGCCCCCAGCTCCCAGCCAGGGCCCAGGA
GGGAAACAGAATGAAGACCTCCAGGTGAAGGTACAAGACATTACAATGCAGTGGTACCAGCAGCTGCAGGATGCT
TCCATGCAGTGTGTGTTGACCTTTGAGGGCCTGACCAACAGCAAGGACAGTCAGGCCAAAAAGATAAAGATGGAC
CTCCAGAAGGCTGCTACCATCCCAGTGAGCCAAATCTCTACCATTGCAGGCTCAAAACTGAAGGAGATCTTTGAC
AAGATCCACAGCCTGCTCTCTGGAAAACCTGTTCAATCTGGTGGGCGCTCTGTGTCTGTCACACTTAACCCACAG
GGGCTGGACTTTGTTCAATACAAACTGGCAGAGAAATTTGTGAAACAAGGCGAGGAGGAAGTGGCCTCTCACCAT
GAAGCAGCATTCCCCATTGCAGTTGTGGCATCCGGGATCTGGGAGCTCCACCCCAGAGTGGGGGACCTCATTCTT
GCTCATCTACATAAGAAGTGTCCTTACTCTGTTCCTTTCTATCCCACTTTCAAGGAGGGAATGGCTTTGGAAGAC
TATCAGAGGATGCTTGGTTACCAAGTAAAGGATTCCAAAGTGGAGCAGCAAGACAACTTTCTAAAACGCATGTCA
GGGATGATCCGTCTCTACGCTGCTATCATCCAGCTCCGGTGGCCATATGGAAACCGACAGGAGATTCACCCTCAT
GGCTTAAATCATGGATGGCGCTGGTTGGCACAGATCTTAAACATGGAGCCCTTGTCAGATGTGACAGCCACCCTC
CTCTTTGACTTCCTGGAGGTGTGTGGGAATGCCCTCATGAAGCAATACCAGGTTCAGTTCTGGAAGATGCTAATT
CTCATCAAAGAGGACTACTTTCCCAGGTATCAGGCTTGT**TGA**GCAGACAGCAGGGGATTAAGTAACTCATAACCA
GGCCTCAGATACCCAAGGGTGCTATTACCTGCTGGTTTTGATTCAAGTTAAAAACACCTGTACTAAGTATGACAT
CTTTCCTACTCCAGTCCCTCTCGTTGATATTTGAATAAATGCTTTTGAACCTTAAAAAAAAAAA

FIGURE 212

MPSEGRCWETLKALRSSDKGRLCYYRDWLLRREDVLEECMSLPKLSSYSGWVVEHVLPHMQENQPLSETSPSSTS
ASALDQPSFVPKSPDASSAFSPASPATPNGTKGKDESQHTESMVLQSSRGIKVEGCVRMYELVHRMKGTEGLRLW
QEEQERKVQALSEMASEQLKRFDEWKELKQHKEFQDLREVMEKSSREALGHQEKLKAEHRHRAKILNLKLREAEQ
QRVKQAEQERLRKEEGQIRLRALYALQEEMLQLSQQLDASEQHKALLKVDLAAFQTRGNQLCSLISGIIRASSES
SYPTAESQAEAERALREMRDLLMNLGQEITRACEDKRRQDEEEAQVKLQEAQMQQGPEAHKEPPAPSQGPGGKQN
EDLQVKVQDITMQWYQQLQDASMQCVLTFEGLTNSKDSQAKKIKMDLQKAATIPVSQISTIAGSKLKEIFDKIHS
LLSGKPVQSGGRSVSVTLNPQGLDFVQYKLAEKFVKQGEEEVASHHEAAFPIAVVASGIWELHPRVGDLILAHLH
KKCPYSVPFYPTFKEGMALEDYQRMLGYQVKDSKVEQQDNFLKRMSGMIRLYAAIIQLRWPYGNRQEIHPHGLNH
GWRWLAQILNMEPLSDVTATLLFDFLEVCGNALMKQYQVQFWKMLILIKEDYFPRYQAC

FIGURE 213

GGTTCACCATCATCCTCACCAACTTTTGGNCCATAATTCACCCAACCCTTTGGTGGAGCCTGAAAAAAATCTGGG
CAGAATGTAGGACTTCTTTATTTTGTTTAAAGGGGTAACACAGAGTGCCCTTATGAAGGAGTTGGAGATCCTGCA
AGGAAGAGAAGGAGTGAAGGAGAGATCAAGAGAGAGAAACAATGAGGAACATTTCATTTGACCCAACATCCTTTA
GGAGCATAAATGTTGACACTAAGTTATCCCTTTTGTGCTAAAATGGACAGTATTGGCAAA**ATG**ATACCACAACTT
CTTATTCTCTGGCTCTATATTGCTTTGGAAACACTTAAACATCAAATGGAGTTAAATACATATTTGAAATTTAGG
TTAGGAAATATTGGTGAGGAGGCCTCAAAAAGGGGGAAACATCTTTTGTCTGGGAGGATATTTTCCATTTTGTGG
ATTTCCCTGATCTTTTTCTACCACCCTGAGGGGTGGTGGGAATTATCATTTTGCTACATTTTAGAGGTCATCCAG
GATTTT**TGA**AACTTTACATTCTTTACGGTTAAGCAAGATGTACAGCTCAGTCAAAGACACTAAATTCTTCTTAGA
AAAATAGTGCTAAGGAGTATAGCAGATGACCTATATGTGTGTTGGCTGGGAGAATATCATCTTAAAGTGAGAGTG
ATGTTGTGGAGACAGTTGAAATGTCAGTGCTAGAGCCTCTGTGGTGTGAATGGGCACGTTAGGTTGTTGCATTAG
AAAGTGACTGTTTCTGACAGAAATTTGTAGCTTTGTGCAAACTCACCCACCATCTACCTCAATAAAATATAGAGA
AAAGAAAAATAGAGCAGTTTGAGTTCTATGAGGTATGCAGGCCCAGAGAGACATAAGTATGTTCCTTTAGTCTTG
CTTCCTGTGTGCCACACTGCCCCTCCACAACCATAGCTGGGGGCAATTGTTTAAAGTCATTTTGTTCCCGACTAG
CTGCCTTGCACATTATCTTCATTTTCCTGGAATTTGATACAGAGAGCAATTTATAGCCAATTGATAGCTTATGCT
GTTTCAATGTAAATTCGTGGTAAATAACTTAGGAACTGCCTCTTCTTTTTCTTTGAAAACCTACTTATAACTGTT
GCTAATAAGAATGTGTATTGTTCAGGACAACTTGTCTCCATACAGTTGGGTTGTAACCCTCATGCTTGGCCCAAA
TAAACTCTCTACTTATATCAGTTTTTCCTACACTTCTTCCTTTTAGGTCAACAATACCAAGAGGGGTTACTGTGC
TGGGTAATGTGTAAACTTGTGTCTTGTTTAGAAAGATAAATTTAAAGACTATCACATTGCTTTTTCATAAAACAA
GACAGGTCTACAATTAATTTATTTTGATGCAAATTGATAGGGGGGCCAAGTAAGCCCCATATGCTTAATGATCAG
CTGATGAATAATCATCTCCTAGCAACATAACTCAATCTAATGCTAAGGTACC

FIGURE 214

MIPQLLILWLYIALETLKHQMELNTYLKFRLGNIGEEASKRGKHLLSGRIFSILWISLIFFYHPEGWWELSFCYI
LEVIQDF

FIGURE 215

AATCTGTGGTTTTTGCTCAAAACTCAGTCTATCTGGATGCGTTGAATTATAGACAG**ATG**TCTGGCCGTGCTGGAA
GAAGAGGTCAAGACCTGATGGGAGATGTATATTTCTTTGATATTCCATTCCCCAAAATAGGAAAACTCATAAAAT
CCAATGTTCCTGAGCTGAGAGGACACTTCCCTCTCAGCATAACCCTGGTCCTGCGACTCATGCTGCTGGCTTCCA
AGGGAGATGACCCAGAGGATGCCAAGGCAAAGGTGCTATCAGTGCTAAAGCATTCATTGCTGTCCTTCAAGCAAC
CCAGAGTCATGGACATGTTAAAACTTTACTTCCTGTTTTCTTTGCAGTTCCTGGTGAAAGAGGGCTATTTAGATC
AAGAAGGTAATCCTATGGGGTTTGCTGGACTTGTGTCACATTTGCATTATCATGAACCTTCTAATCTTGTTTTTG
TGAGTTTTCTTGTAAATGGCCTCTTCCATGATCTCTGTCAGCCAACCAGGAAAGGCTCAAAACATTTTTCTCAAG
ACGTTATGGAAAAGCTAGTATTAGTATTGGCACATCTCTTTGGAAGAAGATATTTTCCACCAAAGTTCCAGGATG
CACACTTCGAGTTTTATCAATCAAAGGTGTTCCTTGATGATCTCCCTGAGGATTTTAGTGATGCTTTAGATGAAT
ATAACATGAAAATTATGGAGGACTTTACCACTTTCCTACGAATTGTTTCCAAACTGGCTGATATGAATCAGGAAT
ATCAACTCCCATTGTCAAAAATCAAATTCACAGGTAAAGAATGTGAAGACTCTCAACTCGTATCTCATTTGATGA
GCTGCAAGGAAGGAAGAGTAGCAATTTCACCATTTGTTTGTCTGTCTGGGAACTTTGATGATGATTTGCTTCGAC
TAGAAACTCCAAACCATGTTACTCTAGGCACAATCGGTGTCAATCGCTCTCAGGCTCCAGTGCTGTTGTCACAGA
AATTTGATAACCGAGGAAGGAAAATGTCGCTTAATGCCTATGCACTGGATTTCTACAAACATGGTTCCTTGATAG
GATTAGTCCAGGATAACAGGATGAATGAAGGAGATGCTTATTATTTGTTGAAGGATTTTGCACTCACCATTAAAT
CTATCAGTGTTTCCTTGCGTGAGCTATGTGAAAATGAAGACGACAACGTTGTCTTAGCCTTTGAACAACTGAGTA
CAACTTTTTGGGAAAAGTTAAACAAAGTC**TAA**AAACAAAGTCTATGCAAACCACTCAAAAATAATTCCATAGTAG
TTTTTCAGGTCACGTTTTTGATTCTTATGCTTCTTGCCAGAAATACATTATGATAAAGTGGAAATACATTACGAT
GAAGTGGAAAGAGCAAACACTTTGGAATCAAACAGAGTTGCAATCAAACCTGCCATGTTCTGTCATGAATACTCA
CAAATTATTTAGTATACCTGAATCTTGGTTTCTTTTTATAACTGAGTAATAATGGTTACATCTCAGGTAGTTTGA
GGATTGACTAAAAAAATGCGAGAATGTTGTATGTGACTGAATAACAATTTTTACTCTGCGAAGCCAAAGTAAATA
TAATATTATCAGTAACTTTATCCCCAGTGTCAGTATTTATAAAATGTTTATTAAGGCTAGAAAAAATGAATACAA
TATCCTGAAGGTGAAATATATTCTCTTCAATTAGCATAAATATGATTTACATAAGTTAGCTATACAGCTATTGAG
ATAGTACTTTCTAGTAAACTTAAACTACTTTTTAAACATACATTTTGTGTTGATTTAACAAAAATATAGAGAATG
ATTTGCTTTATTGTAATTGTATATAAGTGACTGGAAAAGCACAAAGAAATAAAGTGGGTTCGATCTGTTTACCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 216

MSGRAGRRGQDLMGDVYFFDIPFPKIGKLIKSNVPELRGHFPLSITLVLRLMLLASKGDDPEDAKAKVLSVLKHS
LLSFKQPRVMDMLKLYFLFSLQFLVKEGYLDQEGNPMGFAGLVSHLHYHEPSNLVFVSFLVNGLFHDLCQPTRKG
SKHFSQDVMEKLVLVLAHLFGRRYFPPKFQDAHFEFYQSKVFLDDLPEDFSDALDEYNMKIMEDFTTFLRIVSKL
ADMNQEYQLPLSKIKFTGKECEDSQLVSHLMSCKEGRVAISPFVCLSGNFDDDLLRLETPNHVTLGTIGVNRSQA
PVLLSQKFDNRGRKMSLNAYALDFYKHGSLIGLVQDNRMNEGDAYYLLKDFALTIKSISVSLRELCENEDDNVVL
AFEQLSTTFWEKLNKV

FIGURE 217A

AATGCGCTTGCGCACGTGCTGTCTACCAGTTCCTGAGAGGGACGCGTGCCGCGGAGCCAGGCTTACTACGTGACC
CGGACACCAGGCATACGCTAGGGGCAGTCAGCTGTGCCTTCTCTTTCGGAGTTGTTCCGTGCTCCCACGTGCTTC
CCCTTCTCCACTGGCTGGGATCCCCCGGGCTCGGGGCGCAGTAATAATTTTTCACC**ATG**CATCGGAAAAAGGTGG
ATAACCGAATCCGGATTCTCATTGAGAATGGAGTAGCTGAGCGGCAAAGATCTCTCTTTGTTGTAGTTGGGGATC
GAGGAAAAGATCAGGTGGTAATACTTCATCACATGTTATCCAAAGCAACTGTGAAGGCTCGGCCTTCAGTGCTGT
GGTGTTATAAGAAAGAGCTGGGGTTTAGCAGTCACCGGAAGAAAAGAATGCGACAGCTGCAGAAGAAAATAAAGA
ATGGAACACTGAACATAAAGCAGGACGACCCCTTTGAACTCTTCATAGCAGCCACAAACATTCGCTACTGCTACT
ACAACGAGACCCACAAGATCCTGGGCAATACCTTCGGCATGTGTGTGCTGCAGGATTTTGAAGCCTTAACTCCAA
ACTTGCTGGCCAGGACTGTAGAAACAGTGGAAGGTGGTGGGCTAGTGGTCATCCTCCTACGGACCATGAACTCAC
TCAAGCAATTGTACACAGTGACTATGGATGTGCATTCCAGGTACAGAACTGAGGCCCATCAGGATGTGGTGGGAA
GATTTAATGAAAGGTTTATTCTGTCTCTGGCCTCTTGTAAGAAGTGTCTCGTCATTGATGACCAGCTCAACATCC
TGCCCATCTCCTCCCACGTTGCCACCATGGAGGCCCTGCCTCCCCAGACTCCGGATGAGAGTCTTGGTCCTTCTG
ATCTGGAGCTGAGGGAGTTGAAGGAGAGCTTGCAGGACACCCAGCCTGTGGGTGTGTTGGTGGACTGCTGTAAGA
CTCTAGACCAGGCCAAAGCTGTCTTGAAATTTATCGAGGGCATCTCTGAAAAGACCCTGAGGAGTACTGTTGCAC
TCACAGCTGCTCGAGGACGGGGAAAATCTGCAGCCCTGGGATTGGCGATTGCTGGGGCGGTGGCATTTGGGTACT
CCAATATCTTTGTTACCTCCCCATGCCCTGATAACCTCCATACTCTGTTTGAATTTGTATTTAAAGGATTTGATG
CTCTGCAATATCAGGAACATCTGGATTATGAGATTATCCAGTCTCTAAATCCTGAATTTAACAAAGCAGTGATCA
GAGTGAATGTATTTCGAGAACACAGGCAGACTATTCAGTATATACATCCTGCAGATGCTGTGAAGCTGGGCCAGG
CTGAACTAGTTGTGATTGATGAAGCTGCCGCCATCCCCCTCCCCTTGGTGAAGAGCCTACTTGGCCCCTACCTTG
TTTTCATGGCATCCACCATCAATGGCTATGAGGGCACTGGCCGGTCACTGTCCCTCAAGCTAATTCAGCAGCTCC
GTCAACAGAGCGCCCAGAGCCAGGTCAGCACCACTGCTGAGAATAAGACCACGACGACAGCCAGATTGGCATCAG
CGCGGACACTGCATGAGGTTTCCCTCCAGGAGTCAATCCGATACGCCCCTGGGGATGCAGTGGAGAAGTGGCTGA
ATGACTTGCTGTGCCTGGATTGCCTCAACATCACTCGGATAGTCTCAGGCTGCCCCTTGCCTGAAGCTTGTGAAC
TGTACTATGTTAATAGAGATACCCTCTTTTGCTACCACAAGGCCTCTGAAGTTTTCCTCCAACGGCTTATGGCCC
TCTACGTGGCTTCTCACTACAAGAACTCTCCCAATGATCTCCAGATGCTCTCCGATGCACCTGCTCACCATCTCT
TCTGCCTTCTGCCTCCTGTGCCCCCCACCCAGAATGCCCTTCCAGAAGTGCTTGCTGTTATCCAGGTGTGCCTTG
AAGGGGAGATTTCTCGCCAGTCCATCTTGAACAGTCTGTCTCGAGGCAAGAAGGCTTCAGGGGACCTGATTCCAT
GGACAGTGTCAGAACAGTTCCAAGATCCAGACTTTGGTGGTCTGTCTGGTGGAAGGGTCGTTCGCATTGCTGTTC
ACCCAGATTATCAAGGGATGGGCTATGGCAGCCGTGCTCTGCAGCTGCTGCAGATGTACTATGAAGGCAGGTTTC
CTTGTCTGGAGGAAAAGGTCCTTGAGACACCACAGGAAATTCACACCGTAAGCAGCGAGGCTGTCAGCTTGTTGG
AAGAGGTCATCACTCCCCGGAAGGACCTGCCTCCTTTACTCCTCAAATTGAATGAGAGGCCTGCCGAACGCCTGG
ATTACCTGGGTGTTTCCTATGGCTTGACCCCCAGGCTCCTCAAGTTCTGGAAACGAGCTGGATTTGTTCCTGTTT
ATCTGAGACAGACCCCGAATGACCTGACCGGAGAGCACTCGTGCATCATGCTGAAGACGCTCACTGATGAGGATG
AGGCTGACCAGGGAGGCTGGCTTGCAGCCTTCTGGAAAGATTTCCGACGGCGGTTCCTAGCCTTGCTCTCCTACC
AGTTCAGTACCTTCTCTCCTTCCCTGGCTCTGAACATCATTCAGAACAGGAACATGGGGAAGCCAGCCCAGCCTG
CCCTGAGCCGGGAGGAGCTGGAAGCACTCTTCCTCCCCTATGACCTGAAGCGGCTGGAGATGTATTCACGGAATA
TGGTGGACTATCACCTCATCATGGACATGATCCCGGCCATCTCTCGCATCTATTTCCTGAACCAGCTGGGGGACC
TGGCCCTGTCTGCGGCTCAGTCGGCTCTTCTCTTGGGGATTGGCCTGCAGCATAAGTCTGTGGACCGGCTGGAAA
AGGAGATTGAGCTGCCCTCGGGCCAGTTGATGGGACTTTTCAACCGGATCATCCGCAAAGTTGTGAAGCTATTTA
ATGAAGTTCAGGAAAAGGCCATTGAGGAGCAGATGGTGGCAGCGAAGGATGTGGTCATGGAGCCCACGATGAAGA
CCCTCAGTGACGACCTAGATGAAGCAGCAAAGGAATTTCAGGAGAAACACAAGAAGGAAGTAGGGAAGCTGAAGA
GCATGGACCTCTCTGAATACATAATCCGTGGGGACGATGAAGAGTGGAATGAAGTTTTGAACAAAGCTGGGCCGA
ACGCCTCGATCATCAGCCTGAAAAGTGACAAGAAAAGGAAGTTAGAGGCCAAACAAGAACCCAAACAGAGCAAGA
AGTTGAAGAACAGAGAGACAAAGAACAAAAAAGATATGAAACTGAAGCGGAAGAAA**TAG**TGAAGAGAAACTCGGG
CATCTGTGTTTGATCATGGGAAGATACTCTCACTAACTGAACCCTCTCTGGCTGGACTGTTAAAAGCAACGAGAG
GCCCCGGCACACCTGGAAGCTGGCCGCGAATTCGGCCTCTGGGCCTGTGTGTCTGTGAGCTCAACCTGGCTAAAG
GCAGAGTCACTCCCAAATGGGTCTCTTTAGAACTTGATGGCTGGGCACTGCCATCTCTAGAATTGCCACGAGTCT
CTCTCTTCCTGCCCAGTCCAGGGCCCTCCTTTCCTATAAGTTCATATTTTGCTTTGAGCCAGCTTTTTAGTCTCA

FIGURE 217B

TTCCCACACATGTGGAAGCCACGTTGCCTCTCGACCGCCTGAGGCCCTTAAGTACATCGCTTTCTGGTGGTGCCC
AGGAGGCTGCTGCTGGGCCGCTGGGTCTCTCTTTGTGGACTTGTACCTGGAGCAGGAGGAACTCCAGTCCGTCCC
GGCATCCATGGCAGCCCGCGGTTAGGTGCGCCAGGGTTTGCTGATGTTGTCTTGTGCTGTTCCACTCTTGGCTCC
AGCAGACCCACTGTCCCAGAAAAGCCTGATCCTGTAGTTTATGTAGAATGCCACATCTGCGTCCTCAAGACCTGT
TTCATCCATTTGGGAAAAGATGTTGGGAAAGGCCACTTTGCTCGCAGGGGTGAGGGGAAGGATAGAGAATCTATT
TTTAATAAATAACATTCTAGAAAGATC

FIGURE 218

MHRKKVDNRIRILIENGVAERQRSLFVVVGDRGKDQVVILHHMLSKATVKARPSVLWCYKKELGFSSHRKKRMRQ
LQKKIKNGTLNIKQDDPFELFIAATNIRYCYYNETHKILGNTFGMCVLQDFEALTPNLLARTVETVEGGGLVVIL
LRTMNSLKQLYTVTMDVHSRYRTEAHQDVVGRFNERFILSLASCKKCLVIDDQLNILPISSHVATMEALPPQTPD
ESLGPSDLELRELKESLQDTQPVGVLVDCCKTLDQAKAVLKFIEGISEKTLRSTVALTAARGRGKSAALGLAIAG
AVAFGYSNIFVTSPCPDNLHTLFEFVFKGFDALQYQEHLDYEIIQSLNPEFNKAVIRVNVFREHRQTIQYIHPAD
AVKLGQAELVVIDEAAAIPLPLVKSLLGPYLVFMASTINGYEGTGRSLSLKLIQQLRQQSAQSQVSTTAENKTTT
TARLASARTLHEVSLQESIRYAPGDAVEKWLNDLLCLDCLNITRIVSGCPLPEACELYYVNRDTLFCYHKASEVF
LQRLMALYVASHYKNSPNDLQMLSDAPAHHLFCLLPPVPPTQNALPEVLAVIQVCLEGEISRQSILNSLSRGKKA
SGDLIPWTVSEQFQDPDFGGLSGGRVVRIAVHPDYQGMGYGSRALQLLQMYYEGRFPCLEEKVLETPQEIHTVSS
EAVSLLEEVITPRKDLPPLLLKLNERPAERLDYLGVSYGLTPRLLKFWKRAGFVPVYLRQTPNDLTGEHSCIMLK
TLTDEDEADQGGWLAAFWKDFRRRFLALLSYQFSTFSPSLALNIIQNRNMGKPAQPALSREELEALFLPYDLKRL
EMYSRNMVDYHLIMDMIPAISRIYFLNQLGDLALSAAQSALLLGIGLQHKSVDRLEKEIELPSGQLMGLFNRIIR
KVVKLFNEVQEKAIEEQMVAAKDVVMEPTMKTLSDDLDEAAKEFQEKHKKEVGKLKSMDLSEYIIRGDDEEWNEV
LNKAGPNASIISLKSDKKRKLEAKQEPKQSKKLKNRETKNKKDMKLKRKK

FIGURE 219A

TATAAATTGCTTTTTAACTTCGTTGAACAAAACATGAAAATAGAGAGACTGGTTGAAGTAAAGCCTTCCTTAGTT
ATTGACTATTTAAAGACAGAAAAGAAGCTATTCTGGCCAAAGATAAAGAAGGTAAATGTGCAGGTAAGTTTCAAT
CCTGAGAACAAACAAAAAGGCATTTTACTAACTGGCTCAAAGACCGAAGTACTGAAGGCAGTGGACATTGTCAAG
CAAGTCTGGGATTCAGTCTGTGTTAAAAGTGTCCATACTGATAAGCCAGGAGCCAAGCAGTTCTTCCAGGATAAA
GCACGGTTTTATCAAAGTGAGATCAAACGGTTGTTTGGTTGTTACATTGAACTACAGGAGAATGAAGTAATGAAG
GAGGGAGGCAGCCCCGCTGGGCAGAAGTGCTTCTCTCGGACAGTCTTGGCCCCTGGCGTTGTGCTGATTGTGCAG
CAGGGTGACTTGGCACGGCTTCCTGTCGATGTGGTGGTGAATGCATCTAATGAGGACCTTAAGCATTATGGTGGC
CTGGCCGCTGCGCTCTCAAAAGCAGCTGGCCCTGAGCTCCAGGCCGACTGTGACCAGATAGTGAAGAGAGAGGGC
AGACTCCTACCGGGCAATGCCACCATCTCCAAGGCAGGAAAGCTGCCCTACCACCACGTGATCCATGCAGTGGGG
CCCCGCTGGAGCGGATATGAGGCCCCGAGGTGTGTGTACCTATTAAGGAGAGCTGTGCAACTCAGTCTCTGTCTA
GCCGAAAAATACAAGTACCGATCCATAGCCATCCCAGCTATTAGTTCTGGAGTCTTTGGCTTTCCCTTAGGCCGA
TGCGTGGAGACCATTGTTTCTGCCATCAAGGAAAACTTCCAATTCAAGAAGGATGGACACTGCTTGAAAGAAATC
TACCTTGTGGATGTATCTGAGAAGACTGTTGAGGCCTTTGCAGAAGCTGTGAAAACTGTATTTAAAGCCACCCTG
CCAGATACAGCTGCCCCGCCAGGTTTACCACCAGCAGCAGCGGGGCCTGGGAAAACATCATGGGAAAAAGGAAGC
CTGGTGTCCCCGGGAGGCCTGCAGATGCTGTTGGTGAAAGAGGGTGTGCAGAATGCTAAGACCGATGTTGTTGTC
AACTCCGTTCCCTTGGATCTCGTGCTTAGTAGAGGGCCTCTTTCTAAGTCCCTCTTGGAAAAAGCTGGACCAGAG
CTCCAGGAGGAATTGGACACAGTTGGACAAGGGGTGGCTGTCAGCATGGGCACAGTGCTCAAAACCAGCAGCTGG
AATCTGGACTGTCGCTATGTGCTTCACGTGGTAGCTCCGGAGTGGAGAAATGGTAGCACATCTTCACTCAAGATA
ATGGAAGACATAATCAGAGAATGTATGGAGATCACTGAGAGCTTGTCCTTAAAATCAATTGCATTTCCAGCAATA
GGAACAGGAAACTTGGGATTTCCTAAAAACATATTCGCTGAATTAATCATTTCAGAGGTGTTCAAATTTAGTAGC
AAGAATCAGCTGAAAACTTTACAAGAGGTTCACTTTCTGCTGCACCCGAGTGATCATGAAAATATTCAGGCATTT
TCAGATGAATTTGCCAGAAGGGCTAATGGAAATCTCGTCAGTGACAAAATTCCGAAGGCTAAAGATACACAAGGT
TTTTATGGGACTGTTTCTAGCCCTGATTCAGGTGTGTATGAAATGAAGATTGGCTCCATCATCTTCCAGGTGGCT
TCTGGAGATATCACGAAAGAAGAGGCAGATGTGATTGTAAATTCAACATCAAACTCATTCAATCTCAAAGCAGGG
GTCTCCAAAGCAATTTTAGAATGTGCTGGACAAAATGTAGAAAGGGAATGTTCTCAGCAAGCTCAGCAGCGCAAA
AATGATTATATAATCACCGGAGGTGGATTTTTGAGGTGCAAGAATATCATTCATGTAATTGGTGGAAATGATGTC
AAGAGTTCAGTTTCCTCTGTTTTGCAGGAGTGTGAAAAAAAAAATTACTCATCCATTTGCCTCCCAGCCATTGGG
ACAGGAAATGCCAAACAACACCCAGATAAGGTTGCTGAAGCCATAATTGATGCCATTGAAGACTTTGTCCAGAAA
GGATCAGCCCAGTCTGTGAAAAAAGTTAAAGTTGTTATCTTTCTGCCTCAAGTACTGGATGTGTTTTATGCCAAC
ATGAAGAAAAGAGAAGGGACTCAGCTTTCTTCCCAACAGTCTGTGATGTCTAAACTTGCATCATTTTTGGGCTTT
TCAAAGCAATCTCCCCAAAAAAAGAATCATTTGGTTTTGGAAAAGAAAACAGAATCAGCAACTTTTCGGGTGTGT
GGTGAAAATGTCACGTGTGTGGAATACGCTATCTCCTGGCTACAAGACCTGATTGAAAAAGAACAGTGTCCTTAC
ACCAGTGAAGATGAGTGCATCAAAGACTTTGATGAAAAGGAGTATCAGGAGTTGAATGAGCTGCAGAAGAAGTTA
AATATTAACATTTCCCTGGACCATAAGAGACCTTTGATTAAGGTTTTGGGAATTAGCAGAGATGTGATGCAGGCT
AGAGATGAAATTGAGGCGATGATCAAGAGAGTTCGATTGGCCAAAGAACAGGAATCCCGGGCAGATTGTATCAGT
GAGTTTATAGAATGGCAGTATAATGACAATAACACTTCTCATTGTTTTAACAAAATGACCAATCTGAAATTAGAG
GATGCAAGGAGAGAAAAGAAAAAAACAGTTGATGTCAAAATTAATCATCGGCACTACACAGTGAACTTGAACACA
TACACTGCCACAGACACAAAGGGCCACAGTTTATCTGTTCAGCGCCTCACGAAATCCAAAGTTGACATCCCTGCA
CACTGGAGTGATATGAAGCAGCAGAATTTCTGTGTGGTGGAGCTGCTGCCTAGTGATCCTGAGTACAACACGGTG
GCAAGCAAGTTTAATCAGACCTGCTCACACTTCAGAATAGAGAAGGTAAGCCTTCTGCTAGAATGCAGTTTCTGG
ATGGTGGAAATAAGTTCTGTCATGGTCCTATATAAAATCCATTTTCATTCACTTCCTATCACATTTTTT**TAA**ACC
CAGAATTAGAATTTGTATGGTAATTAGTAGTTCTAGATTCTACTCATGTGACCATAATTACTGAGGCATTAAGAT
TCTTGTGTCAGTGATTACAATATTTGATTGTAATATGATAGAACACTAAAGACATATATTTACTTTGTGAAGCAA
GCTAATACAAATTCAAAGATATGGCTTTAAAATTGGATTTGATAGCTAGCAAATTCCACAGAGAGCCATGCAGAG
GCTCCTTAGATCAGGACCATGTTACTCTGCCCCATTATTCACAGATCAACAGTGCTTCCTTGATAAAGCCAGCAG
GCCTTTTCTCGTTTATCATAATTATTTTGGGCAGGTGAATGTGATGATTCGTGCCTGTAGTCCCAGCTATTGGGA
GGCTGAGGTGGAAGGATTGCATGAGCCCAGGAGTTTGACGCCAGTCTGGGTAACATAGTGAGATCCTGCTCTCAA
ATAAAAACAACCAATTATTTTGGCATCTTCTTCCATTTTTAAACATTTTTGATATTGCTGTTTGAAATTATATTT

FIGURE 219B

TCCTTGACTTCTCTAGCAAAATTATTATGATTTTTTTTTTCCTTGACTAATTTTCTTTTCATTTTTGCAGGCACG
CTGTTTCTCTTCCAAACCCCTAATTCTAGCTTTATTCACGCCATTTATGCTTAAACGGTCTTTTGTCTCTGTACC
TCACCAGGGAATATATTTACCCTTCTTGGATTCAACTATTAGTTCAATGTCGATAGCTCCCAAATCAACATTACC
AACCTGGGTCTTTGACTCAAGCTCTAGAACATACTCCCAGTGGCCTAAAAAAATCTCCACTTGAGGCTGGGCACA
GTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGTGGATCACGAGGTCAGGGGTTCAAGACCAT
CCTGGTGAAGATGGTGAAACCACGTCTCTACTAAAACTACAAAAATTAGCCGGGCATGTTGGCAGGTGCCTATAA
TCCCACCTACTTGGGAGGCTGAGGCAGGATAATTGCTTGAACATGGGCGGCAGAGATTGCAGTGAGCCAAGATCA
CGCCACTGCACTCCAGCCTGGTCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAATCTCCACTTGAATATCTAAC
TGCAAAATCAACTTCTCTAAAATCTAATGCATCATACGTAAGTAATTCTCTTTCCCTTTCCTTCCTCATTTCTGT
TTTTGGTTCTACCACTTTCTGAGTAAAGCCGGAGATCTTTGATCCACCATAAGTCTGCCAGTAAGACCTACATTT
TCTTTGCAAATTTTTCTTACTCTCTATTTGAACTGCCAACACTGTTTATTCATGTTGTTAAGTACATCATAATTT
AAAAAGATTCAAAGTGCCCTACAAAGATATAAACTATACCTTCAGATAAAATAAATATACAAAGAAAAATGGTTA
AAGAGAAAAGAATGGCAGGGAAAATAAGATAATACAGACGAACTGCTAGTTCTCAAAAATATATAACATGAGGTT
ACCAATTTGTCCCTGAGCTTCCTAGTAGACAAAGCAAGAAGTAAACATTCAGGTACAAGACTCATAATGTCCGTA
AATCAAAAAGCAAACCATTTGATAAGGAGGCTCACAGCTCCTCACAATACTGAGACTGACTCCTGAGAGATTTCT
CTTGTGGATCAAGTACTAGAGAATATCCTCAACGTCATCCTCACAATAAATTAAATATCAACTTTTATATCACTG
TTTTTTTTTAATGTAAAACTGGTTGAACAAAACCGATGCCTGATTGAATGAAAACAATTCTATGAGGCACCAAGA
CAATATGATTCAAGTATGCAGCTCTATGATGGTCTATTTCTGAGATAACAAGTAAGTCTCACTCCAAGTACCAAT
TACTACTAACTGGTAGTGGCTGATTGGCACATTGTGATGAGATGCTAAGTTTAGATTGAGCAGGAATGAATGTTC
TGCTTGACCAGCAATATCTACAGTGGGCCCTGTGGATGCCTGCTGTGTATTGGCAGACCCTGGCCAGAGAATTGA
TTTCAACACTTTTTTGCAGTGAAACCTTTTTTTTCAATAAAATCTTATGTGAAATCCCAGTGTATGAACCAGATA
AAAGCAGAGGTGTGGGTAGTACTTAAGGTGCCTCCATGGAGGTCCCTAGAATTGTG

FIGURE 220

YKLLFNFVEQNMKIERLVEVKPSLVIDYLKTEKKLFWPKIKKVNVQVSFNPENKQKGILLTGSKTEVLKAVDIVK
QVWDSVCVKSVHTDKPGAKQFFQDKARFYQSEIKRLFGCYIELQENEVMKEGGSPAGQKCFSRTVLAPGVVLIVQ
QGDLARLPVDVVVNASNEDLKHYGGLAAALSKAAGPELQADCDQIVKREGRLLPGNATISKAGKLPYHHVIHAVG
PRWSGYEAPRCVYLLRRAVQLSLCLAEKYKYRSIAIPAISSGVFGFPLGRCVETIVSAIKENFQFKKDGHCLKEI
YLVDVSEKTVEAFAEAVKTVFKATLPDTAAPPGLPPAAAGPGKTSWEKGSLVSPGGLQMLLVKEGVQNAKTDVVV
NSVPLDLVLSRGPLSKSLLEKAGPELQEELDTVGQGVAVSMGTVLKTSSWNLDCRYVLHVVAPEWRNGSTSSLKI
MEDIIRECMEITESLSLKSIAFPAIGTGNLGFPKNIFAELIISEVFKFSSKNQLKTLQEVHFLLHPSDHENIQAF
SDEFARRANGNLVSDKIPKAKDTQGFYGTVSSPDSGVYEMKIGSIIFQVASGDITKEEADVIVNSTSNSFNLKAG
VSKAILECAGQNVERECSQQAQQRKNDYIITGGGFLRCKNIIHVIGGNDVKSSVSSVLQECEKKNYSSICLPAIG
TGNAKQHPDKVAEAIIDAIEDFVQKGSAQSVKKVKVVIFLPQVLDVFYANMKKREGTQLSSQQSVMSKLASFLGF
SKQSPQKKNHLVLEKKTESATFRVCGENVTCVEYAISWLQDLIEKEQCPYTSEDECIKDFDEKEYQELNELQKKL
NINISLDHKRPLIKVLGISRDVMQARDEIEAMIKRVRLAKEQESRADCISEFIEWQYNDNNTSHCFNKMTNLKLE
DARREKKKTVDVKINHRHYTVNLNTYTATDTKGHSLSVQRLTKSKVDIPAHWSDMKQQNFCVVELLPSDPEYNTV
ASKFNQTCSHFRIEKVSLLLECSFWMVEISSVMVLYKIHFHSLPITFF

FIGURE 221

GCGTCGGGGGAGGACAACAAAGGGCCGCGGGCGGCGGGCAGTGGTGTCCCAGTCTCCCGGTGCTTCCCTGAGGCT
GAGGCGCCCGGCCTCCCGCCCGCCGCGCTCCAG**ATG**AAGTGTGAGCACTGCACGCGCAAGGAATGTAGTAAGAAA
ACAAAAACTGATGACCAAGAGAATGTGTCAGCCGATGCACCGAGTCCAGCCCAGGAAAATGGAGAGAAGGGAGAA
TTCCACAAGTTGGCTGATGCCAAGATATTTTTGAGCGACTGCCTGGCATGTGACAGCTGTATGACTGCAGAGGAA
GGAGTCCAACTTTCCCAGCAAAATGCCAAGGACTTCTTCCGCGTTCTGAACCTTAACAAGAAATGTGATACCTCA
AAGCACAAAGTGCTGGTAGTGTCTGTGTGTCCTCAATCTTTGCCTTATTTTGCTGCTAAATTCAACCTCAGTGTA
ACTGATGCATCCAGAAGACTCTGTGGTTTCCTCAAAAGTCTTGGGGTGCACTATGTATTTGATACGACGATAGCT
GCGGATTTTAGTATCCTGGAGAGTCAAAAAGAATTCGTGCGTCGCTATCGCCAGCACAGTGAGGAGGAACGCACC
CTGCCCATGCTGACCTCTGCCTGTCCTGGCTGGGTCCGATACGCCGAGCGGGTGCTGGGTCGCCCCATCACTGCC
CACCTCTGCACCGCCAAGTCCCCCCAGCAGGTCATGGGCTCTTTGGTGAAGGATTATTTCGCCAGACAGCAGAAC
CTGTCTCCAGAGAAGATTTTCCACGTCATTGTGGCCCCTTGTTATGACAAGAAGCTGGAGGCTCTTCAGGAAAGC
CTTCCCCCTGCTTTGCATGGCTCCCGGGGCGCTGACTGCGTGTTAACATCAGAAATTAGCCAGGCGTGGTGGTGC
ACACCTGTGATCACAGCTACTCGGGAGGCTGCGGCAAGAGAATCACTTGAACCCGGGAGGCAGAGGTTACAGCGA
GACAAGATTGCACCACTGGACTCCAGCCTGGGCGGCGGAGGTGAAATTGCTCAAATAATGGAGCAAGGTGACCTC
TCAGTGAGAGATGCTGCCGTCGACACTCTGTTTGGAGACTTGAAGGAGGACAAAGTGACGCGTCATGATGGAGCC
AGCTCAGACGGGCACCTGGCACACATCTTCAGACATGCGGCCAAGGAGCTGTTCAACGAGGATGTGGAGGAGGTC
ACTTACCGAGCCCTGAGAAACAAAGACTTCCAAGAGGTCACCCTTGAGAAGAACGGAGAGGTGGTGTTACGCTTT
GCTGCAGCCTATGGCTTTCGAAACATCCAGAACATGATCCTGAAGCTTAAGAAGGGCAAGTTCCCATTCCACTTT
GTGGAGGTCCTCGCCTGTGCTGGAGGATGCTTAAATGGCAGAGGCCAAGCCCAGACTCCAGACGGACATGCGGAT
AAGGCCCTGCTGCGGCAGATGGAAGGCATTTACGCTGACATCCCTGTGCGGCGTCCGGAGTCCAGTGCACACGTG
CAGGAGCTGTACCAGGAGTGGCTGGAGGGGATCAACTCCCCCAAGGCCCGAGAGGTGCTGCATACCACGTACCAG
AGCCAGGAGCGTGGCACACACAGCCTGGACATCAAGTGG**TGA**AGTCAGGCCAGGGCCTTCCAGCTGCTCTTGGGG
CCAGAGCCAAGAGCCTCTCAGTAGAGGGAGGGGCTGCCCTGAGTGGAGTATTAAAGACACTTAAGAAAACCGCTC
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 222

MKCEHCTRKECSKKTKTDDQENVSADAPSPAQENGEKGEFHKLADAKIFLSDCLACDSCMTAEEGVQLSQQNAKD
FFRVLNLNKKCDTSKHKVLVVSVCPQSLPYFAAKFNLSVTDASRRLCGFLKSLGVHYVFDTTIAADFSILESQKE
FVRRYRQHSEEERTLPMLTSACPGWVRYAERVLGRPITAHLCTAKSPQQVMGSLVKDYFARQQNLSPEKIFHVIV
APCYDKKLEALQESLPPALHGSRGADCVLTSEISQAWWCTPVITATREAAARESLEPGRQRLQRDKIAPLDSSLG
GGGEIAQIMEQGDLSVRDAAVDTLFGDLKEDKVTRHDGASSDGHLAHIFRHAAKELFNEDVEEVTYRALRNKDFQ
EVTLEKNGEVVLRFAAAYGFRNIQNMILKLKKGKFPFHFVEVLACAGGCLNGRGQAQTPDGHADKALLRQMEGIY
ADIPVRRPESSAHVQELYQEWLEGINSPKAREVLHTTYQSQERGTHSLDIKW

FIGURE 223

TTTCACCTCAGCAAGGCCAGGGGATCTGCACGTTGTGTTAGAC**ATG**GCTAAAGTAGCTGATACCATCCTGTTCCT
CCTTGATCCACTAGAAGGCTGGGACAGCACCGGTGATTACTGTCTTTCCTGCCTCTTTGCTCAGGGCCTTCCGAC
CTATACACTAGCTGTCCAGGGGATTTCTGGCCTCCCACTGAAGAAACAAATAGATACCAGGAAGAAGCTAAGTAA
AGCAGTGGAGAAGCGCTTTCCGCATGACAAACTCCTCTTGTTAGACACTCAACAGGAGGCAGGGATGCTGCTTAG
GCAGTTGGCTAACCAGAAGCAACAGCATCTTGCTTTTCGAGATCGGCGGGCCTACCTATTTGCCCATGCTGTTGA
TTTTGTTCCTAGTGAAGAGAATAACTTGGTGGGCACCTTGAAAATTTCAGGCTATGTTCGAGGGCAGACTCTGAA
TGTCAATAGGTTGCTGCATATCGTTGGATATGGTGATTTCCAGATGAAACAGATAGATGCCCCCGGAGACCCTTT
CCCTTTAAATCCTAGAGGAATTAAACCCCAAAAGGACCCAGACATGGCAATGGAGATTTGTGCTACGGATGCTGT
AGATGATATGGAAGAAGGTCTTAAAGTCCTAATGAAGGCAGACCCTTGTAGACAGGAATCCTTGCAAGCAGAGGT
TATCCCAGATCCAATGGAGGGAGAGCAAACCTGGCCCACTGAGGAGGAGCTGAGCGAGGCAAAGGATTTCTTGAA
GGAAAGTTCTAAGGTGGTAAAGAAGGTCCCCAAAGGAACATCCAGTTACCAAGCTGAATGGATTTTGGATGGTGG
CAGCCAAAGTGGTGGGGAAGGAGATGAATATGAATATGATGATATGGAACATGAGGATTTTATGGAGGAGGAATC
TCAGGATGAGAGTAGTGAAGAAGAGGAAGAATATGAAACTATGACTATTGGGGAGTCTGTGCATGATGATCTGTA
TGATAAGAAAGTAGATGAAGAAGCTGAGGCAAAAATGTTGGAGAAATATAAACAAGAAAGACTGGAAGAGATGTT
TCCAGATGAAGTGGACACGCCCCGTGATGTGGCTGCTCGAATTCGATTTCAGAAATACAGAGGCCTTAAGAGCTT
CCGGACATCTCCATGGGATCCTAAGGAAAACCTTCCTCAAGATTATGCTCGAATATTTCAGTTTCAGAACTTTAC
TAACACTAGGAAAAGCATCTTTAAAGAGGTTGAAGAAAAAGAGGTTGAAGGAGCTGAGGTTGGCTGGTATGTCAC
ACTTCATGTCTCTGAAGTCCCCGTCTCAGTGGTCGAGTGCTTCAGGCAAGGAACACCCTTGATTGCATTTTCTTT
ACTACCTCATGAACAGAAGATGTCAGTATTGAATATGGTGGTGAGGCGTGACCCTGGCAACACTGAACCTGTGAA
AGCCAAGGAGGAGCTCATATTTCACTGTGGATTCAGGCGCTTCCGAGCCTCACCTTTATTCTCTCAGCACACTGC
AGCGGACAAACATAAATTGCAGAGATTCCTGACTGCTGACATGGCCCTGGTGGCGACAGTCTATGCGCCAATCAC
TTTTCCTCCTGCATCTGTGCTGCTTTTCAAGCAGAAAAGCAATGGAATGCACAGCCTCATTGCTACAGGCCATCT
TATGTCAGTAGATCCAGACAGAATGGTCATCAAGAGAGTTGTTCTGAGTGGTCATCCTTTCAAAATTTTTACTAA
GATGGCAGTAGTACGTTACATGTTCTTCAACAGAGAGGATGTGCTGTGGTTTAAACCAGTGGAACTGAGAACGAA
GTGGGGCCGGAGAGGACATATCAAGGAACCTTTAGGTACCCATGGCCACATGAAATGCAGCTTTGATGGGAAGCT
AAAATCTCAAGACACAGTACTGATGAACCTGTATAAACGAGTCTTCCCCAAATGGACTTATGATCCATATGTACC
AGAACCAGTACCCTGGCTGAAAAGTGAGATTTCTTCAACAGTGCCTCAAGGGGGCATGGAG**TAA**TGGATTCAAAG
AGATTCTGTCCTACCGGTGCCAGTCAGTACTCCAGGGATGGGAGGCACAAGTTGTGATTGGGCAAAGTTTATTTT
CTATGTCAGCCTGTCAGTCCACTGCCCCATTTTGCAAGACTTTTTTTTAGCCTTGACAAAATGTCTCAGTTAAGT
ATAAAAGTTTTTCCACTACTTAGTCCAAAAAAAAACTATTAAATCTTAATGAAT

FIGURE 224

MAKVADTILFLLDPLEGWDSTGDYCLSCLFAQGLPTYTLAVQGISGLPLKKQIDTRKKLSKAVEKRFPHDKLLLL
DTQQEAGMLLRQLANQKQQHLAFRDRRAYLFAHAVDFVPSEENNLVGTLKISGYVRGQTLNVNRLLHIVGYGDFQ
MKQIDAPGDPFPLNPRGIKPQKDPDMAMEICATDAVDDMEEGLKVLMKADPCRQESLQAEVIPDPMEGEQTWPTE
EELSEAKDFLKESSKVVKKVPKGTSSYQAEWILDGGSQSGGEGDEYEYDDMEHEDFMEEESQDESSEEEEEYETM
TIGESVHDDLYDKKVDEEAEAKMLEKYKQERLEEMFPDEVDTPRDVAARIRFQKYRGLKSFRTSPWDPKENLPQD
YARIFQFQNFTNTRKSIFKEVEEKEVEGAEVGWYVTLHVSEVPVSVVECFRQGTPLIAFSLLPHEQKMSVLNMVV
RRDPGNTEPVKAKEELIFHCGFRRFRASPLFSQHTAADKHKLQRFLTADMALVATVYAPITFPPASVLLFKQKSN
GMHSLIATGHLMSVDPDRMVIKRVVLSGHPFKIFTKMAVVRYMFFNREDVLWFKPVELRTKWGRRGHIKEPLGTH
GHMKCSFDGKLKSQDTVLMNLYKRVFPKWTYDPYVPEPVPWLKSEISSTVPQGGME

FIGURE 225A

CCGGTTCCCGCGGTCGCAGCTCCAGCCGCCTCCTCCGCGCAGCCGCCGCCTCAGCTGCTCGCTCTGTGGGTCGGT
CCTCTCCGGCACTTGGGCTCCAGTCGCGCCCTCCAAGCCCTTCAGGCCGCCCCAGTGTCCTCCTCCTTCTCCGGC
CAGACCCAGCCCCGCGAAG**ATG**GTGGACCGCGAGCAACTGGTGCAGAAAGCCCGGCTGGCCGAGCAGGCGGAGCG
CTACGACGACATGGCCGCGGCCATGAAGAACGTGACAGAGCTGAATGAGCCACTGTCGAATGAGGAACGAAACCT
TCTGTCTGTGGCCTACAAGAACGTTGTGGGGGCACGCCGCTCTTCCTGGAGGGTCATCAGTAGCATTGAGCAGAA
GACATCTGCAGACGGCAATGAGAAGAAGATTGAGATGGTCCGTGCGTACCGGGAGAAGATAGAGAAGGAGTTGGA
GGCTGTGTGCCAGGATGTGCTGAGCCTGCTGGATAACTACCTGATCAAGAATTGCAGCGAGACCCAGTACGAGAG
CAAAGTGTTCTACCTGAAGATGAAAGGGGACTACTACCGCTACCTGGCTGAAGTGGCCACCGGAGAGAAAAGGGC
GACGGTGGTGGAGTCCTCCGAGAAGGCCTACAGCGAAGCCCACGAGATCAGCAAAGAGCACATGCAGCCCACCCA
CCCCATCCGATTAGGCCTGGCTCTTAACTACTCCGTCTTCTACTATGAGATCCAGAACGCCCCAGAGCAAGCGTG
CCACTTGGCCAAGACCGCGTTCGACGACGCCATCGCCGAGCTTGACACCCTCAACGAGGACTCCTACAAGGACTC
CACGCTCATCATGCAGCTCCTCCGCGACAACCTCACGCTCTGGACGAGCGACCAGCAGGACGACGATGGCGGCGA
AGGCAACAAT**TAA**GGCCCCAGGGGAACTGGCAGCGCACGCGGATGCTACTACTGCAGTCTTTATTTTTTTCCCAT
GAGTTGGGGGTCGGGTGGGGGAGGGAAAGGGAGGGATGACCTTCCCAGGGAGAAACCCACGACCTGTCCTGTCTT
TGATCGCCTCTTTGACATTTTTGCCAAAATACCACTAGTGGAAAGTCAGGCTAGCTGTGCTGGTATTGGAATAGC
AGCCTCACACTGGCGTCTGGACTGTTCTGTAGATTCATGCAAGTGGAGCTGTCTGTCTCTAATTTAACTTATTGC
TAGATAATAGGGTTTTCAGATGAAAAGAAAACTTAAAGAGGAATGGCCCTCATTCAGTAAGTTCTGTGGTTCCAG
TAAGGATTTTTATGTACATACGCTCTCGTCTCTCGTTTTGGGTACTTTCTATCTCATCTGTCTCGGCTCTGCATG
TTTTCCAGGGTGTAGCCTACAGACATGGAACAGTGTAAATCCCAGACTGACAGACTTAGAACCTGAGGTCTCATT
CATCCTTATGGTTTAGGCCTTGCCAGTTTTCCGAAGTCTCTGATTAGTTGACAGTATTAACACTAAATTGCAGTT
TACAGTATTTCTACATTACAGCCATATGTAACATCAAGCCATCGATTGTGTACTTTTCCTTTGCTAGTTGTTTGG
GCTTTAACATCCTTATTCAGCCTTATCCAGGTTGGTTTTGCTGTTGATCGGTCTCCTAGGCTAAATGAGAATGAA
AGCGACTTCAGGTTTTTGGTTCATAGGTGCTCGGCAGGTGGCTGTGGGATTTTTTTTTTTGGTCCTTCTTTCCTC
TTAACGTAAATCCACCACCAAAATTATTAATCCTCTTGAGAGAAACGTGAAACGCCACAAAAATAGAGAAAATTC
AGGTCTGTATGTCATGGATCGTGTTGGTATTTTCAGAGAACATCCCGCTTCTGAAGCTGCTGCAGCTCCCTCCTC
AGGGATCACACTGCCGTCACCCACTCTGCACTGGGGCGTTTCCTACTGCGCCTCGTGCTGGCGGACGCAGCTGGG
TGCAGAAGCTGTGGGGTCGGAGAGGCGTTTGGAGAAGGTCTGTGGTGCAGTGTGTGAAAATTCAGGTGCTAGAAG
CCTACTGGTAGAAAAACCCAAAAGGAAGAGCTATATCCTTAACCATTCTGTCCAATTTCGGGAGCCTTGTCAGTG
TGTCAGTTTTTCCTCCCCGAAGACACTCCTTCCCCAAGTAATTGTAGGAAGATAAAAAAACTGTTACCAGATAAC
AAACACTTAACTCCTATTTGACCAGAACTTTTTCCTCTCGAGATAGTTTTTTCTTTTTAATGAAAAAAGCATAGG
AATTGGAGATTGGCTTGTCTCACGCAGCCAGTGCACATTTGGAATTGACGGAAACAACGTTGCTATTTCCACCCA
TTTGTTTTCGGCAGCCTTAAGGCCCTCATTCTCATTTCGGGTGAATCTGTCTATCTGTGAACGTGGCCCGCATGT
GCATTCTTTTTTTTATATATATAAAGTCAGTGACGAGGCACTCCCGAGACGTGTAATGACACCACACTTGTTTTC
TTTGTTTCTTTGTTTTATTTAGGCAAGAAGAGGTGTGAGTAATTGAGGAAAAACTGACAGATGCTTTTGCTAATA
CCAAAATTGAGCTTACAATTAGGAACTGAGTATGTGTAACAGGATACAGGTGACAGTGAAGATAGAAGAACCACG
ATGACCACAGACTCAATGTGCTCTGTAACATCGCACAGTTTACCCAGCATGACTTTCCTTAGGAGGCCCCCTCCT
CACGCTAGAGTAAAAGTCCCAGTTAAGTGAAGCCTACCAGAAGAACTAGTAGAAGAAGCTTTGCCGCTTTTGTGC
CTCTCACAGGCGCCTAAAGTCATTGCCATGGGAGGAAGACGATTTGGGGGGGGAGGGGGGGGGCAGGGTAGGTGG
GGCTTTCCCTAATTTATCTTCATGTCCAGTGAGCAGTGTTGCGTTTTTCCTTGTAGCATTTGGAAATGATTTACT
GGAATTACAAAACCTATTTTTCCTTTAAATTTCAGCTTTGGCTCTGGCTGCTTTTTAGAATAATGCAAGATAAAA
ATCACACCTGAGGGCTGAAAACGGAGAGGGAATGGGAGACTTGATATTTAAGCAGCTTGAATGGTTTTTCTTTTC
TTTATTTTTAAAGAAATGCACTTGCCTATGATACTGTCTCTCCAGTGAAATGATTACTCCTCCATTACTCTATTG
ATACAATATTGTGCATGCTAGTGTTGTATTTCTATACAGTAGCTTGAAATTGATTAACTTATACTGTAGGTGTTA
TGTATTCCTATGACAAAAAAAATTAAGTCTTCAAATTTTTTAAAGGTTTTTTTTTTTTAATTTAATTTTTCCTTT
TGGGGGTAAAGTTTGCTCTACCAAATAGTGATTGTAACAAATTGATCTGTTTTGGATGTTGCTATAGTGACATGC
AGTTATATATTTTGTTTTTAAAAGGGGGGGAGCAAAAGAAACACCAGTGTTAGCTTAATCTTAATGTCTGGTGTT
TGTCATGGTGAAATTATAACTATTACAGTGTTGGAGAACAACAAATATGTTCTCTGAATGAGCCTTTGTGCTTTT
TGTCATGTTATGCAGTGAACTATTTTTAAGGTCTAATCAGTGATTATTTTTCCAGCTCCGTGTTTCTCTAAGGAA

FIGURE 225B

TTATTTCACACACGGACCATCTTTAGCAGTTTCCTCAGTGATGGAATATCATGAATGTGAGTCATTATGTAGCTG
TCGTACATTGAGCAAATAAACTTACAGATCTGACGCC

FIGURE 226

MVDREQLVQKARLAEQAERYDDMAAAMKNVTELNEPLSNEERNLLSVAYKNVVGARRSSWRVISSIEQKTSADGN
EKKIEMVRAYREKIEKELEAVCQDVLSLLDNYLIKNCSETQYESKVFYLKMKGDYYRYLAEVATGEKRATVVESS
EKAYSEAHEISKEHMQPTHPIRLGLALNYSVFYYEIQNAPEQACHLAKTAFDDAIAELDTLNEDSYKDSTLIMQL
LRDNLTLWTSDQQDDDGGEGNN

FIGURE 227A

ATCCAGTTCACGCAGTCGTCATTCCAGTATCTCACCTGTCAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACT
CAGTAGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCCAGCTACGAAAG
AAGTGGCTCTTACAGCGGGCGATCGCCCAGTCCCTATGGTCGAAGGCGGTCCAGCAGCCCTTTCCTGAGCAAGCG
GTCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCCTGCATATTCAAGACA
TTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGTCATTCCAGTATCTCACCTGTCAGGCTTCC
ACTTAATTCCAGTCTGGGAGCTGAACTCAGTAGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGAT
GGATGGAAAGGAGTCCAAGGGTTCACCTGTATTTTTGCCTAGAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTC
AGGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAAAATTGGAAAAATCTGCCCCAGATACTGAACTGGTGAATGT
AACACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAAGTAAAGTTGGATGAGAACTCCGAGAAGCA
TCTTGTTAAAGATTTGAAAGCACAGGGAACAAGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCC
AAAGGAGACAGAAACATCAGAAAAGGAGACCCCTCCACCTCTTCCCACAATTGCTTCTCCCCCACCCCCTCTACC
AACTACTACCCCTCCACCTCAGACACCCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTTCCACAGCAACCACC
TCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCCTGCTTCCAGTACTTCAACTTTGCCCCCTTCTACTCACTC
AAAGACATCTGCTGTGTCCTCTCAGGCAAATTCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGT
AACAGCTGCTATTCCACACCTGAAAACTTCAACGTTGCCTCCTTTGCCCCTCCCACCCTTATTACCTGGAGATGA
TGACATGGATAGTCCAAAAGAAACTCTTCCTTCAAAACCTGTGAAGAAAGAGAAGGAACAGAGGACACGTCACTT
ACTCACAGACCTTCCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTGTCTCCCCCAGACTCTCCAGAACCAAAGGC
AATCACACCACCTCAGCAACCATATAAAAAGAGACCAAAAATTTGTTGTCCTCGTTATGGAGAAAGAAGACAAAC
AGAAAGCGACTGGGGGAAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCA
AGTATATAAAGCCAAGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTAGACAATGAGAAAGA
GGGCTTCCCAATCACAGCCATTCGTGAAATCAAAATCCTTCGTCAGTTAATCCACCGAAGTGTTGTTAACATGAA
GGAAATTGTCACAGATAAACAAGATGCACTGGATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTTGAGTA
TATGGACCATGACTTAATGGGACTGCTAGAATCTGGTTTGGTGCACTTTTCTGAGGACCATATCAAGTCGTTCAT
GAAACAGCTAATGGAAGGATTGGAATACTGTCACAAAAAGAATTTCCTGCATCGGGATATTAAGTGTTCTAACAT
TTTGCTGAATAACAGTGGGCAAATCAAACTAGCAGATTTTGGACTTGCTCGGCTCTATAACTCTGAAGAGAGTCG
CCCTTACACAAACAAAGTCATTACTTTGTGGTACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACC
AGCCATAGATGTTTGGAGCTGTGGATGTATTCTTGGGGAACTATTCACAAAGAAGCCTATTTTTCAAGCCAATCT
GGAACTGGCTCAGCTAGAACTGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGGCCTGATGTTATCAA
ACTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGGCGTCTACGAGAAGAATTCTCTTTCATTCC
TTCTGCAGCACTTGATTTATTGGACCACATGCTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCT
ACAGAGCGACTTCCTTAAAGATGTCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCA
TGAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTTGTAGTCGAAGAGCCACCTCCATCCAAAAC
TTCTCGAAAAGAAACTACCTCAGGGACAAGTACTGAGCCTGTGAAGAACAGCAGCCCAGCACCACCTCAGCCTGC
TCCTGGCAAGGTGGAGTCTGGGGCTGGGGATGCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGA
ATTGGCAGTGTTATTAAACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACAT
CCACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTGACGGAAGCTACTTC
CCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAGGAAGCACCCTCTGCCCCAGTGATCCTGCC
TTCAGCAGAACAGACGACCCTTGAAGCTTCAAGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAG
TCAGCTGATGAAAACCCAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGG
GCCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGGTAGGAGCAACGGTGGGAATGCCCTC**TGA**GGAAT
GCAGTGATGTCCATCAGTCACCTCTCACCCAGAGCCTGGCAAATTCAGTCTCTTTCACAGAACCTAAAGCCAAGC
CAGGTTCAGTGGGAAATCCCACCTGTCCAAACACTGTGTGAGACACCAGAATTAGAGGCCTGCAAGCCTGCTTCC
TTCATCCCCAATGCCCAGATGGGACAGGTCACCAGCCTCCTGTGTCTACCCCCACCTTTCTTGCTTGCTGGCCTC
CTCTCTCTGCAGTGCCTCTCTCATCCCTGCAATCCAGACAGCACATGCAGCAGCTCAACCAATTCCATTCCTGGC
TACCTCATCCCCTCCAGTCTGAAAGGACGTGTGAATGCCACCAGGATCTGAACCCAAGATTCCAGCCTCGGTCAC
CACCCTGACCCTGAGAATGCCACTGGGATGGGGAGAACTTGTCAGTCTTCATCCTTCCCCACAAGTATACTGAAG
CCAGGACAGCACCTGCCTTAGAGAGCTCTTAGAGGGATTATCCGCAGCCTGAAGAAAGAAGGTTACAACTGAGGA
AGAACTTCTGAACAGGGAAGAGTGGAAGAAAAGACTGCAGCTCAGCTCCAGAAGCAGACCCAGAATGGCATCCTT

FIGURE 227B

CTCTGAGACCCAGACCCCAGCCCCTTTTCATGGAAGACCAGCACAAAGGAGGAAGTAGGTTAGGGAATGGTAAGG
CTCCATGTGATGGGACTAATGTGGAGAGGCCTGGGGCCTTTCCCTGAGGACTGGATGGCTGGAGTTTGGGAGCCT
GAGTTGACAGAGGAGGCTAAGCCCGGGCAGCTACTTTGTTCCAGAAATCTAAGGTCCCTGGAGGGAGGCTCTGCT
TTGGGAGGGGGAAGGGAGCTAACATTGCAGAGCACCAACTGTGAACCAGGTACAATGGCAGAGCCTTTCCATACC
TGTACTCACAACTAGCGGGTGAGGAGTCAAGGCAAATAGGTGTCTCATAGCTCCCCATATCTCGGCAGTCGACCA
CCTCCTCTTTTGATTCTCTGATGTCACTGCCAGTTCTCCTCCTATTGCTCTGACCTGTCTTTCTCTGTGTCCTTT
GCAAACTCATTCTCAACTCCTTAGACTCAGTCAAGTCCCCCAGTTACACACTTCCATGGTACTATATATCATTCC
TTCAGAGCACTTAACACAGTTATTTCCTATGTATTTGTCCAGTCATTTGAATAATGATCCTAGTTTCATTGGATG
GAAAGTTCCACAAGGTCAGTGACCATTTCTATCTGTGTTCACCAATGTGTTCCCAGTGCCCAGAAACAATGCCTA
GCATAAAGCAGCTGTTTTGTAAATACTTGTTCAATGAATGAATAAATGACAAAAGAACATC

FIGURE 228

SSSRSRHSSISPVRLPLNSSLGAELSRKKKERAAAAAAAKMDGKESSYERSGSYSGRSPSPYGRRRSSSPFLSKR
SLSRSPLPSRKSMKSRSRSPAYSRHSSSHSKKKRSSSRSRHSSISPVRLPLNSSLGAELSRKKKERAAAAAAAKM
DGKESKGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELVNVTHLNTEVKNSSDTGKVKLDENSEKH
LVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPLPTTTPPPQTPPLPPLPPIPALPQQPP
LPPSQPAFSQVPASSTSTLPPSTHSKTSAVSSQANSQPPVQVSVKTQVSVTAAIPHLKTSTLPPLPLPPLLPGDD
DMDSPKETLPSKPVKKEKEQRTRHLLTDLPLPPELPGGDLSPPDSPEPKAITPPQQPYKKRPKICCPRYGERRQT
ESDWGKRCVDKFDIIGIIGEGTYGQVYKAKDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQLIHRSVVNMK
EIVTDKQDALDFKKDKGAFYLVFEYMDHDLMGLLESGLVHFSEDHIKSFMKQLMEGLEYCHKKNFLHRDIKCSNI
LLNNSGQIKLADFGLARLYNSEESRPYTNKVITLWYRPPELLLGEERYTPAIDVWSCGCILGELFTKKPIFQANL
ELAQLELISRLCGSPCPAVWPDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLLDHMLTLDPSKRCTAEQTL
QSDFLKDVELSKMAPPDLPHWQDCHELWSKKRRRQRQSGVVVEEPPPSKTSRKETTSGTSTEPVKNSSPAPPQPA
PGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDLSIPQMAQLLNIHSNPEMQQQLEALNQSISALTEATS
QQQDSETMAPEESLKEAPSAPVILPSAEQTTLEASSTPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQG
PRRTPTMPQEEAAGRSNGGNAL

FIGURE 229

AATCGCGAAACCCGGCGAGCGGCGCGCTGGCTATCGAGCGAGCGGGGCGGAACCGGGAGTTGCGCCGCCGCTCGG
GCGCCGGGCTCCGTCGCGGCCGCAGCCCCGCGGGTCGCCCTCCCGTGCCTCGCCCGCGGACACCCTGGCCGTGGA
CACCCTGGCCGTGGGCACCCGCGGGGCGCGGCGCGGGCGCTGCGCGGCGGCGGCGGCGGC**ATG**AAGGTCACGTCG
CTCGACGGGCGCCAGCTGCGCAAGATGCTCCGCAAGGAGGCGGCGGCGCGCTGCGTGGTGCTCGACTGCCGGCCC
TATCTGGCCTTCGCTGCCTCGAACGTGCGCGGCTCGCTCAACGTCAACCTCAACTCGGTGGTGCTGCGGCGGGCC
CGGGGCGGCGCGGTGTCGGCGCGCTACGTGCTGCCCGACGAGGCGGCGCGCGCGGCTCCTGCAGGAGGGCGGC
GGCGGCGTCGCGGCCGTGGTGGTGCTGGACCAGGGCAGCCGCCACTGGCAGAAGCTGCGAGAGGAGAGCGCCGCG
CGTGTCGTCCTCACCTCGCTACTCGCTTGCCTACCCGCCGGCCCGCGGGTCTACTTCCTCAAAGGGGGATATGAG
ACTTTCTACTCGGAATATCCTGAGTGTTGCGTGGATGTAAAACCCATTTCACAAGAGAAGATTGAGAGTGAGAGA
GCCCTCATCAGCCAGTGTGGAAAACCAGTGGTAAATGTCAGCTACAGGCCAGCTTATGACCAGGGTGGCCCAGTT
GAAATCCTTCCCTTCCTCTACCTTGGAAGTGCCTACCATGCATCCAAGTGCGAGTTCCTCGCCAACTTGCACATC
ACAGCCCTGCTGAATGTCTCCCGACGGACCTCCGAGGCCTGCATGACCCACCTACACTACAAATGGATCCCTGTG
GAAGACAGCCACACGGCTGACATTAGCTCCCACTTTCAAGAAGCAATAGACTTCATTGACTGTGTCAGGGAAAAG
GGAGGCAAGGTCCTGGTCCACTGTGAGGCTGGGATCTCCCGTTCACCCACCATCTGCATGGCTTACCTTATGAAG
ACCAAGCAGTTCCGCCTGAAGGAGGCCTTCGATTACATCAAGCAGAGGAGGAGCATGGTCTCGCCCAACTTTGGC
TTCATGGGCCAGCTCCTGCAGTACGAATCTGAGATCCTGCCCTCCACGCCCAACCCCCAGCCTCCCTCCTGCCAA
GGGGAGGCAGCAGGCTCTTCACTGATAGGCCATTTGCAGACACTGAGCCCTGACATGCAGGGTGCCTACTGCACA
TTCCCTGCCTCGGTGCTGGCACCGGTGCCTACCCACTCAACAGTCTCAGAGCTCAGCAGAAGCCCTGTGGCAACG
GCCACATCCTGC**TAA**AACTGGGATGGAGGAATCGGCCCAGCCCCAAGAGCAACTGTGATTTTTGTTTTTAAGACT
CATGGACATTTCATACCTGTGCAATACTGAAGACCTCATTCTGTCATGCTGCCCCAGTGAGATAGTGAGTGGTCA
CCAGGCTTGCAAATGAACTTCAGACGGACCTCAGGGTAGGTTCTCGGGACTGAAGGAAGGCCAAGCCATTACGGG
AGCACAGCATGTGCTGACTACTGTACTTCCAGACCCCTGCCCTCTTGGGACTGCCCAGTCCTTGCACCTCAGAGT
TCGCCTTTTCATTTCAAGCATAAGCCAATAAATACCTGCAGCAACGTGGGAGAAAGAAGTTGCTGGACCAGGAGA
AAAGGCAGTTATGAAGCCAATTCATTTTGAAGGAAGCACAATTTCCACCTTATTTTTTGAACTTTGGCAGTTTCA
ATGTCTGTCTCTGTTGCTTCGGGGCATAAGCTGATCACCGTCTAGTTGGGAAAGTCACCCTACAGGGTTTGTAGG
GACATGATCAGCATCCTGATTTGAACCCTGAAATGTTGTGTAGACACCCTCTTGGGTCCAATGAGGTAGTTGGTT
GAAGTAGCAAGATGTTGGCTTTTCTGGATTTTTTTTGCCATGGGTTCTTCACTGACCTTGGACTTTGGCATGATT
CTTAGTCATACTTGAACTTGTCTCATTCCACCTCTTCTCAGAGCAACTCTTCCTTTGGGAAAAGAGTTCTTCAGA
TCATAGACCAAAAAAGTCATACCTTCGAGGTGGTAGCAGTAGATTCCAGGAGGAGAAGGGTACTTGCTAGGTATC
CTGGGTCAGTGGCGGTGCAAACTGGTTTCCTCAGCTGCCTGTCCTTCTGTGTGCTTATGTCTCTTGTGACAATTG
TTTTCCTCCCTGCCCCTGGAGGTTGTCTTCAACTGTGGACTTCTGGGATTTGCAGATTTTGCAACGTGGTACTAC
TTTTTTTTCTTTTTGTCTGTTAGTTATTTCTCCAGGGGAAAAGGCAATAATTTTCTAAGACCCGTGTGAATGTGA
AGAAAAGCAGTATGTTACTGGTTGTTGTTGTTGTTCTTGTTTTTTATATGTAAAATAAAAATAGTGAAAGGAG

FIGURE 230

MKVTSLDGRQLRKMLRKEAAARCVVLDCRPYLAFAASNVRGSLNVNLNSVVLRRARGGAVSARYVLPDEAARARL
LQEGGGGVAAVVVLDQGSRHWQKLREESAARVVLTSLLACLPAGPRVYFLKGGYETFYSEYPECCVDVKPISQEK
IESERALISQCGKPVVNVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSRRTSEACMTHLHY
KWIPVEDSHTADISSHFQEAIDFIDCVREKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMV
SPNFGFMGQLLQYESEILPSTPNPQPPSCQGEAAGSSLIGHLQTLSPDMQGAYCTFPASVLAPVPTHSTVSELSR
SPVATATSC

FIGURE 231

GCAGCCCAGCCAAGCACTGTCAGGAATCCTGTGAAGCAGCTCCAGCT**ATG**TGTGAAGAAGAGGACAGCACTGCCT
TGGTGTGTGACAATGGCTCTGGGCTCTGTAAGGCCGGCTTTGCTGGGGACGATGCTCCCAGGGCTGTTTTCCCAT
CCATTGTGGGACGTCCCAGACATCAGGGGGTGATGGTGGAATGGGACAAAAAGACAGCTACGTGGGTGACGAAG
CACAGAGCAAAAGAGGAATCCTGACCCTGAAGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGG
AAAAGATCTGGCACCACTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTGCTCACGGAGG
CACCCCTGAACCCCAAGGCCAACCGGGAGAAAATGACTCAAATTATGTTTGAGACTTTCAATGTCCCAGCCATGT
ATGTGGCTATCCAGGCGGTGCTGTCTCTCTATGCCTCTGGACGCACAACTGGCATCGTGCTGGACTCTGGAGATG
GTGTCACCCACAATGTCCCCATCTATGAGGGCTATGCCTTGCCCCATGCCATCATGCGTCTGGATCTGGCTGGCC
GAGATCTCACTGACTACCTCATGAAGATCCTGACTGAGCGTGGCTATTCCTTCGTTACTACTGCTGAGCGTGAGA
TTGTCCGGGACATCAAGGAGAAACTGTGTTATGTAGCTCTGGACTTTGAAAATGAGATGGCCACTGCCGCATCCT
CATCCTCCCTTGAGAAGAGTTACGAGTTGCCTGATGGGCAAGTGATCACCATCGGAAATGAACGTTTCCGCTGCC
CAGAGACCCTGTTCCAGCCATCCTTCATCGGGATGGAGTCTGCTGGCATCCATGAAACCACCTACAACAGCATCA
TGAAGTGTGATATTGACATCAGGAAGGACCTCTATGCTAACAATGTCCTATCAGGGGGCACCACTATGTACCCTG
GCATTGCCGACCGAATGCAGAAGGAGATCACGGCCCTAGCACCCAGCACCATGAAGATCAAGATCATTGCCCCTC
CGGAGCGCAAATACTCTGTCTGGATCGGTGGCTCCATCCTGGCCTCTCTGTCCACCTTCCAGCAGATGTGGATCA
GCAAACAGGAATACGATGAAGCCGGGCCTTCCATTGTCCACCGCAAATGCTTC**TAA**AACACTTTCCTGCTCCTCT
CTGTCTCTAGCACACAACTGTGAATGTCCTGTGGAATTATGCCTTCAGTTCTTTTCCAAATCATTCCTAGCCAAA
GCTCTGACTCGTTACCTATGTGTTTTTAATAAATCTGAAATAGGCTACTGGTAA

FIGURE 232

MCEEEDSTALVCDNGSGLCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSKRGILTLKYPIEH
GIITNWDDMEKIWHHSFYNELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMYVAIQAVLSLYASGRT
TGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKEKLCYVALDF
ENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRKDLYANNV
LSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHRK
CF

FIGURE 233

CGGGAAGCGCGGCGGGGCCTCCAGACCGGGGCGGGCTTAAGGGTGACATCTGCGCTTTAAAGGGTCCGGGTCAGC
TGACTCCCGACTCTGTGGAGTCTAGCTGCCAGGGTCGCGGCAGTGCGGGGAGAG**ATG**ACTGGGGAGCGACCCAGC
ACGGCGCTCCCGGACAGACGCTGGGGGCCGCGGATTCTGGGCTTCTGGGGAGGCTGTAGGGTTTGGGTGTTTGCC
GCGATCTTCCTGCTGCTGTCTCTGGCAGCCTCCTGGTCCAAGGCTGAGAACGACTTCGGTCTGGTGCAGCCGCTG
GTGACCATGGAGCAACTGCTGTGGGTGAGCGGGAGACAGATCGGCTCAGTGGACACCTTCCGCATCCCGCTCATC
ACAGCCACTCCGCGGGGCACTCTTCTCGCCTTTGCTGAGGCGAGGAAAATGTCCTCATCCGATGAGGGGGCCAAG
TTCATCGCCCTGCGGAGGTCCATGGACCAGGGCAGCACATGGTCTCCTACAGCGTTCATTGTCAATGATGGGGAT
GTCCCCGATGGGCTGAACCTTGGGGCAGTAGTGAGCGATGTTGAGACAGGAGTAGTATTTCTTTTCTACTCCCTT
TGTGCTCACAAGGCCGGCTGCCAGGTGGCCTCTACCATGTTGGTATGGAGCAAGGATGATGGTGTTTCCTGGAGC
ACACCCCGGAATCTCTCCCTGGATATTGGCACTGAAGTGTTTGCCCCTGGACCGGGCTCTGGTATTCAGAAACAG
CGGGAGCCACGGAAGGGCCGCCTCATCGTGTGTGGCCATGGGACGCTGGAGCGGGACGGAGTCTTCTGTCTCCTC
AGCGATGATCATGGTGCCTCCTGGCGCTACGGAAGTGGGGTCAGCGGCATCCCCTACGGTCAGCCCAAGCAGGAA
AATGATTTCAATCCTGATGAATGCCAGCCCTATGAGCTCCCAGATGGCTCAGTCGTCATCAATGCCCGAAACCAG
AACAACTACCACTGCCACTGCCGAATTGTCCTCCGCAGCTATGATGCCTGTGATACACTAAGGCCCCGTGATGTG
ACCTTCGACCCTGAGCTCGTGGACCCTGTGGTAGCTGCAGGAGCTGTAGTCACCAGCTCCGGCATTGTCTTCTTC
TCCAACCCAGCACATCCAGAGTTCCGAGTGAACCTGACCCTGCGATGGAGCTTCAGCAATGGTACCTCATGGCGG
AAAGAGACAGTCCAGCTATGGCCAGGCCCCAGTGGCTATTCATCCCTGGCAACCCTGGAGGGCAGCATGGATGGA
GAGGAGCAGGCCCCCCAGCTCTACGTCCTGTATGAGAAAGGCCGGAACCACTACACAGAGAGCATCTCCGTGGCC
AAAATCAGTGTCTATGGGACACTC**TGA**GCTGTGCCACTGCCACAGGGGTATTCTGCCTTCAGGACTCTGCCTTCA
GGAACACGGGTCTGTAGAGGGTCTGCTGGAGACGCCTGAAAGACAGTTCCATCTTCCTTTAGACTCCAGCCTTGG
CAAAATCACCTTCCCTTTACCAGGGAAATCACTTCCTTTAGGACTGAAAGCTAGGCGTCCTCTCCCACAAAAAAG
TCCTGCCCTCATCTGAGAATACTGTCTTTCCATATGGCTAAGTGTGGCCCCACCACCCTCTCTGCCTCCCGGGAC
ATTGATTGGTCCTGTCTTGGGCAGGTCTAGTGAGCTGTAGAATTGAATCAATGTGAACTCAGGGAACTGGGGAAG
GCTGAGCCTCCTCTTTGGTGTTGCGGTAAGATAACCGACAGGGCTGGTGAAAGTCCCCAGATGGCAGGATATTTG
GTTTCAGAGTAAGGACTAGGTGCACCACCATGACTGACTATCAATCAAAATGTTTGTAACTTAAAATTTTTAATG
AAGGATAATGAATATTTTA

FIGURE 234

MTGERPSTALPDRRWGPRILGFWGGCRVWVFAAIFLLLSLAASWSKAENDFGLVQPLVTMEQLLWVSGRQIGSVD
TFRIPLITATPRGTLLAFAEARKMSSSDEGAKFIALRRSMDQGSTWSPTAFIVNDGDVPDGLNLGAVVSDVETGV
VFLFYSLCAHKAGCQVASTMLVWSKDDGVSWSTPRNLSLDIGTEVFAPGPGSGIQKQREPRKGRLIVCGHGTLER
DGVFCLLSDDHGASWRYGSGVSGIPYGQPKQENDFNPDECQPYELPDGSVVINARNQNNYHCHCRIVLRSYDACD
TLRPRDVTFDPELVDPVVAAGAVVTSSGIVFFSNPAHPEFRVNLTLRWSFSNGTSWRKETVQLWPGPSGYSSLAT
LEGSMDGEEQAPQLYVLYEKGRNHYTESISVAKISVYGTL

FIGURE 235

GCTCGTGGGTTTTCCGTGAAGTCGCGGTGCAGCGGTGGGCGGC**<u>ATG</u>**TCTGTGGCCGGTGGGGAGATTCGTGGGGA
CACGGGGGGAGAGGACACTGCTGCTCCCGGCCGGTTCAGCTTCAGCCCGGAGCCCACGCTCGAGGACATCCGCCG
CCTCCATGCTGAGTTTGCTGCGGAACGAGACTGGGAACAGTTCCATCAGCCTCGGAATCTCCTCCTGGCCTTGGT
TGGGGAAGTGGGGGAGCTGGCAGAACTCTTTCAGTGGAAAACCGATGGGGAACCTGGCCCCCAAGGCTGGTCCCC
CAGGGAACGGGCAGCCCTTCAAGAGGAGCTTAGTGACGTCCTCATCTACCTGGTGGCATTAGCAGCCCGCTGCCG
TGTGGATCTGCCGCTAGCAGTGCTCTCCAAAATGGACATCAACCGGCGACGCTACCCAGCCCATCTGGCCCGCAG
CTCTTCCCGCAAGTATACAGAATTGCCCCATGGGGCCATCTCTGAAGACCAGGCTGTGGGGCCTGCGGACATTCC
CTGTGACTCCACAGGCCAGACCTCAACC**<u>TAG</u>**AAAGATGGCCACAGGACTTGCAACTCAGGGTGGTGTCTGAAGAG
CAGAGAGTGGCCTGGCCCTGGAGCCTTTTTCTAGTCTTTTCAGAATAGATCATGGGCCTGAGGCCTCCACTTCTT
GAGGTCTGAGGCCCAGCAGCCTCTAGAAGGTAGCCTCCTGGTGTTTGTTCTCCCAGTAAAATGGTTTTGGGCGAT
AACTTCTAGATTATTCCTGGATGGCCAGGGAGGCTCTCTGTCTCAGCAGGTGATGACGGGGGTACCAGGGGTGCC
TCTGAGACCCATTCTCGTGTTTCCCTGTTGTACCTTTTGCCTGCAGGGCAGAGAGATCTGGTTTCTAGCAAATTC
CCAGTAGGATGTCATGTAAGTTCCTTCCCCCTCTTAGAGATTGAAGGCTGTAAGAGTCCAGATGGTGGAGCCAGG
CTGTCTGGGTTCAAATGCCATCTTTGACACTTGCAAGCTAAATGACATTACTCAAATTAATCGTTCTGCACTTCA
GCTTCCTTGTCTATCAAATAAAAAGAATAGTACCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 236

MSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRRLHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKT
DGEPGPQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDINRRRYPAHLARSSSRKYTELPHGAIS
EDQAVGPADIPCDSTGQTST

FIGURE 237

GTGGAATTC**<u>ATG</u>**GCATCTACTTCGTATGACTATTGCAGAGTGCCCATGGAAGACGGGGATAAGCGCTGTAAGCTT
CTGCTGGGGATAGGAATTCTGGTGCTCCTGATCATCGTGATTCTGGGGGTGCCCTTGATTATCTTCACCATCAAG
GCCAACAGCGAGGCCTGCCGGGACGGCCTTCGGGCAGTGATGGAGTGTCGCAATGTCACCCATCTCCTGCAACAA
GAGCTGACCGAGGCCCAGAAGGGCTTTCAGGATGTGGAGGCCCAGGCCGCCACCTGCAACCACACTGTGATGGCC
CTAATGGCTTCCCTGGATGCAGAGAAGGCCCAAGGACAAAAGAAAGTGGAGGAGCTTGAGGGAGAGATCACTACA
TTAAACCATAAGCTTCAGGACGCGTCTGCAGAGGTGGAGCGACTGAGAAGAGAAAACCAGGTCTTAAGCGTGAGA
ATCGCGGACAAGAAGTACTACCCCAGCTCCCAGGACTCCAGCTCCGCTGCGGCGCCCCAGCTGCTGATTGTGCTG
CTGGGCCTCAGCGCTCTGCTGCAG**<u>TGA</u>**GATCCCAGGAAGCTGGCACATCTTGGAAGGTCCGTCCTGCTCGGCTTT
TCGCTTGAACATTCCCTTGATCTCATCAGTTCTGAGCGGGTCATGGGGCAACACGGTTAGCGGGGAGAGCACGGG
GTAGCCGGAGAAGGGCCTCTGGAGCAGGTCTGGAGGGGCCATGGGGCAGTCCTGGGTGTGGGGACACAGTCGGGT
TGACCCAGGGCTGTCTCCCTCCAGAGCCTCCCTCCGGACAATGAGTCCCCCCTCTTGTCTCCCACCCTGAGATTG
GGCATGGGGTGCGGTGTGGGGGGCATGTGCTGCCTGTTGTTATGGGTTTTTTTTGCGGGGGGGGTTGCTTTTTTC
TGGGGTCTTTGAGCTCCAAAAAATAAACACTTCCTTTGAGGGAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAA

FIGURE 238

MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQELT
EAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIAD
KKYYPSSQDSSSAAAPQLLIVLLGLSALLQ

FIGURE 239

ATGGCGGCCTCAGCAGCGCGAGGTGCTGCGGCGCTGCGTAGAAGTATCAATCAGCCGGTTGCTTTTGTGAGAAGA
ATTCCTTGGACTGCGGCGTCGAGTCAGCTGAAAGAACACTTTGCACAGTTCGGCCATGTCAGAAGGTGCATTTTA
CCTTTTGACAAGGAGACTGGCTTTCACAGAGGTTTGGGTTGGGTTCAGTTTTCTTCAGAAGAAGGACTTCGGAAT
GCACTACAACAGGAAAATCATATTATAGATGGAGTAAAGGTCCAGGTTCACACTAGAAGGCCAAAACTTCCGCAA
ACATCTGATGATGAAAAGAAAGATTTT**TGA**

FIGURE 240

MAASAARGAAALRRSINQPVAFVRRIPWTAASSQLKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRN
ALQQENHIIDGVKVQVHTRRPKLPQTSDDEKKDF

FIGURE 241

GGCTCTTTTAAATGACCCCAGGCGTCGTGTATTGAATCCTAGACTCACGTCCGTCTCGCCGGCGCCCGAGCCAGT
CCGCGCGCACCGCGTCTGCGTCCCCGAAAGCCCCGCCCGCAAGGGCTGCCCTGCCTACCTGGTCTCCGACGTGCT
CGTCTGGAGGGCGGTGCGAGGGGCCGAGCCGACGAG**<u>ATG</u>**TTCTTGCTGCCTCTTCCGGCTGCGGGGCGAGTAGTC
GTCCGACGTCTGGCCGTAGTACGTTCTGGGAGCCGGAGTCTCTCCACCGCAGACATGACGAAGGGCCTTGTTTTA
GGAATCTATTCCAAAGAAAAAGAAGATGATGTGCCACAGTTCACAAGTGCAGGAGAGAATTTTGATAAATTGTTA
GCTGGAAAGCTGAGAGAGACTTTGAACATATCTGGACCACCTCTGAAGGCAGGGAAGACTCGAACCTTTTATGGT
CTGCATCAGGACTTCCCCAGCGTGGTGCTAGTTGGCCTCGGCAAAAAGGCAGCTGGAATCGACGAACAGGAAAAC
TGGCATGAAGGCAAAGAAAACATCAGAGCTGCTGTTGCAGCGGGGTGCAGGCAGATTCAAGACCTGGAGCTCTCG
TCTGTGGAGGTGGATCCCTGTGGAGACGCTCAGGCTGCTGCGGAGGGAGCGGTGCTTGGTCTCTATGAATACGAT
GACCTAAAGCAAAAAAAGAAGATGGCTGTGTCGGCAAAGCTCTATGGAAGTGGGGATCAGGAGGCCTGGCAGAAA
GGAGTCCTGTTTGCTTCTGGGCAGAACTTGGCACGCCAATTGATGGAGACGCCAGCCAATGAGATGACGCCAACC
AGATTTGCCGAAATTATTGAGAAGAATCTCAAAAGTGCTAGTAGTAAAACCGAGGTCCATATCAGACCCAAGTCT
TGGATTGAGGAACAGGCAATGGGATCATTCCTCAGTGTGGCCAAAGGATCTGACGAGCCCCCAGTCTTCTTGGAA
ATTCACTACAAAGGCAGCCCCAATGCAAACGAACCACCCCTGGTGTTTGTTGGGAAAGGAATTACCTTTGACAGT
GGTGGTATCTCCATCAAGGCTTCTGCAAATATGGACCTCATGAGGGCTGACATGGGAGGAGCTGCAACTATATGC
TCAGCCATCGTGTCTGCTGCAAAGTTAAATTTGCCCATTAATATTATAGGTCTGGCCCCTCTTTGTGAAAATATG
CCCAGCGGCAAGGCCAACAAGCCGGGGGATGTTGTTAGAGCCAAAAACGGGAAGACCATCCAGGTTGATAACACT
GATGCTGAGGGGAGGCTCATACTGGCTGATGCGCTCTGTTACGCACACACGTTTAACCCGAAGGTCATCCTCAAT
GCCGCCACCTTAACAGGTGCCATGGATGTAGCTTTGGGATCAGGTGCCACTGGGGTCTTTACCAATTCATCCTGG
CTCTGGAACAAACTCTTCGAGGCCAGCATTGAAACAGGGGACCGTGTCTGGAGGATGCCTCTCTTCGAACATTAT
ACAAGACAGGTTGTAGATTGCCAGCTTGCTGATGTTAACAACATTGGAAAATACAGATCTGCAGGAGCATGTACA
GCTGCAGCATTCCTGAAAGAATTCGTAACTCATCCTAAGTGGGCACATTTAGACATAGCAGGCGTGATGACCAAC
AAAGATGAAGTTCCCTATCTACGGAAAGGCATGACTGGGAGGCCCACAAGGACTCTCATTGAGTTCTTACTTCGT
TTCAGTCAAGACAATGCT**<u>TAG</u>**TTCAGATACTCAAAAATGTCTTCACTCTGTCTTAAATTGGACAGTTGAACTTAA
AAGGTTTTTGAATAAATGGATGAAAATCTTTTAACGGAGACAAAGGATGGTATTTAAAAATGTAGAACACAATGA
AATTTGTATGCCTTGATTTTTTTTTCATTTCACACAAAGATTTATAAAGGTAAAGTTAATATCTTACTTGATAAG
GATTTTTAAGATACTCTATAAATGATTAAAATTTTTAGAACTTCCTAATCACTTTTCAGAGTATATGTTTTTCAT
TGAGAAGCAAAATTGTAACTCAGATTTGTGATGCTAGGAACATGAGCAAACTGAAAATTACTATGCACTTGTCAG
AAACAATAAATGCAACTTGTTGTGAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 242

MFLLPLPAAGRVVVRRLAVVRSGSRSLSTADMTKGLVLGIYSKEKEDDVPQFTSAGENFDKLLAGKLRETLNISG
PPLKAGKTRTFYGLHQDFPSVVLVGLGKKAAGIDEQENWHEGKENIRAAVAAGCRQIQDLELSSVEVDPCGDAQA
AAEGAVLGLYEYDDLKQKKKMAVSAKLYGSGDQEAWQKGVLFASGQNLARQLMETPANEMTPTRFAEIIEKNLKS
ASSKTEVHIRPKSWIEEQAMGSFLSVAKGSDEPPVFLEIHYKGSPNANEPPLVFVGKGITFDSGGISIKASANMD
LMRADMGGAATICSAIVSAAKLNLPINIIGLAPLCENMPSGKANKPGDVVRAKNGKTIQVDNTDAEGRLILADAL
CYAHTFNPKVILNAATLTGAMDVALGSGATGVFTNSSWLWNKLFEASIETGDRVWRMPLFEHYTRQVVDCQLADV
NNIGKYRSAGACTAAAFLKEFVTHPKWAHLDIAGVMTNKDEVPYLRKGMTGRPTRTLIEFLLRFSQDNA

FIGURE 243

CCGCTGTTATACGTCACTTCCACGGCTCAGCGTCAGGGAGGAGAGAGA**ATG**TCTTTTCGAGGCGGAGGTCGTGGA
GGCTTTAATCGAGGTGGTGGAGGTGGCGGCTTCAACCGAGGCGGCAGCAGCAACCACTTCCGAGGTGGAGGCGGC
GGTGGAGGCGGCGGCAATTTCAGAGGCGGCGGCAGGGGAGGATTTGGACGAGGGGGTGGCCGCGGAGGCTTTAAC
AAAGGCCAAGACCAAGGACCTCCAGAACGTGTAGTCTTATTAGGAGAGTTCCTGCATCCCTGTGAAGATGACATA
GTTTGTAAATGTACCACAGATGAAAATAAGGTGCCTTATTTCAATGCTCCTGTTTACTTAGAAAACAAAGAACAA
ATTGGAAAAGTGGATGAAATATTTGGACAACTCAGAGATTTTTATTTTTCAGTTAAGTTGTCAGAAAACATGAAG
GCTTCATCCTTTAAAAAACTACAGAAGTTTTATATAGACCCATATAAGCTGCTGCCACTGCAGAGGTTTTTACCT
CGACCTCCAGGTGAGAAAGGACCTCCAAGAGGTGGTGGCAGGGGAGGCCGAGGAGGAGGAAGAGGAGGAGGTGGC
AGAGGTGGTGGCAGAGGCGGTGGTTTTAGAGGTGGAAGAGGAGGTGGAGGTGGGGGCTTCAGAGGAGGAAGAGGT
GGTGGTTTCAGAGGGAGAGGACAT**TAA**GTGAAACAGTTGACAGACATCACCAGTTGACTTCTGCATTAACCTGCA
TGATCTGTTTCTACTATGGATTGGAAACTTGTTTCTTGAACAAGTCTTGAAGATCTTGGTCATTTTATGACAATG
GATCTAAAATGTCAGCATCATGCAAAGTGCAACGGAATAGTGAATTTTGCTCTAAAAGAGCATGAACAAGTCTTT
CTAATGTTTTGTACAGTGCCTGGCACTCTGTGGGTGCTCAATAAATGGATAGGAGTTTTCATTTGAAGCATATTT
GAATTTTTAAAATAAAGTGTTTATTCCCTTAAAAAAAAAAAAAAA

FIGURE 244

MSFRGGGRGGFNRGGGGGGFNRGGSSNHFRGGGGGGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGE
FLHPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLRDFYFSVKLSENMKASSFKKLQKFYIDPYK
LLPLQRFLPRPPGEKGPPRGGGRGGRGGGRGGGGRGGGRGGGFRGGRGGGGGGFRGGRGGGFRGRGH

FIGURE 245

CTGGAAGGAGTC**ATG**GCGGATGGTCAGGTGGCGGAACTGCTGCTCCGGCGGCTGGAGGCGTCTGATGGCGGCCTG
GACAGCGCCGAGTTGGCGGCTGAGCTGGGCATGGAGCACCAGGCGGTGGTGGGCGCCGTGAAGAGCCTTCAGGCG
CTGGGCGAGGTCATCGAGGCTGAACTTCGGTCCACCAAGCACTGGGAGCTTACTGCGGAGGGCGAGGAGATTGCC
CGGGAGGGCAGCCATGAGGCCCGTGTGTTTCGAAGCATTCCCCCAGAGGGCCTGGCCCAGAGCGAGCTTATGCGA
CTGCCCAGTGGCAAAGTGGGCTTCAGCAAGGCCATGTCCAACAAGTGGATTCGGGTGGACAAGAGTGCGGCTGAC
GGGCCCCGGGTGTTCCGAGTGGTGGACAGCATGGAGGATGAGGTGCAGCGGCGGCTCCAGCTGGTCCGGGGGGGA
CAGGCTGAGAAGCTGGGGGAGAAGGAGAGGAGCGAGCTGAGGAAGAGGAAGCTGTTGGCTGAAGTGACTCTGAAG
ACCTACTGGGTGAGCAAAGGCAGTGCCTTTAGTACCAGCATCTCCAAGCAAGAGACAGAGCTGAGCCCAGAGATG
ATCTCCAGTGGCTCTTGGCGGGACCGGCCCTTCAAGCCCTACAACTTCTTGGCCCACGGTGTCCTCCCCGACAGC
GGCCACCTTCACCCGCTGCTCAAGGTCCGCTCCCAGTTCCGACAGATCTTCCTGGAGATGGGGTTCACCGAGATG
CCGACTGATAACTTCATTGAGAGCTCCTTCTGGAACTTTGACGCCCTCTTCCAGCCCCAGCAGCACCCAGCCCGT
GACCAGCACGACACCTTCTTCCTTCGAGATCCAGCGGAGGCCCTGCAGCTCCCAATGGACTATGTCCAGCGGGTC
AAGCGGACCCACTCTCAGGGCGGCTACGGCTCACAGGGGTACAAGTATAACTGGAAGCTGGACGAGGCCCGGAAA
AACCTACTGCGAACCCACACCACATCAGCCAGCGCCCGTGCGCTCTACCGCCTTGCCCAGAAGAAGCCCTTCACT
CCGGTCAAGTACTTCTCCATCGACCGCGTATTCCGGAATGAGACCCTGGACGCCACGCACCTGGCTGAGTTCCAC
CAGATCGAGGGCGTGGTGGCGGATCATGGTCTCACCTTGGGCCACCTCATGGGCGTTCTGCGGGAGTTCTTCACC
AAGCTGGGTATCACGCAACTCCGCTTCAAGCCAGCCTACAACCCATACACAGAGCCCAGCATGGAGGTGTTCAGC
TACCACCAAGGCCTGAAGAAGTGGGTGGAGGTCGGAAACTCGGGGGTCTTCCGTCCAGAGATGCTGCTGCCCATG
GGGCTTCCCGAGAACGTGTCGGTCATTGCCTGGGGCCTCTCCCTGGAGCGCCCAACGATGATCAAATATGGCATC
AACAATATCCGGGAGCTGGTGGGCCACAAGGTGAACCTGCAGATGGTGTATGACAGTCCCCTGTGCCGCCTGGAT
GCCGAGCCGAGGCCCCCTCCCACACAGGAGGCTGCG**TGA**CATGGGCCACTCTAGGACAGGTCATCCTCCCCGAGT
CCCTGCTGCTGCGCTCCTTTGCATCCCTGGCCAGTGACCTTGTATTTATGAGGCTCTGTGAGGCCAGCCCCCACC
TTCCTCTTTCCCACCTGTCCCAGGACCAGAATCCCAGGGACAGAGGACTGGGTAGCAGGTTCCTTCTGTTGTCCT
GTGTGGTGTGTCTACTGTGAGGGTGGGCCCTGAGGAGACCTGTGGGCCACCTATTGTCTAATAAAGTGGGCAGTT
GCCCCCA

FIGURE 246

MADGQVAELLLRRLEASDGGLDSAELAAELGMEHQAVVGAVKSLQALGEVIEAELRSTKHWELTAEGEEIAREGS
HEARVFRSIPPEGLAQSELMRLPSGKVGFSKAMSNKWIRVDKSAADGPRVFRVVDSMEDEVQRRLQLVRGGQAEK
LGEKERSELRKRKLLAEVTLKTYWVSKGSAFSTSISKQETELSPEMISSGSWRDRPFKPYNFLAHGVLPDSGHLH
PLLKVRSQFRQIFLEMGFTEMPTDNFIESSFWNFDALFQPQQHPARDQHDTFFLRDPAEALQLPMDYVQRVKRTH
SQGGYGSQGYKYNWKLDEARKNLLRTHTTSASARALYRLAQKKPFTPVKYFSIDRVFRNETLDATHLAEFHQIEG
VVADHGLTLGHLMGVLREFFTKLGITQLRFKPAYNPYTEPSMEVFSYHQGLKKWVEVGNSGVFRPEMLLPMGLPE
NVSVIAWGLSLERPTMIKYGINNIRELVGHKVNLQMVYDSPLCRLDAEPRPPPTQEAA

FIGURE 247

CTATCTGAAATGCAGAGATTAAGCCAAATACCTGATGTATTGTGAAAGCCACTGATTTTAAGAATGGAGAGAAAG
GGATTTTTTACTGCATCCCTCTGTATGAATATGAAATCAGAGACCAGGGCATGATGTTGCTAGGATTAGAGCCTC
TCAGTCTGGCCTCTTCACCCAAGTGCAAGAACTCAGTCTCTTACTGTTCAAAGAAAGAATCTTAACAGTTGAATT
ATGGAGGGAAATTCCCTTTTGCCCCAAGCGTTTCTATATTTAAAGCAATATCCCAGGAGAATATGTCAGACTTAG
GATGATACCTTCAGCCACTTGAAGAAGAAATAGAAGGCGCTCATTCCAATATAGTCTTTATTTCCCATTCAGATA
CAGGTTGAGCATCCCTAATCTGAACAGTTAAAACCCCCAAATGCCCCAAAATCCAAACCTTCCTGAACGCTATGA
CACCATGAGTGGAAAATTCCACACCTAACAAACACATTTGCTTTCTTATGGTTCAATGTACACAAACTGTTTTAT
ATAGAAAATGATTTCAAATATCATAAAATTACCTTCAGGCTATGTGCATAAAGTATATATGAGCCATAA**ATG**AAT
TTTGTGTTTAGACTTTGTGTCCATCCCCAAGATCTCTCATTATATATATA

FIGURE 248

MNFVFRLCVHPQDLSLY

FIGURE 249

CGAAAAAAGAGGGGAAGAGTATTAAAGACCATTTCTGGCTGGGCAGGGCACTCTCAGCAGCTCAACTGCCCAGCG
TGACCAGTGGCCACCTCTGCAGTGTCTTCCACAACCTGGTCTTGACTCGTCTGCTGAACAAATCCTCTGACCTCA
GGCCGGCTGTGAACGTAGTTCCTGAGAGATAGCAAAC**ATG**CCCAACAGTGAGCCCGCATCTCTGCTGGAGCTGTT
CAACAGCATCGCCACACAAGGGGAGCTCGTAAGGTCCCTCAAAGCGGGAAATGCGTCAAAGGATGAAATTGATTC
TGCAGTAAAGATGTTGGTGTCATTAAAAATGAGCTACAAAGCTGCCGCGGGGGAGGATTACAAGGCTGACTGTCC
TCCAGGGAACCCAGCACCTACCAGTAATCATGGCCCAGATGCCACAGAAGCTGAAGAGGATTTTGTGGACCCATG
GACAGTACAGACAAGCAGTGCAAAAGGCATAGACTACGATAAGCTCATTGTTCGGTTTGGAAGTAGTAAAATTGA
CAAAGAGCTAATAAACCGAATAGAGAGAGCCACCGGCCAAAGACCACACCACTTCCTGCGCAGAGGCATCTTCTT
CTCACACAGAGATATGAATCAGGTTCTTGATGCCTATGAAAATAAGAAGCCATTTTATCTGTACACGGGCCGGGG
CCCCTCTTCTGAAGCAATGCATGTAGGTCACCTCATTCCATTTATTTTCACAAAGTGGCTCCAGGATGTATTTAA
CGTGCCCTTGGTCATCCAGATGACGGATGACGAGAAGTATCTGTGGAAGGACCTGACCCTGGACCAGGCCTATGG
CGATGCTGTTGAGAATGCCAAGGACATCATCGCCTGTGGCTTTGACATCAACAAGACTTTCATATTCTCTGACCT
GGACTACATGGGGATGAGCTCAGGTTTCTACAAAAATGTGGTGAAGATTCAAAAGCATGTTACCTTCAACCAAGT
GAAAGGCATTTTCGGCTTCACTGACAGCGACTGCATTGGGAAGATCAGTTTCCTGCCATCCAGGCTGCTCCCTC
CTTCAGCAACTCATTCCCACAGATCTTCCGAGACAGGACGGATATCCAGTGCCTTATCCCATGTGCCATTGACCA
GGATCCTTACTTTAGAATGACAAGGGACGTCGCCCCCAGGATCGGCTATCCTAAACCAGCCCTGTTGCACTCCAC
CTTCTTCCCAGCCCTGCAGGGCGCCCAGACCAAAATGAGTGCCAGCGACCCAAACTCCTCCATCTTCCTCACCGA
CACGGCCAAGCAGATCAAAACCAAGGTCAATAAGCATGCGTTTTCTGGAGGGAGAGACACCATCGAGGAGCACAG
GCAGTTTGGGGGCAACTGTGATGTGGACGTGTCTTTCATGTACCTGACCTTCTTCCTCGAGGACGACGACAAGCT
CGAGCAGATCAGGAAGGATTACACCAGCGGAGCCATGCTCACCGGTGAGCTCAAGAAGGCACTCATAGAGGTTCT
GCAGCCCTTGATCGCAGAGCACCAGGCCCGGCGCAAGGAGGTCACGGATGAGATAGTGAAAGAGTTCATGACTCC
CCGGAAGCTGTCCTTCGACTTTCAG**TAG**CACTCGTTTTACATATGCTTATAAAAGAAGTGATGTATCAGTAATGT
ATCAATAATCCCAGCCCAGTCAAAGCACCGCCACCTGTAGGCTTCTGTCTCATGGTAATTACTGGGCCTGGCCTC
TGTAAGCCTGTGTATGTTATCAATACTGTTTCTTCCTGTGAGTTCCATTATTTCTATCTCTTATGGGCAAAGCAT
TGTGGGTAATTGGTGCTGGCTAACATTGCATGGTCGGATAGAGAAGTCCAGCTGTGAGTCTCTCCCCAAAGCAGC
CCCACAGTGGAGCCTTCGGCTGGAAGTCCATGGGCCACCCTGTTCTTGTCCATGGAGGACTTCCGAGGGTTCCAA
GTATACTCTTAAGACCCACTCTGTTTAAAAATATATATTCTATGTATGCGTATATGGAATTGAAATGTCATTATT
GTAACCTAGAAAGTGCTTTGAAATATTGATGTGGGGAGGTTTATTGAGCACAAGATGTATTTCAGCCCATGCCCC
CTCCCAAAAAGAAATTGATAAGTAAAAGCTTCGTTATACATTTGACTAAGAAATCACCCAGCTTTAAAGCTGCTT
TTAACAATGAAGATTGAACAGAGTTCAGCAATTTTGATTAAATTAAGACTTGGGGGTGAAACTTTCCAGTTTACT
GAACTCCAGACCATGCATGTAGTCCACTCCAGAAATCATGCTCGCTTCCCTTGGCACACCAGTGTTCTCCTGCCA
AATGACCCTAGACCCTCTGTCCTGCAGAGTCAGGGTGGCTTTTCCCCTGACTGTGTCCGATGCCAAGGAGTCCTG
GCCTCCGCAGATGCTTCATTTTGACCCTTGGCTGCAGTGGAAGTCAGCACAGAGCAGTGCCCTGGCTGTGTCCTG
GACGGGTGGACTTAGCTAGGGAGAAAGTCGAGGCAGCAGCCCTCGAGGCCCTCACAGATGTCTAGGCAGGCCTCA
TTTCATCACGCAGCATGTGCAGGCCTGGAAGAGCAAAGCCAAATCTCAGGGAAGTCCTTGGTTGATGTATCTGGG
TCTCCTCTGGAGCACTCTGCCCTCCTGTCACCCAGTAGAGTAAATAAACTTCCTTGGCTCCTAAAAAA

FIGURE 250

MPNSEPASLLELFNSIATQGELVRSLKAGNASKDEIDSAVKMLVSLKMSYKAAAGEDYKADCPPGNPAPTSNHGP
DATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAY
ENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIAC
GFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDR
TDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH
AFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRK
EVTDEIVKEFMTPRKLSFDFQ

FIGURE 251

CACCGCGCAAGCGCATCCTGGCCTTTCTTCAGTCCCCACGTGCGATCCTTCCCGGCAACTTTTTCGAGAAAAATG
CCCAAATTCAAGGCGGCCCGTGGGGTGGGGGGTCAGGAAAAACATGCGCCCCTGGCCGATCAGATCCTGGCTGGG
AATGCGGTGCGGGCGGGGGTCCGGGAGAAGCGGCGGGGTCGCGGGACAGGAGAAGCGGAGGAAGAGTATGTGGGG
CCCCGGCTGAGCCGACGGATTTTGCAGCAAGCACGGCAGCAACAGGAGGAACTCGAGGCCGAGCATGGGACTGGG
GACAAGCCCGCGGCGCCGCGGGAACGCACCACGCGGCTGGGTCCAAGAATGCCTCAGGATGGATCAGATGACGAG
GACGAGGAGTGGCCCACCCTGGAGAAGGCTGCCACAATGACAGCAGCGGGCCATCATGCAGAGGTGGTTGTGGAC
CCTGAGGATGAGCGTGCCATAGAGATGTTC**ATG**AACAAGAACCCTCCTGCCAGGCGCACCCTGGCTGACATCATC
ATGGAGAAGCTGACTGAGAAGCAGACAGAGGTTGAGACAGTCATGTCAGAGGTGTCGGGCTTCCCTATGCCCCAG
CTGGACCCCCGGGTCCTAGAAGTGTACAGGGGGGTCCGGGAGGTATTATCTAAGTACCGCAGTGGAAAACTGCCC
AAGGCATTTAAGATCATCCCTGCACTCTCCAACTGGGAGCAAATCCTCTACGTCACAGAGCCGGAGGCCTGGACT
GCAGCTGCCATGTACCAGGCCACCAGGATTTTTGCCTCTAACCTGAAGGAACGCATGGCCCAGCGCTTCTACAAC
CTTGTCCTGCTCCCTCGAGTACGAGATGACGTTGCTGAATACAAACGACTCAACTTCCATCTCTACATGGCTCTC
AAGAAGGCCCTTTTCAAACCTGGAGCCTGGTTCAAAGGGATCCTGATTCCACTGTGCGAGTCTGGCACTTGTACC
CTCCGGGAAGCCATCATTGTGGGTAGCATCATCACCAAGTGCTCCATCCCTGTGTTGCACTCCAGTGCGGCCATG
CTGAAAATTGCTGAGATGGAATACAGCGGTGCCAACAGCATCTTCCTGCGACTGCTGCTGGATAAGAAGTATGCA
CTGCCTTACCGGGTGCTGGATGCCCTAGTCTTCCACTTCCTGGGGTTCCGGACAGAGAAGCGTGAACTGCCTGTG
CTGTGGCACCAGTGCCTCCTGACTTTGGTCCAGCGCTACAAGGCCGACTTGGCCACAGACCAGAAAGAGGCCCTC
TTAGAACTGCTCCGGCTGCAGCCCCATCCACAGCTATCGCCCGAAATCAGGCGTGAGCTTCAGAGTGCAGTCCCC
CGCGATGTGGAAGATGTTCCCATCACCGTGGAG**TGA**GGAAAACAGTCAGCTGTCCTGGCCAAAGGGGTTTGGAAG
GACACCAAGACCCCCGTTGGTGACTGAAGATGACACTGAGCTTTAATGGCTGAAGACCCAGATCAGGGCAGTGAC
AGATCACAGGGACATCTGTGGCTCCCAGTCCAGGACAGGAAGGACTGAGGGTCTGGCTGGTTCCCTCTTCCATTC
TAGGCCCTTATCCCTGTTTAGTTCTGAGAGCCAACTTGAGATACCATATGCTAGCATTCCCAGTCCCCAGCTGGG
GCTTGGTGTGAGTACTTTTTCTATGGCTATTGTGTCAGGTCACTGTGGATAAAGGCAAAGACAGATATTTATTGA
AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MNKNPPARRTLADIIMEKLTEKQTEVETVMSEVSGFPMPQLDPRVLEVYRGVREVLSKYRSGKLPKAFKIIPALS
NWEQILYVTEPEAWTAAAMYQATRIFASNLKERMAQRFYNLVLLPRVRDDVAEYKRLNFHLYMALKKALFKPGAW
FKGILIPLCESGTCTLREAIIVGSIITKCSIPVLHSSAAMLKIAEMEYSGANSIFLRLLLDKKYALPYRVLDALV
FHFLGFRTEKRELPVLWHQCLLTLVQRYKADLATDQKEALLELLRLQPHPQLSPEIRRELQSAVPRDVEDVPITV
E

FIGURE 253

TGGAGACTCACCAATCTATCTCCCTACATCAAGGTCCTCTTAGAAGTCACCTTTCTGCTGTATAATACAGCGTAA
CCCTACTTGAGACATTTCCATTTAAATTGCTCTGTTCCACATGTTTCATCCTGTCCTTGCTGTAACTGTGTAGGT
GGGTGACAACATTTTCGAACTGTATATTTGTCACCTCTGTTAGTCTATCTCTAAGAACACAGCCAATAAGACATC
ACTTGACAAGCCATTACCTTATTGACCAAGACTATTTTGTGAATCAAATGCAATGTGACTTGAAAATCAAATCGT
TTCAATGGTCATTTAAGTTGTTAATTTTAAAAAATGGTCATTTCAGCTTG**ATG**CATAAGAGCGTTCTTTGCAGGA
ACTTCATTTTTGACTACAAAGGCTTTGAATTTTATTTTGCTGCTTGCAGTAATTTTTGTTTTCTTTTTCTTCCAG
GGTATATGAGAAAATAT**TGA**CTCCTATCTGGCCTTCATCAACTGACCTCGAAAAGCCTCATGAGATGCTTTTTCT
TAATGTGATTTTGTTCAGCCTCACTGTTTTTACCTTAATTTCAACTGCCCACACACTTGACCGTGCAGTCAGGAG
TGACTGGCTTCTCCTTGTCCTCATTTATGCATGTTTGGAGGAGCTGATTCCTGAACTCATATTTAAACTCTACTG
CCAGGGAAATGCTACATTATTTTTCTAATTGGAAGTATAATTAGAGTGATGTTGGTAGGGTAGAAAAAGAGGGAG
TCACTTGATGCTTTCAGGTTAATCAGAGCTATGGGTGCTACAGGCTTGTCTTTCTAAGTGACATATTCTTATCTA
ATTCTCAGATCAGGTTTTGAAAGCTTTGGGGGTCTTTTTAGATTTTAATCCCTACTTTCTTTATGGTACAAATAT
GTACAAAAGAAAAAGGTCTTATATTCTTTTACACAAATTTATAAATAAATTTTGAACTCCTTCTGTAAAAAAA

FIGURE 254

MHKSVLCRNFIFDYKGFEFYFAACSNFCFLFLPGYMRKY

FIGURE 255

ATGAGTGAGAACAATAAGAATTCCTTGGAGAGCAGCCTACGGCAACTAAAATGCCATTTCACCTGGAACTTGATG
GAGGGAGAAAACTCCTTGGATGATTTTGAAGACAAAGTATTTTACCGGACTGAGTTTCAGAATCGTGAATTCAAA
GCCACAATGTGCAACCTACTGGCCTATCTAAAGCACCTCAAAGGGCAAAACGAGGCAGCCCTGGAATGCTTACGT
AAAGCTGAAGAGTTAATCCAGCAAGAGCATGCTGACCAGGCAGAAATCAGAAGTCTGGTCACCTGGGGAAACTAT
GCCTGGGTCTACTATCACATGGGCCGACTCTCAGACGTTCAGATTTATGTAGACAAGGTGAAACATGTCTGTGAG
AAGTTTTCCAGTCCCTATAGAATTGAGAGTCCAGAGCTTGACTGTGAGGAAGGGTGGACACGGTTAAAGTGTGGA
GGAAACCAAAATGAAAGAGCGAAGGTGTGCTTTGAGAAGGCTCTGGAAAAGAAGCCAAAGAACCCAGAATTCACC
TCTGGACTGGCAATAGCAAGCTACCGTCTGGACAACTGGCCACCATCTCAGAACGCCATTGACCCTCTGAGGCAA
GCCATTCGGCTGAATCCTGACAACCAGTACCTTAAAGTCCTCCTGGCTCTGAAGCTTCATAAGATGCGTGAAGAA
GGTGAAGAGGAAGGTGAAGGAGAGAAGTTAGTTGAAGAAGCCTTGGAGAAAGCCCCAGGTGTAACAGATGTTCTT
CGCAGTGCAGCCAAGTTTTATCGAAGAAAAGATGAGCCAGACAAAGCGATTGAACTGCTTAAAAAGGCTTTAGAA
TACATACCAAACAATGCCTACCTGCATTGCCAAATTGGGTGCTGCTATAGGGCAAAAGTCTTCCAAGTAATGAAT
CTAAGAGAGAATGGAATGTATGGGAAAAGAAAGTTACTGGAACTAATAGGACACGCTGTGGCTCATCTGAAGAAA
GCTGATGAGGCCAATGATAATCTCTTCCGTGTCTGTTCCATTCTTGCCAGCCTCCATGCTCTAGCAGATCAGTAT
GAAGACGCAGAGTATTACTTCCAAAAGGAATTCAGTAAAGAGCTTACTCCTGTAGCGAAACAACTGCTCCATCTG
CGGTATGGCAACTTTCAGCTGTACCAAATGAAGTGTGAAGACAAGGCCATCCACCACTTTATAGAGGGTGTAAAA
ATAAACCAGAAATCAAGGGAGAAAGAAAAGATGAAAGACAAACTGCAAAAAATTGCCAAAATGCGACTTTCTAAA
AATGGAGCAGATTCTGAGGCTTTGCATGTCTTGGCATTCCTTCAGGAGCTGAATGAAAAAATGCAACAAGCAGAT
GAAGACTCTGAGAGGGGTTTGGAGTCTGGAAGCCTCATCCCTTCAGCATCAAGCTGGAATGGGGAATGA

FIGURE 256

MSENNKNSLESSLRQLKCHFTWNLMEGENSLDDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDKVKHVCEKFSSPYRIESPELDCEEGWTRLKCG
GNQNERAKVCFEKALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPDNQYLKVLLALKLHKMREE
GEEEGEGEKLVEEALEKAPGVTDVLRSAAKFYRRKDEPDKAIELLKKALEYIPNNAYLHCQIGCCYRAKVFQVMN
LRENGMYGKRKLLELIGHAVAHLKKADEANDNLFRVCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHL
RYGNFQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRLSKNGADSEALHVLAFLQELNEKMQQAD
EDSERGLESGSLIPSASSWNGE

FIGURE 257

TGAACTGAGCGGCCCCTGAGCTGACAGATACACTGCGCAGTGGAACGGCGAGCGAGCCGACGGGCGAGTGAGGGG
CGCAC**ATG**ATCACCTCGGCCGCTGGAATTATTTCTCTTCTGGATGAAGATGAACCACAGCTTAAGGAATTTGCAC
TACACAAATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATTTCCGAGTCCGTAGACAAAATAGAGGTTTTAT
ACGAAGATGAAGGTTTCCGGAGTCGGCAGTTTGCAGCCTTAGTGGCATCTAAAGTATTTTATCACCTGGGGGCTT
TTGAGGAGTCTCTGAATTATGCTCTTGGAGCAAGGGACCTCTTCAATGTCAATGATAACTCTGAATATGTGGAAA
CTATTATAGCAAAATGCATTGATCACTACACCAAACAATGTGTGGAAAATGCAGATTTGCCTGAAGGAGAAAAAA
AACCAATTGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTCCAGCGATGTCTAGATGATCACAAGTATAAAC
AGGCTATTGGCATTGCTCTGGAGACACGAAGACTGGACGTCTTTGAAAAGACCATACTGGAGTCGAATGATGTCC
CAGGAATGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGCAGAATAAACAGTTTCGGAATAAAGTACTAA
GAGTTCTAGTTAAAATCTACATGAACTTGGAGAAACCTGATTTCATCAATGTTTGTCAGTGCTTAATTTTCTTAG
ATGATCCTCAGGCTGTGAGTGATATCTTAGAGAAACTGGTAAAGGAAGACAACCTCCTGATGGCATATCAGATTT
GTTTTGATTTGTATGAAAGTGCTAGCCAGCAGTTTTTGTCATCTGTAATCCAGAATCTTCGAACTGTTGGCACCC
CTATTGCTTCTGTGCCTGGATCCACTAATACGGGTACTGTTCCGGGATCAGAGAAAGACAGTGACTCGATGGAAA
CAGAAGAAAAGACAAGCAGTGCATTTGTAGGAAAGACACCAGAAGCCAGTCCAGAGCCTAAGGACCAGACTTTGA
AAATGATTAAAATTTTAAGTGGTGAAATGGCTATTGAGTTACATCTGCAGTTCTTAATACGAAACAATAATACAG
ACCTCATGATTCTAAAAAACACAAAGGATGCAGTACGGAATTCTGTATGTCATACTGCAACCGTTATAGCAAACT
CTTTTATGCACTGTGGGACAACCAGTGACCAGTTTCTTAGAGATAATTTGGAATGGTTAGCCAGAGCCACTAACT
GGGCAAAATTTACTGCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGAAAAAGAAGCATTACAGTTAATGG
CAACATACCTTCCCAAGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGGAGGTCTCTATGCACTAGGTCTTA
TTCATGCCAATCATGGTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAGAACGCCAGCAATGATATCGTTA
GACACGGTGGCAGTCTGGGCCTTGGTTTGGCAGCCATGGGAACTGCACGTCAAGATGTTTATGATTTGCTAAAAA
CAAACCTTTATCAGGATGATGCAGTAACAGGGGAAGCAGCTGGCCTGGCCCTAGGTTTGGTTATGTTGGGCTCTA
AAAATGCTCAGGCTATTGAGGACATGGTTGGTTATGCACAAGAAACTCAACATGAGAAGATTCTGCGTGGTCTTG
CAGTTGGCATAGCTTTAGTAATGTATGGGAGGATGGAAGAGGCTGATGCTCTCATTGAATCTCTCTGTCGTGACA
AGGACCCAATTCTTCGAAGGTCTGGAATGTATACTGTAGCCATGGCTTATTGTGGCTCTGGTAACAACAAAGCAA
TTCGACGCCTGCTACATGTGGCTGTAAGTGATGTGAATGATGATGTCAGGAGTGCAGCAGTAGAATCACTTGGGT
TCATTCTATTCAGAACCCCTGAACAGTGCCCAAGTGTTGTCTCTTTGTTGTCAGAGAGTTACAACCCTCATGTGC
GCTACGGAGCTGCAATGGCCTTGGGGATATGCTGTGCTGGTACAGGAAACAAGGAAGCCATTAATTTGCTAGAAC
CAATGACAAACGACCCCGTGAACTACGTGAGGCAAGGGGCACTCATAGCTTCAGCTCTCATCATGATCCAGCAGA
CTGAAATCACTTGTCCAAAGGTGAATCAGTTCAGACAGCTGTATTCCAAAGTCATCAATGATAAGCATGATGATG
TCATGGCCAAGTTTGGCGCTATTCTGGCCCAGGGCATACTGGATGCAGGTGGTCATAATGTCACAATCTCCTTGC
AGTCCAGGACTGGGCATACTCATATGCCTTCTGTGGTTGGCGTCCTTGTATTTACCCAGTTTTGGTTCTGGTTTC
CTCTTTCACACTTCCTGTCATTGGCTTATACCCCTACCTGTGTCATTGGCCTTAACAAGGACTTAAAGATGCCGA
AAGTTCAGTATAAATCGAACTGTAAACCATCCACATTTGCATATCCTGCCCCTCTGGAAGTACCAAAAGAAAAAG
AAAAGGAAAAGGTTTCTACTGCTGTATTATCTATAACTGCCAAGGCTAAAAAGAAGGAAAAAGAAAAGGAAAAAA
AGGAGGAGGAGAAAATGGAAGTGGATGAGGCAGAGAAAAAGGAGGAAAAAGAGAAGAAAAAAGAACCTGAGCCAA
ACTTCCAGTTATTGGATAACCCAGCCCGAGTTATGCCTGCCCAGCTTAAGGTCCTAACCATGCCGGAGACCTGTA
GATACCAGCCTTTCAAACCACTCTCTATTGGAGGCATCATCATTCTGAAGGATACCAGTGAAGACATTGAGGAGC
TGGTGGAACCTGTGGCAGCACATGGCCCAAAAATCGAGGAGGAGGAACAAGAGCCAGAACCCCCAGAACCATTTG
AGTATATTGATGAT**TAA**GGACCAGAGGATCTCACTTGCTTATCTGAAGAAGATTGTCCAGGCTCATATTGGGAAT
GCTTATGAGGAAATTCATGCCGAGACCTGCTATTCAATGCATGTATCGTTGCCTCTGCACTGACCTGAAGAACCC
TGTCTCCAAGTCTTTGGTTGAAGAGAAGATATATGACTGTTGAGTGTGCTCTTTCACAGAACTTGGTTTTCAAAT
AAATATAAGATCTCCAGATGGACAAG

FIGURE 258

MITSAAGIISLLDEDEPQLKEFALHKLNAVVNDFWAEISESVDKIEVLYEDEGFRSRQFAALVASKVFYHLGAFE
ESLNYALGARDLFNVNDNSEYVETIIAKCIDHYTKQCVENADLPEGEKKPIDQRLEGIVNKMFQRCLDDHKYKQA
IGIALETRRLDVFEKTILESNDVPGMLAYSLKLCMSLMQNKQFRNKVLRVLVKIYMNLEKPDFINVCQCLIFLDD
PQAVSDILEKLVKEDNLLMAYQICFDLYESASQQFLSSVIQNLRTVGTPIASVPGSTNTGTVPGSEKDSDSMETE
EKTSSAFVGKTPEASPEPKDQTLKMIKILSGEMAIELHLQFLIRNNNTDLMILKNTKDAVRNSVCHTATVIANSF
MHCGTTSDQFLRDNLEWLARATNWAKFTATASLGVIHKGHEKEALQLMATYLPKDTSPGSAYQEGGGLYALGLIH
ANHGGDIIDYLLNQLKNASNDIVRHGGSLGLGLAAMGTARQDVYDLLKTNLYQDDAVTGEAAGLALGLVMLGSKN
AQAIEDMVGYAQETQHEKILRGLAVGIALVMYGRMEEADALIESLCRDKDPILRRSGMYTVAMAYCGSGNNKAIR
RLLHVAVSDVNDDVRSAAVESLGFILFRTPEQCPSVVSLLSESYNPHVRYGAAMALGICCAGTGNKEAINLLEPM
TNDPVNYVRQGALIASALIMIQQTEITCPKVNQFRQLYSKVINDKHDDVMAKFGAILAQGILDAGGHNVTISLQS
RTGHTHMPSVVGVLVFTQFWFWFPLSHFLSLAYTPTCVIGLNKDLKMPKVQYKSNCKPSTFAYPAPLEVPKEKEK
EKVSTAVLSITAKAKKKEKEKEKKEEEKMEVDEAEKKEEKEKKKEPEPNFQLLDNPARVMPAQLKVLTMPETCRY
QPFKPLSIGGIIILKDTSEDIEELVEPVAAHGPKIEEEEQEPEPPEPFEYIDD

FIGURE 259

CGCAAAGAGTAGTCAGTCCCTTCTTGGCTCTGCTGACACTCGAGCCCACATTCCATCACCTGCTCCCAATC**ATG**C
AGGTCTCCACTGCTGCCCTTGCCGTCCTCCTCTGCACCATGGCTCTCTGCAACCAGGTCCTCTCTGCACCACGTG
AGTCCATGTTGTTGTTGTGGGTATCACCACTCTCTGGCCATGGTTAGACCACATCAGTCTTTTTTTGCGGCCTGA
GAGCCCCGAAGAGAAAAGAAGGAAGTTCTTAAAGCGCTGCCAAACACCTTGGTCTTTTTCTTCACAACTTTTATT
TTTATCTCTAGAAGGGGTCTTAGCCCTCCTAGTCTCCAGTTGCTGCTGACACGCCGACCGCCTGCTGCTTCAGCT
ACACCTCCCGACAGATTCCACAGAATTTCATAGCTGACTACTTTGAGACGAGCAGCCAGTGCTCCAAGCCCAGTG
TCATCTTCCTAACCAAGAGAGGCCGGCAGGTCTGTGCTGACCCCAGTGAGGAGTGGGTCCAGAAATACGTCAGTG
ACCTGGAGCTGAGTGCC**TGA**GGGGTCCAGAAGCTTCGAGGCCCAGCGACCTCAGTGGGCCCAGTGGGGAGGAGCA
GGAGCCTGAGCCTTGGGAACATGCGTGTGACCTCTACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCC
ACACTGTGGGACTCTTCTTAACTTAAATTTTAATTTATTTATACTATTTAGTTTTTATAATTTATTTTTGATTTC
ACAGTGTGTTTGTGATTGTTTGCTCTGAGAGTTCCCCCTGTCCCCTCCACCTTCCCTCACAGTGTGTCTGGTGAC
AACCGAGTGGCTGTCATCGGCCTGTGTAGGCAGTGATGGCACCAAAGCCACCAGACTGACAAATGTGTGATCAGA
TGCTTTTGTTCAGGGCTGTGATCGGCCTGGGGAAATAATAAAGATGTTCTTTTAAACGGT

FIGURE 260

MQVSTAALAVLLCTMALCNQVLSAPLAADTPTACCFSYTSRQIPQNFIADYFETSSQCSKPSVIFLTKRGRQVCA
DPSEEWVQKYVSDLELSA

FIGURE 261

GAGAGAGAAGGAGAAGATAATATACTGAAAAGAAGAGGAGGAGGAGAGCGACGGGACGGGACGCGAGCGGGAGCG
CAGCCGCCCTCTCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCGAGGGGAGACGCCGTGA
CAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTCGGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGG
AGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCACTGGCTGCTCCAAAGCATCTTTTGTTGTGGAATGGTTATT
CCAGTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGG
AAAGAGAAAGAGACATTCACTTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCACCAG
CCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAA
TTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTC**ATG**GCCCATGAGATGATTGGAACTCAAATTGTTACTG
AGAGGTTGGTGGCTCTGCTGGAAAGTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACA
ATACATCCCACATTTTGGAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGACAAAG
TGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTT
ACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGA
AGAGCTTCAACTCTGTTCACCTGCTTGCAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAG
GAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGAATTC
TTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATG
TGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATG
ACAGCTTTTGTGAGAAAATTTTGCCGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCTCCAATG
GATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGA
TGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAAGACCTACTATATCTCCAAACTTCAATTTTC
TGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGC
TGCTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCTCA
GTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCCAGCG
TGCCCAGCGTGCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGCAG
ACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTCTGGATATCAAATCAGTTTCATATTCAGCCAGCA
TGGCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTGGATG
GGACCAACAAGCTATGCCAGTTCTCCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCAGTCCTGATAAGG
AGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCGGTCA
GAACCAGCAGCAGTGGCACCGCCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATT
ACCACACCAGCTTCCTTTTCGGCCTTTCCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGG
GCTGGCACTCGGATATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCAGCAGCTGGTATTTGCCACAGAGT
CCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGC
CCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGACAGAGCTGACTCGCGGCGGAGCT
GGCATGAAGAGAGCCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGT
CAGAGAACAGGTCACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATCATTG
AGGTCTCC**TGA**GAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTCTTGTTCACAAAAAAAATTCCCTGT
AAATCTGAAATATATATATGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAAAAGCAACAGGTGGA
TCAACCCAGTTGGTTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGG
GCAGATGCTAGAATCCCCCCTAGACGGAGGAAAACCATTTTATTCAGTGAATTACACATCCTCTTGTTCTTAAAA
AAGCAAGTGTCTTTGGTGTTGGAGGACAAAATCCCCTACCATTTTCACGTTGTGCTACTAAGAGATCTCAAATAT
TAGTCTTTGTCCGGACCCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGAC
CCTGTTAGGGACAGAGCCTAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTCACAAACCCACGCTC
ACCTGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCCTTGCCAAGGTCTACCTTAGAG
CAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTAGCCCATTTTCTAGGCATTG
TGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATTCCCGTGGGCCTAGA
TGGAGATAATTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTCAGCTGAACCACCAGGA
ACCTGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAAATCAAAGAATT
GTTTAAAATGGGATTGTCAATCCTTTAAATAAAGATGAACTTGGTTTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 262

MAHEMIGTQIVTERLVALLESGTEKVLLIDSRPFVEYNTSHILEAININCSKLMKRRLQQDKVLITELIQHSAKH
KVDIDCSQKVVVYDQSSQDVASLSSDCFLTVLLGKLEKSFNSVHLLAGGFAEFSRCFPGLCEGKSTLVPTCISQP
CLPVANIGPTRILPNLYLGCQRDVLNKELMQQNGIGYVLNASNTCPKPDFIPESHFLRVPVNDSFCEKILPWLDK
SVDFIEKAKASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPNFNFLGQLLDYEKKIKN
QTGASGPKSKLKLLHLEKPNEPVPAVSEGGQKSETPLSPPCADSATSEAAGQRPVHPASVPSVPSVQPSLLEDSP
LVQALSGLHLSADRLEDSNKLKRSFSLDIKSVSYSASMAASLHGFSSSEDALEYYKPSTTLDGTNKLCQFSPVQE
LSEQTPETSPDKEEASIPKKLQTARPSDSQSKRLHSVRTSSSGTAQRSLLSPLHRSGSVEDNYHTSFLFGLSTSQ
QHLTKSAGLGLKGWHSDILAPQTSTPSLTSSWYFATESSHFYSASAIYGGSASYSAYSCSQLPTCGDQVYSVRRR
QKPSDRADSRRSWHEESPFEKQFKRRSCQMEFGESIMSENRSREELGKVGSQSSFSGSMEIIEVS

FIGURE 263

AGCTGAAGTTGAGGATCTCTTACTCTCTAAGCCACGGAATTAACCCGAGCAGGC**ATG**GAGGCCTCTGCTCTCACC
TCATCAGCAGTGACCAGTGTGGCCAAAGTGGTCAGGGTGGCCTCTGGCTCTGCCGTAGTTTTGCCCCTGGCCAGG
ATTGCTACAGTTGTGATTGGAGGAGTTGTGGCCATGGCGGCTGTGCCCATGGTGCTCAGTGCCATGGGCTTCACT
GCGGCGGGAATCGCCTCGTCCTCCATAGCAGCCAAGATGATGTCCGCGGCGGCCATTGCCAATGGGGGTGGAGTT
GCCTCGGGCAGCCTTGTGGGTACTCTGCAGTCACTGGGAGCAACTGGACTCTCCGGATTGACCAAGTTCATCCTG
GGCTCCATTGGGTCTGCCATTGCGGCTGTCATTGCGAGGTTCTAC**TAG**CTCCCTGCCCCTCGCCCTGCAGAGAAG
AGAACCATGCCAGGGGAGAAGGCACCCAGCCATCCTGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGT
GAAATATACCAAATTCTGCATCTCCAGAGGAAAATAAGAAATAAAGATGAATTGTTGCAACTCTTAAAAAAA

FIGURE 264

MEASALTSSAVTSVAKVVRVASGSAVVLPLARIATVVIGGVVAMAAVPMVLSAMGFTAAGIASSSIAAKMMSAAA
IANGGGVASGSLVGTLQSLGATGLSGLTKFILGSIGSAIAAVIARFY

FIGURE 265

ATGGGGCTTGGGGCTGGGCGGCCAGACGCTAACTCGGATGCTCCCAGGCTACGCCTTGGCCATGACCCGTGCGGC
CGCGCGCCCCCGCCTTCACCTTCGGCGCGCGCTTCCCCACGCAGCAGACGACGTGCGGCCCCGGGCCAGGCCACC
TGGTGCCCGCTCGCA**TGA**CCGTGCGCGGCACCGACGGCGCCCCCGCCTACTCCATCTACGGCCGCCCACGCCGCT
CAGCGCCCTTCCTCACTCCGGGACCTGGTCAGGACCCCCGGGCCCCTGGCCACCCCAACGCCGAACTGCGTCCAG
GGAGGCCCACCTGGGAACCCCCGACCTGAACCCCGAGTCCCCCTCGGATACCCTAACACGATATTCGGTACCCCC
ATATCCGGATCTCAAATCCCAAACCCCGAACCCACGGGGCTTTGATAAATCGTGGCTCAGACTCCCCACTAGTCC
CAGGACCCCATCTCGGGTACCCACCAGGCTCCCACGCAGTTCTAGCCCCCCACACCCTTGATCCGCCCCGCAGGC
AGGTACTTCCCGGAGCGAGCGGGGAACGCGACGTACCCCAGTGCGCCTCGGCACACCATTGCTCCCCGAAACTGG
GGTGTCCAGGCGGAACAGCAGAGCCCAGGTCCCGCGGCCTATACGGTGCCCTCGCTCTTGGGTCCGCGCGTCATC
GGCAAAGTCTCCGCCCCAACTTGCTCCATCTACGGCCGCAGAGCGGCTGGCAGTTTCTTCGAGGACCTCAGCAAG
GTCGTGAGTCCAGGGGTCTACAAGTCCCGGGCCCCCCAGTTCACGATTCTGGCGCGGACTTCGCTCCCCCAAGAC
AACACTCGGAAGCCAGGGCCCGCGGCCTACAACGTGGATCAGCACCGGAAGCCCCGCGGCTGGAGTTTCGGGATC
CGGCACTCGGACTACCTGGCCCCGCTGGTGACCGACGCGGACAACTGACCCGCCAGGCGGGAGCGGCCCCACACG
TGTTTGCTTAAAGTCTGCGAGTCCGCATCGTGTCCGCCTCTCTCTCTCTCTCTGCGCGTCCTGGCGCAAGGCC
TGGGGTGGAGCCACGGCTGGGGCCGTGTCCCAACTCCGAACCCAGCGGGGCGGGGCCCGAGCGTCGGGCGAGGCC
GGGACCCCAGCGCTGCGCCGCGTCCGAACGTCGAGACCCCACCGAGGGCGGGAGGGGGACTCTCGGGAGCCACAG
ACGCCCGAGACCCACGCCGGGCGGGACCGGCCAGGGATCACCCCCGCCGACGGCCCCGGGCCCCGACGGCCCGGA
AGTTCCGCGTGTCCGGGGGCACCGGGGGATTGGCCGGGGCGCGGCGTGCAAGGCTTCCCGGGGGCGGCGACTGCC
GAGCTCCGCCCTCCAGGCGGCCCCACCCGCCTGCCGTCCTGGGGCGCCGCCGCCCCGCCGCCGGCAGTGGACCGC
TGTGCGCGAACCCTGAACCCTACGGTCCCGACCCGCGGGCGAGGCCGGGTACCTGGGCTGGGATCCGGAGCAAGC
GGGCGAGGGCAGCGCCCTAAGCAGGTACGGGCGGGGCTCAAGTCGCGAGGCGGGGAAGCGGGAGGCAGACACGGA
CGAGGGCGACACAGACACGGACCGAGGGGCGGACACCGGAGAGACACGGGAAAGGGGTCGGGACAGGAGCACGT
GGCTCAGACACCGACGCCGGGAGGCCGCAGACCCCGGACGTGTCAGGCATCCCCGCAGGCCCGGAGCG

FIGURE 266

MGLGAGRPDANSDAPRLRLGHDPCGRAPPPSPSARASPRSRRRAAPGQATWCPLA

FIGURE 267

AGACTGACCACTAGCCGACGCGGGCGAGAGGGACAGGAGCGTGACCTCCCCATCCCGAGGGGCCGGACGCTCGGG
CGCCTCCCCGCTCCCCCCACTCGGAGGCCGCGCGCGCCGTTAGCCCCTTCCTCGCTCCCCCGCCCCAGTCCCGCA
GTCCGGGAGGCGGGGGTCGGCAGCCGGCTGAGTGGGAACCGCGCGGTGTCTGAGGAGGCAGTCGGCGACCGGTTT
CCACTTCAAGCGTGACCCTTTTGCCTGTGGGATGAGCTCCAGCATGGGGTGAGGTACAGAAGAGAGACTTGAAGA
GCGTGCCTTGGGACTCAAGCGCCAAACCTGTACCCTAGCGAGTGTCCTACTCCGCATCCGTAATGGAAGGAAATG
CACATCTTACTCCAGAGGCACAAGAGGAGGACATCCCATGCGGCTACTCCTGCCCAGCGTGGTGGGGCAGCAGAA
GCTCCAGAGCCCAGACTTGCAGGCTCACGGTGCAGGGTGAACCTGGCCACAGCTCACCCTGGAACAGCCACAATG
TCTGCCCCTTAGAGAAGAACCCTGAAATCAGACCAGTTTTTGCGGCCTCCCCCTTTCCTCTCTGTTACAGTGCCC
TTTCCAGGCCTTAAGAGAAGTAAAACTTAGCTGCAGCGCCAGGAGGTGGACCCCAGAGTGTGAGTGGCACGCTTC
CCTGTGAACCCGTCCTCACC**ATG**TTTGCCACATCTGGGGCAGTGGCAGCGGGGAAGCCTTACTCGTGCAGCGAAT
GTGGCAAGAGCTTCTGCTACAGCTCAGTGCTGCTGCGACATGAACGAGCTCACGGCGGTGACGGCCGCTTCCGTT
GCCTAGAATGCGGTGAGCGCTGTGCACGGGCTGCTGACCTCCGAGCGCACAGGCGCACGCATGCTGGCCAGACCC
TCTACATCTGCAGTGAGTGCGGACAAAGCTTCCGCCACAGCGGCCGTCTTGACCTACACTTGGGCGCACACCGGC
AGCGATGCCGCACTTGCCCCTGCCGCACATGCGGCCGGCGCTTCCCGCACCTCCCGGCGCTGCTGCTACACCGGC
GCCGCCAGCATCTGCCAGAGCGGCCCCGCCGCTGCCCGCTGTGCGCCCGCACCTTCCGGCAGAGCGCGCTGCTCT
TCCACCAGGCGCGGGCGCACCCCTTGGGGACAACCTCTGACCCTGCTGCCCCACCCCACCGCTGCGCGCAGTGCC
CGCGAGCCTTCCGAAGCGGCGCCGGGCTGCGGAGTCACGCGCGCATCCACGTGTCCCGGAGCCCCACGCGACCCC
GTGTCTCAGACGCCCACCAGTGTGGCGTGTGCGGCAAGTGCTTTGGCAAGAGCTCTACGCTGACGCGACACCTGC
AGACGCACTCGGGGGAGAAACCCTTCAAGTGCCCGGAGTGCGGCAAGGGCTTCCTGGAGAGTGCCACGCTGGTGC
GCCACCAGCGCACACACACGGGCGAGAAGCCGTACGCATGTGGCGACTGTGGACGCTGCTTCAGCGAGAGTTCCA
CGCTGCTGCGCCATCGGCGCAGCCATCAGGGCGAGCGGCCACATGCGTGCGCCACTTGCGGCAAGGGTTTCGGGC
AGCGCTCCGACCTGGTGGTGCACCAGCGCATCCACACGGGCGAGAAGCCCTTCGCGTGCCCCGAGTGCGGCCGCC
GCTTCAGCGACCGCTCGGACCTCACCAAGCACCGGCGCACGCACACGGGCGAGAAGCCCTACCGCTGCGAACTGT
GCGGCAAGCGGTTCACGTGCGTGTCCAATCTCAACGTGCATCGGCGCAACCATGCCGGCCACAAGCCACACAAAT
GCCCCGAGTGCAGCAAGGCCTTCAGCGTCGCCTCCAAGCTTGCACTGCACCGCAAGACGCACCTGGGCGAACGGC
CAGCGGAGTGCGCAGAGTGCGGCAAGTGCTTCAGCCACAGCCGCTCGCTGTCACAGCATCAGCGGGCCCACACGC
GCGCCCGCACCGCTGCCGCCGTTGCCATCCAGTCCGCAGTGGGCACTGCCCTCGTCTTTGAGGGGCCGGCTGAAC
AGGAAAAGCCAGGGTTCTCTGTGTCC**TAG**TTGAGGGAGGCTTGCTGAGGCTTCTCTAAAGGTGGTTGGGCAAGCA
CCTATATAGTATCACGGGGACAGTTGAGGCAACTCGTAGATGGAGATTTGGGAAAAGACGATGTGGCCTCCTACC
TTTCCAGTTTCTGTTGGCAGCCCTTCACGTAGCCTCCTGCCTCGCCTCTACACCTACTACCCTGTCGGCCCTTTT
GCCATGCTGTCCTCGTATAACTCGGATTCTCTCCTCAGGTGTAGGTGCAGGGAGTCAGGGAACCCTTAGACTCCC
CTGTGTGCAAGAGCCCAGGTGTTGGTGTGTCCCTTTAATGCTACTGTGCTCTCTGGTGTTTCTGATTTTCCTGCC
TTTATTCTGTCTTCTCTTGTCCTATCTCATTCCAGCCCACATCTTCTCCTTTCCTGATTACTTTTGTTGTCCTGC
CTCTTCAGGTAATGGTCACAGATTTGGCTGTAGGCACGTTACCAGCCCTGTGGCTTCTTGACTCTTGGTTCCCTG
TTAACTCTGTTTCTGAGAAATGTGGGTATGGAGGTGGGTGGGAAAGCTCACTTCCATGAAGGATGTCTCCATGCT
AGGAGCTGCCTGCACCCTGGCAGAGGTGGCCAGTCACGTGAAGGTGGGCAGGGCCCTTAGCATGGCCACACATGT
CCCCAGGGCAGATCAAGGGGCCTCTCAGAACCATGTTCCCCAGCCAGGTGAGGACCATTTTCACTGGACCCAGG
CCAAAACCATGTGGGTGCACAAAGCCAGGCACTGCCAAGTGGAACATGAGGTTATTTCCAAATCATGGGAGCCAC
CAGCAGGGAGAGGGCAGGATGGAAAATCCCCTGGAGCCGGTCAACTTTTTGCTCATGGCTAGTGAAATAAAGTTG
TTTGAGTACTAAAAAAAAAAAAAAAAAA

FIGURE 268

MFATSGAVAAGKPYSCSECGKSFCYSSVLLRHERAHGGDGRFRCLECGERCARAADLRAHRRTHAGQTLYICSEC
GQSFRHSGRLDLHLGAHRQRCRTCPCRTCGRRFPHLPALLLHRRRQHLPERPRRCPLCARTFRQSALLFHQARAH
PLGTTSDPAAPPHRCAQCPRAFRSGAGLRSHARIHVSRSPTRPRVSDAHQCGVCGKCFGKSSTLTRHLQTHSGEK
PFKCPECGKGFLESATLVRHQRTHTGEKPYACGDCGRCFSESSTLLRHRRSHQGERPHACATCGKGFGQRSDLVV
HQRIHTGEKPFACPECGRRFSDRSDLTKHRRTHTGEKPYRCELCGKRFTCVSNLNVHRRNHAGHKPHKCPECSKA
FSVASKLALHRKTHLGERPAECAECGKCFSHSRSLSQHQRAHTRARTAAAVAIQSAVGTALVFEGPAEQEKPGFS
VS

FIGURE 269

GGCCGTGCCTTCTCTCGCTTCGGACTGCGCAACGCTGCGCTCTGGGCTGACAGGCGGATAAAACGGTCCCATCAA
GACTGAGAAAAAGCACACCAGCTATTGGCACAGCGTGGGCAGTGGGGCCTACAGGATGACTGACTTAGTCTACAG
AGATCCCGGCGTACTTAAGCAGATGAAGACTCTTAAGATGACAGAAGGTGATTTTTCTGGTGATCGAGGACTTCC
GGGGTAATGACAGTGATGAA**ATG**CAGGGGACCTGGTTGCCCCCAAGTTTCCTGGCAGTGTGTGATACTGAGGAGG
TGAGCTTGTTTCTGGAGCTGTGCTTTAAGATTCATGTTACATGTAAAGCTGTCCTCATTTGTGACTATGGACCTA
TGGAGTTGGGACAATCTCTATGGGAAGCAGAAGGCAAGGACCCCGGTCATTTTAGG**TAG**AAACAACAGCATGCTA
ATGCAAAAAATTATGCAGTGTGCTACTGAACTTCAGAGGTGATCAATAAAAGAAGAATAAAAAGACTAATAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 270

MQGTWLPPSFLAVCDTEEVSLFLELCFKIHVTCKAVLICDYGPMELGQSLWEAEGKDPGHFR

FIGURE 271

GAGGAACATGATTTTATTGGTTCTTTCAGTTCACCACATCCGACTCGCGTCTCGGCCCTGGCCCGCCTTGCGGAC
CTTAAAGCAGTCAGTCCAGGGTTTGGGGGAAACGTGCTCACCCGACGGCAGCTCACAGGACCCCGGAGAGTCCTG
GCATGGTATCTCGGTCCGGACTCTCCGCTGGGCCCACGAAGGAGAAAGGCTGCCTCGGATTCCTGCGCCCAAGCC
AAGGTCCGGCGCCCACGGAGGCAAGTCCGGTCTCACGGTGACCTCCCGCTGGCGCCGCCTTCGCCGCCAACCATC
CAGTTCTTCCTCCAGGCCACGTTCTCCTGCGTGGTCGCTGCCTCCTGCAGAGTGGCCAGCAATAGCTGCTGGGTC
CTGGCCGCCTCCTCCCTGCTCCTTGGGTCCTGCAGTGGCATCTCCTGAGGGCAGGAAGGGGAGTTCGCAGGAGCT
CCAGTCCGGGGCTCTCCACCCGCCCACCCTTCCTCGGGACTACCAGTTGCTTCTACCTTTAGCATTTCCTGCTTC
CGCCGCTCTCCCGGGGTCACGATAACGAGGAGCGCGTAGCCCACGCCAGCCCCTGCGCCCAGCATTGCGACTGAG
ATCAGCATTTTCCGCAAGGAATCCATGGCCGCCTGCACAGCCAGCGGAGCGCCCACGGGAGCTCCCCGCAGCCGC
AAGCTGTTGCCGCGCGGTCTCACTACCCCTTGGCGCAGGCTAGAGCGCCCTATAGCAGAAACCATAGATAAGCGG
CCGGCTAGAGAGGACCTGCTCGAGGAAACGTTTGGAATCCGGAGCGCTTGGATCTCAGGTTTAGCTGAGGGGGTT
GAGGTGTCCAAGAAGTGCTGGCACCAAGGGCTGAGCGCGGGGACCCTGTGTCCTCAATTCCGGGGTGGGATTGCT
AGGGGGAGAGTGCGTGTCTTCATGGTTGCCGTGGGTTTTATGATTGCCCATTTTTCTGTCTTCCGACGTTTCCCG
ATCAGTAGAGGCCCGAGCTGTGCTCTGTGGTTTCCTGCAGTCACCCGCGAGTTTTCAACACAGCGCATGGAGGGC
ATCTACACACATACACATCCCTCTCCATCCCCTCAACTCTGGAACAAACACTCAAAGTCAAGTATACTGGTTGGA
GAAATGGGTAATAGTTACTTATCTTTAACATTTATTTTACAAACAACCTATTCCTTTTCTCGTCATGGTACACAC
TTGGTATTGTTTGGGTTTTTTTTTGGTTTTGTTGTTGTTGTTAGTGTGTGGGCGTGGTTTTGTTTGTTTTTGGAG
ACAAGGTCTCGCTCTGTCGCCCAGGGCTGGAGTGCAGTGGCGCGATCATGGCTCACTGAAGCCTCGACTTCCAGG
GCCCAAGCGATCCTCCTGCCTCAACCTCCCGGATAGCTGGGATTACAGGCGTGCACCACCACGCCCGGCTGGTAT
TGCTTTTTGTTTTGCTTCGTTTTCTTTTTTGCTTTTTGAGACAGAGTCTCACTCTGTTGCCCAGCTGGAGTGCAG
TGGCGTGATCTCGGCTCACTGCAAGCTCTGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGC
TGGGACTACAGGCGCCCGCCACCACGGCCGGCTAATTTTTTGTATTTTTAGTAGAGAAAGAGTTTCACTATGTAG
GTCAGGCTGGTCTCGAACTCCTGACCTCGTGATCCGCCCAATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATT
ACAGGTGTGAGCCACCGCGCCCGGCTGTTTTGCTTTGTTTTCAACCACTAAAAGGCTGGATTCGTGTAACATACT
GAATTCTGCTTTACAGAAGAAAACACCTCTTAGCTGTGTGACTGATTATAGGCAAGTTCTTGTGCCCCGGTTTCT
GCATCAGAAAATGAAGCTTATAACAACAGTACTTGTCTCACAGTTTTAGGATAATTAAATTAGTTATATGTAAAG
CAATTAAAACAGCTCCTGCCAAAGAGTAAACACCATATAAATATTCATTAAATAACATACAAACATACCAGGTTG
GGAAAAATCAGTAAGCATAGGAGTCAGGAAATTCCAAGTTGGTTATCACAACTCTTGGCCCACAGGGCTTTAATC
CAGGTGCCCTTGTCTCCTACCCTTGTTGCCATCCCAGTGTCTCCAGGGAGTAAGTAGAAATAAAGATCCTATCTC
ACCTCTTGGGCATTTTCCCCTGCCCTGAAAGCGTATAATCGCTTAGCACAGTCGGTGCTTAAGGGGCCAGGCTCC
AAAGAAGATTAAAGGAACAGTTTGTGGGGTGCACTGGGCAGCAGTACTCTCCTCTGAGTTCAATCATCTTGCACT
CTAAGAATCACCACCATGGCCCTTGTGCCAGGGAGAAGCAAGGAGGATGGGCTTTGGACTAGAAATAGCCCAGGC
TCCTCCCAGCATCCAGAAAGTCCCAGGCTGCCCAACCCTCTCTGGGACAGAGGAAAAATTGGCAAGGTTGAAGGT
CACCAGCACATTCAGGATTTCTCTCAAAAGTCCCATCTGCCGTCTATTGTGGTGGAATCCAGTGAGGTGAATGAA
GAGAGTGGGGATCTCCATTTGCCCCATGAGGAGCTGCTGCTGCTCACTGATGGTGAGGAAGAGGATGCTGAGGCC
TTCTTCCAAGACCAAAGTGAAGAGCCAGGCTGGGCTTGGAGCCCACAGGACCCTAGAAGTCCTTTAAGAACATTT
AACGCTGGACTCAGCTGGGGGCAGGACCAGG**ATG**AAGAAGATGCTTGTTGGATTCTTGAGGACACAGCATGTCTG
GAAGCCACCAACCACTGTCCCTTCTGGGACTCAACAGGCTCCCGTGTTTGTAGAAGTGGCTTTGTGGAATATTCC
CATCTCCTGCCTCCTAATAGCTTTGAGGGAGCTGAAGAAGAAGCTGTTCAAACGCCGGCGGGTGTTGAATCGGGA
GCGGCGTCTGAGGCACCGGGTGGTCGGGGCTGTGATAGACCAAGGGCTGATCACGCGGCACCACCTCAAGAAGCG
GGCGTCCAGTGCACGTGCCAACATTACACTGTCAGGGAAGAAGCGCAGAAAACTCCTCCAGCAGATCCGGCTTGC
CCAGAAAGAGAAGACAGCCATGGAAGTGGAAGCCCCTTCAAAGCCAGCCAGGACTAGTGAACCACAGCTCAAAAG
GCAAAAGAAGACAAAAGCCCCCCAGGATGTAGAAATGAAGGACCTTGAAGATGAGAGC**TAA**ACCTCTTCCACTAG
AAGATTCTCAACTGGAGCCAGCCTTCAGACTCAGTGGTTGTTTCAGAGGACTTTGACAAAAGCAAGGCCCCTTTT
CACTCTCCAGATTTCCTCCTACCTAATGGCCTACTGACCTCCCCTAGAGGGATGTCTTTGGGAGGGAAGAAGGTA
CAGAAGAAAGATTGGAGAAGGGCCTCTCTAGCAGTCAACTCCATTTGTAATAAAGCCCTAGCACTCTGAAAAAAA
AAAAAAAAAAA

FIGURE 272

MKKMLVGFLRTQHVWKPPTTVPSGTQQAPVFVEVALWNIPISCLLIALRELKKKLFKRRRVLNRERRLRHRVVGA
VIDQGLITRHHLKKRASSARANITLSGKKRRKLLQQIRLAQKEKTAMEVEAPSKPARTSEPQLKRQKKTKAPQDV
EMKDLEDES

FIGURE 273

CTCACTGAATCTGCCTTAGTGAGAATGTCACTACCTTATTGCTTATAT**<u>TAA</u>**TGCAGATGTCTTTCTCTGCCCTCC
TTGTTTCCAGATTGTACCATCATAATCAACCCTTCATAGGGCTTCCTATCAGAGCAGAGGTTCTAATGACTCTCT
ATTCCCTGCAGGATGAAGTGCAAACTCTTTAGTATGGCCTGTGTTTTCCATGACTCGCCCCTGCCTACATCCATG
GCTTCATCTACTACCTTTCCCCTCACAATGGTCTCTCCTTAGTAGATAGTGAAATATTAGTGTACTATTCTTTTT
ACATGAAAATGACATAGTGAAAGAGAAGGACTAGTTTAGCCTGTCTTTGCAGAAAGAATGAAGAATAAATAATGA
CATACTTGAAAGTAACAGACATGGATTTGAACCCTAGATTTGCCATGAAATGTCTGAATGCCTTTGGTCAATTTA
CATAATGGCAGAAAGCCTTACAAATTCCTAGTGAAGATTAAACTCAATAACGCGGGCAAAGTGCTTAACAAAATT
GCTGGAACATAGTACACCTCTACATGCTCAATAAATGGGAGTTAATTACCTTTTTTACCTCCCCTTCCCTTCCCA
AATAGTATGCATTACCTTTTAAATTTTAAATTGAGAAGTTTACAGTTGAATTAAAAAATGCAATGAATCACA

FIGURE 274

LTESALVRMSLPYCLY

FIGURE 275

AGGGGAGAGCGGCCGCCGCCGCTGCCGCTTCCACCACAGTTTGAAGAAAACAGGTCTGAAACAAGGTCTTACCCC
CAGCTGCTTCTGAACACAGTGACTGCCAGATCTCCAAACATCAAGTCCAGCTTTGTCCGCCAACCTGTCTGAC**AT**
GTCGGGACCCGTGCCAAGCAGGGCCAGAGTTTACACAGATGTTAATACACACAGACCTCGAGAATACTGGGATTA
CGAGTCACATGTGGTGGAATGGGGAAATCAAGATGACTACCAGCTGGTTCGAAAATTAGGCCGAGGTAAATACAG
TGAAGTATTTGAAGCCATCAACATCACAAATAATGAAAAAGTTGTTGTTAAAATTCTCAAGCCAGTAAAAAAGAA
GAAAATTAAGCGTGAAATAAAGATTTTGGAGAATTTGAGAGGAGGTCCCAACATCATCACACTGGCAGACATTGT
AAAAGACCCTGTGTCACGAACCCCCGCCTTGGTTTTTGAACACGTAAACAACACAGACTTCAAGCAATTGTACCA
GACGTTAACAGACTATGATATTCGATTTTACATGTATGAGATTCTGAAGGCCCTGGATTATTGTCACAGCATGGG
AATTATGCACAGAGATGTCAAGCCCCATAATGTCATGATTGATCATGAGCACAGAAAGCTACGACTAATAGACTG
GGGTTTGGCTGAGTTTTATCATCCTGGCCAAGAATATAATGTCCGAGTTGCTTCCCGATACTTCAAAGGTCCTGA
GCTACTTGTAGACTATCAGATGTACGATTATAGTTTGGATATGTGGAGTTTGGGTTGTATGCTGGCAAGTATGAT
CTTTCGGAAGGAGCCATTTTTCCATGGACATGACAATTATGATCAGTTGGTGAGGATAGCCAAGGTTCTGGGGAC
AGAAGATTTATATGACTATATTGACAAATACAACATTGAATTAGATCCACGTTTCAATGATATCTTGGGCAGACA
CTCTCGAAAGCGATGGGAACGCTTTGTCCACAGTGAAAATCAGCACCTTGTCAGCCCTGAGGCCTTGGATTTCCT
GGACAAACTGCTGCGATATGACCACCAGTCACGGCTTACTGCAAGAGAGGCAATGGAGCACCCCTATTTCTACAC
TGTTGTGAAGGACCAGGCTCGAATGGGTTCATCTAGCATGCCAGGGGGCAGTACGCCCGTCAGCAGCGCCAATAT
GATGTCAGGGATTTCTTCAGTGCCAACCCCTTCACCCCTTGGACCTCTGGCAGGCTCACCAGTGATTGCTGCTGC
CAACCCCCTTGGGATGCCTGTTCCAGCTGCCGCTGGCGCTCAGCAG**TAA**CGGCCCTATCTGTCTCCTGATGCCTG
AGCAGAGGTGGGGGAGTCCACCCTCTCCTTGATGCAGCTTGCGCCTGGCGGGGAGGGGTGAAACACTTCAGAAGC
ACCGTGTCTGAACCGTTGCTTGTGGATTTATAGTAGTTCAGTCATAAAAAAAAAATTATAATAGGCTGATTTTCT
TTTTTCTTTTTTTTTTTAACTCGAACTTTTCATAACTCAGGGGATTCCCTGAAAAATTACCTGCAGGTGGAATAT
TTCATGGACAAATTTTTTTTTCTCCCCTCCCAAATTTAGTTCCTCATCACAAAAGAACAAAGATAAACCAGCCTC
AATCCCGGCTGCTGCATTTAGGTGGAGACTTCTTCCCATTCCCACCATTGTTCCTCCACCGTCCCACACTTTAGG
GGGTTGGTATCTCGTGCTCTTCTCCAGAGATTACAAAAATGTAGCTTCTCAGGGGAGGCAGGAAGAAAGGAAGGA
AGGAAAGAAGGAAGGGAGGACCCAATCTATAGGAGCAGTGGACTGCTTGCTGGTCGCTTACATCACTTTACTCCA
TAAGCGCTTCAGTGGGGTTATCCTAGTGGCTCTTGTGGAAGTGTGTCTTAGTTACATCAAGATGTTGAAAATCTA
CCCAAAATGCAGACAGATACTAAAAACTTCTGTTCAGTAAGAATCATGTCTTACTGATCTAACCCTAAATCCAAC
TCATTTATACTTTTATTTTTAGTTCAGTTTAAAATGTTGATACCTTCCCTCCCAGGCTCCTTACCTTGGTCTTTT
CCCTGTTCATCTCCCAACATGCTGTGCTCCATAGCTGGTAGGAGAGGGAAGGCAAAATCTTTCTTAGTTTTCTTT
GTCTTGGCCATTTTGAATTC

FIGURE 276

MSGPVPSRARVYTDVNTHRPREYWDYESHVVEWGNQDDYQLVRKLGRGKYSEVFEAINITNNEKVVVKILKPVKK
KKIKREIKILENLRGGPNIITLADIVKDPVSRTPALVFEHVNNTDFKQLYQTLTDYDIRFYMYEILKALDYCHSM
GIMHRDVKPHNVMIDHEHRKLRLIDWGLAEFYHPGQEYNVRVASRYFKGPELLVDYQMYDYSLDMWSLGCMLASM
IFRKEPFFHGHDNYDQLVRIAKVLGTEDLYDYIDKYNIELDPRFNDILGRHSRKRWERFVHSENQHLVSPEALDF
LDKLLRYDHQSRLTAREAMEHPYFYTVVKDQARMGSSSMPGGSTPVSSANMMSGISSVPTPSPLGPLAGSPVIAA
ANPLGMPVPAAAGAQQ

FIGURE 277

AGGTTAATCTTAAAAGCCCAGGTTACCCGCGGAAATTTATGCTGTCCGGTCACCGTGACA**ATG**CAGCTGAGGAAC
CCAGAACTACATCTGGGCTGCGCGCTTGCGCTTCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGA
GCACTGGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGGAGCGCTTCATGTGCAACCTTGAC
TGCCAGGAAGAGCCAGATTCCTGCATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGAAGGC
TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGAGATTCAGAAGGCAGA
CTTCAGGCAGACCCTCAGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTCACAGCAAAGGACTGAAG
CTAGGGATTTATGCAGATGTTGGAAATAAAACCTGCGCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGAT
GCCCAGACCTTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCT
CTTTATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTACTGCAATCACTGGCGAAATTTTGCT
GACATTGATGATTCCTGGAAAAGTATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTTGAT
GTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACACATCAGCCCT
CAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAG
CTTAGACAGGGAGACAACTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGGGCTGTAGCTATGATAAAC
CGGCAGGAGATTGGTGGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCT
GCCTGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACTTCAAGGTTAAGAAGT
CACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACTT**TAA**

FIGURE 278

MQLRNPELHLGCALALRFLALVSWDIPGARALDNGLARTPTMGWLHWERFMCNLDCQEEPDSCISEKLFMEMAEL
MVSEGWKDAGYEYLCIDDCWMAPQRDSEGRLQADPQRFPHGIRQLANYVHSKGLKLGIYADVGNKTCAGFPGSFG
YYDIDAQTFADWGVDLLKFDGCYCDSLENLADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNH
WRNFADIDDSWKSIKSILDWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQQVTQMALWAIMAAPLFMSNDL
RHISPQAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIGGPRSYTIAVASLGKG
VACNPACFITQLLPVKRKLGFYEWTSRLRSHINPTGTVLLQLENTMQMSLKDLL

FIGURE 279

TGTTCAGTCCCCCGAGGTCCATGCAGGTTACAAGTGGCACCCCAAACAGCAACAGGATCGGGTGCTCTGCATAGT
GGCATCCGAACACAGGACTTCGAGGACATGAATGAAGAAAGTCCGCTGGAGCAGAGGAACTGAAATGACAAGGCG
AATGGGGACCCCGAAACGAGTCTGCCAGCAGCAGAGATAAGGTCAGTGCCCTAAAGAGGTACTGATCAGTGCCGT
AAAGAGGTACTGGGAGCAGTGCTTTAAAGAAGTACTAGGAACAGGAAGTTTTCTGAATCAGGCTAACAAGGGGAA
GAATTTGTCTATTGAAGAAAAACATTATGTGCAGTTGCTTAAAGTTCTGTAGAGACAGTCTGGAGCTTAGGTTAA
TTCGCAGACACTAACCTCCTGCAGAAGCCACAAAAGGTTATTACGCATAACCCATGGTTCCCACAGGCAGGCATC
CTTGATATGGAAAATTGAGACAAAGCAGGAGAAGGATTAAAACAGGCTCATCAAAAAGGTCTTAGCTGATTCTTA
GTTGATTCTTCTGTTTTCTCCACTTGGAGTTTAGTTTGTACTGTACTTCTACCATTATCTCCTTATTATTCTGTG
GGACAACAGCCTGAATCTAAAAATCTGAAAGAAT**ATG**TTGTCCCACCCACAGCTCCAATTGAAAATAAAAAACAG
AGAGGATAAAAATTGGCCTATACCGCCTCCTCCAATTGCAGAAACATCTGTACTGCCTCCTTCAGTAGCACAAAT
AGAAACCCCAATACAAAGAATTTTACGCTCTGCTGTCATAGCTGGAGAGCCCTTAGGACCTTGCGCTGTTCCTGT
TTCCATAAGGCCTGATCCCAATAATCCACAGCAGTTTATTCATGAACACACCCCACTAGAATTTCAGTTGTTGAA
GGAATTAAAAACTAGTGTGGTCAATAATGGAGTACAAAGCCCATGGTTCCCAGAGGAAAGAACACTAGATGTAGA
ACTCTGGGAACAAGTGGGGAGAAATCTTAAACAACATCAGGTGCAAAGGCATCAGGTCCCAGTAAAATCTTTAAT
GTTATGGGCTTTAATTAGAGCAGCCCTGGCTCAGTTACACACAGAAGAGCCTAAAAAGAGGAAGGAGGAGAAAAT
GTCACCTGCCTTATCACCTCCTCTTCCCTCAGTCCCAATATCACTGGGTCAAAATAACAGGAAACGGAGGTCTCA
CCTAAGTCTCCTCCTCCAA**TAG**ATAGGAAAAAGGACAGAGGATATGCTATAGCCATCAGTGTGTTAGATATGAGT
TCTAAATTTCTCTTTAAAGAATCAGTATGTCAGTATGTTCAATTCTTTGCCTTCTACTTCTAAACTTAACTTCCT
CATAAAGCAACCTTTTTCGATTACCTGCTCCATCCTGACTCATTCCGATTTCCTGCTCTGCCATAACCATTTTTC
CCGCCAAACCACTCACCCTGTCACTCTCTTTAAATTAGCCAGTTGGAGTTAGTTTGGCCTGTGTGGTCTAACCCT
AGCCAATAGGGGAATGACACAGCAGCAGGGGCCATGTGCATCAGGGATAAGAACCCTTTCCCTCCCTTGTCCAGG
TGTNCACTNAACCATTGCTCCATCTGTAAGGCGCACCCTTCTGTAGAAGTACATTGACTTGCTGAGAATTAAAAA
GNACATTTTA

FIGURE 280

MLSHPQLQLKIKNREDKNWPIPPPPIAETSVLPPSVAQIETPIQRILRSAVIAGEPLGPCAVPVSIRPDPNNPQQ
FIHEHTPLEFQLLKELKTSVVNNGVQSPWFPEERTLDVELWEQVGRNLKQHQVQRHQVPVKSLMLWALIRAALAQ
LHTEEPKKRKEEKMSPALSPPLPSVPISLGQNNRKRRSHLSLLLQ

FIGURE 281

ATGCCTAAATCAAAGGAACTTGTTTCTTCAAGCTCTTCTGGCAGTGATTCTGACAGTGAGGTTGACAAAAAGTTA
AAGAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGTAAAGAAACAAAAGACAGGTGAGACTTCGAGAGCCCTGTCA
TCTTCTAAACAGAGCAGCAGCAGCAGAGATGATAACATGTTTCAGATTGGGAAAATGAGGTACGTTAGTGTTCGC
GATTTTAAAGGCAAAGTGCTAATTGATATTAGAGAATATTGGATGGATCCTGAAGGTGAAATGAAACCAGGAAGA
AAAGGTATTTCTTTAAATCCAGAACAATGGAGCCAGCTGAAGGAACAGATTTCTGACATAGATGACGCAGTAAGA
AAGCTG**TAA**

FIGURE 282

MPKSKELVSSSSSGSDSDSEVDKKLKRKKQVAPEKPVKKQKTGETSRALSSSKQSSSSRDDNMFQIGKMRYVSVR
DFKGKVLIDIREYWMDPEGEMKPGRKGISLNPEQWSQLKEQISDIDDAVRKL

FIGURE 283

GACGCGGGGCCGGAACGCGAAGAGGGTGGTGGAGTCGGGCTACCCACTGATTTTCCTTCCCTTACTTCCCCTGAG
CCCTTGGGCCCACTTCCCAGCCTACCGCTTCCGTCCCCGCCCGACTCTTGGGCCAGCGCCTGGGCCCACACTTTC
CTATCCCCCGCAG**ATG**CCGGTGGCCGTGGGTCCCTACGGACAGTCCCAGCCAAGCTGCTTCGACCGTGTCAAAAT
GGGCTTCGTGATGGGTTGCGCCGTGGGCATGGCGGCCGGGGCGCTCTTCGGCACCTTTTCCTGTCTCAGGATCGG
AATGCGGGGTCGAGAGCTGATGGGCGGCATTGGGAAAACCATGATGCAGAGTGGCGGCACCTTTGGCACATTCAT
GGCCATTGGGATGGGCATCCGATGC**TAA**CCATGGTTGCCAACTACATCTGTCCCTTCCCATCAATCCCAGCCCAT
GTACTAATAAAAGAAAGTCTTTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 284

MPVAVGPYGQSQPSCFDRVKMGFVMGCAVGMAAGALFGTFSCLRIGMRGRELMGGIGKTMMQSGGTFGTFMAIGM
GIRC

FIGURE 285

GCGCCCAGCCTGCCAGCCGCGCTGCTGCTGCTCCTCCTGCTGTGGGACCGCTGACCGCGCGGCTGCTCCGCTCTC
CCCGCTCCAAGCGCCGATCTGGGCACCCGCCACCAGC**ATG**GACGCTCGCCGCGTGCCGCAGAAAGATCTCAGAGT
AAAGAAGAACTTAAAGAAATTCAGATATGTGAAGTTGATTTCCATGGAAACCTCGTCATCCTCTGATGACAGTTG
TGACAGCTTTGCTTCTGATAATTTTGCAAACACGAGGCTGCAGTCAGTTCGGGAAGGCTGTAGGACCCGCAGCCA
GTGCAGGCACTCTGGACCTCTCAGGGTGGCGATGAAGTTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAAAAA
AGCAGAGTCCCGCCAGCCCTCAGAGAATTCTGTGACTGATTCCAACTCCGATTCAGAAGATGAAAGTGGAATGAA
TTTTTTGGAGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAATTAGAAAG
CTTCCCTGGCTCGTTCCGTGGAAGACATCCCCTCCCAGGCTCCGACTCACAATCAAGGAGACCGCGAAGGCGTAC
ATTCCCGGGTGTTGCTTCCAGGAGAAACCCTGAACGGAGAGCTCGTCCTCTTACCAGGTCAAGGTCCCGGATCCT
CGGGTCCCTTGACGCTCTACCCATGGAGGAGGAGGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAAGAC
CGTGGATGGCTACATGAATGAAGATGACCTGCCCAGAAGCCGTCGCTCCAGATCATCCGTGACCCTTCCGCATAT
AATTCGCCCAGTGGAAGAAATTACAGAGGAGGAGTTGGAGAACGTCTGCAGCAATTCTCGAGAGAAGATATATAA
CCGTTCACTGGGCTCTACTTGTCATCAATGCCGTCAGAAGACTATTGATACCAAAACAAACTGCAGAAACCCAGA
CTGCTGGGGCGTTCGAGGCCAGTTCTGTGGCCCCTGCCTTCGAAACCGTTATGGTGAAGAGGTCAGGGATGCTCT
GCTGGATCCGAACTGGCATTGCCCGCCTTGTCGAGGAATCTGCAACTGCAGTTTCTGCCGGCAGCGAGATGGACG
GTGTGCGACTGGGGTCCTTGTGTATTTAGCCAAATATCATGGCTTTGGGAATGTGCATGCCTACTTGAAAAGCCT
GAAACAGGAATTTGAAATGCAAGCA**TAA**TATCTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTTTCTTG
TAAAAGTTTCCAATTTTTTCACTGAAACCTGAGTTAAAAATCTTGATGATCAGCCTGTTTCATAAGAAACTCCAA
TCAAGTTAATCTTAGCAGACATGTGTTTCTGGAGCATCACAGAAGGTATATTGCTAGTTACACTTTGCCCTCCTG
CAGTTTCTTCTCTGCTCCCAACCCCCATCTCATAGCATCCCCCTCTATTTCCAATGCTCCTCTCCAACCGCTTAG
TTTCTGAATTTCTTTTAAATTACAGTTTTATGAAAGCATATTTTATTTACTTGGTGTTGAAATAGCCCTCATAAA
ACCTAAGCACTTGGAAACACAATAATAGTATTAACTAACTAGATCTATTGAATTTCAGAGAAGAGCCTTCTAACT
TGTTTACACAAAAACGAGTATGATTTAGCATTCATACTAGTTGAAATTTTTAATAGAATCAAGGCACAAAAGTCT
TAAAACCATGTGGAAAAATTAGGTAATTATTGCAGATTGATGTCTCTCAATCCCATGTATTGCGCTTATGTTACA
AGTTGTTGTCACAGTTGAGACTTAATTTCTCCTAATTTCTTCTGCCCGAAGGGTAAGTGGTGCGTCCAGCTTACA
CAATCATAATTCAAAGGTTGGTGGGCAATGTAATACTTAATTAAAATAATGATGGAAGAGCTATCTGGAGATTAT
GAGTAAGCTGATTTGAATTTTCAGTATAAAACTTTAGTATAATTGTAGTTTGCAAAGTTTATTTCAGTTCACATG
TAAGGTATTGCAAATAAATTCTTGGACAATTTTGTATGGAAACTTGATATTAAAAACTAGTCTGTGGTTCTTTGC
AGTTTCTTGTAAATTTATAAACCAGGCACAAGGTTCAAGTTTAGATTTTAAGCACTTTTATAACAATGATAAGTG
CCTTTTTGGAGATGTAACTTTTAGCAGTTTGTTAACCTGACATCTCTGCCAGTCTAGTTTCTGGGCAGGTTTCCT
GTGTCAGTATTCCCCCTCCTCTTTGCATTAATCAAGGTATTTGGTAGAGGTGGAATCTAAGTGTTTGTATGTCCA
ATTTACTTGCATATGTAAACCATTGCTGTGCCATTCAATGTTTGATGCATAATTGGACCTTGAATCGATAAGTGT
AAATACAGCTTTTGATCTGTAATGCTTTTATACAAAAGTTTATTTAATAATAAAATGTTTGTTCTAACTTGTCT
GCTTTTTTAAAAATAATCTTACTGTACTTAATTCTAATTTTTTCCTCATATTTAAATAAAAGGCCATTTCCACCT
TTTCT

FIGURE 286

MDARRVPQKDLRVKKNLKKFRYVKLISMETSSSSDDSCDSFASDNFANTRLQSVREGCRTRSQCRHSGPLRVAMK
FPARSTRGATNKKAESRQPSENSVTDSNSDSEDESGMNFLEKRALNIKQNKAMLAKLMSELESFPGSFRGRHPLP
GSDSQSRRPRRRTFPGVASRRNPERRARPLTRSRSRILGSLDALPMEEEEEEDKYMLVRKRKTVDGYMNEDDLPR
SRRSRSSVTLPHIIRPVEEITEEELENVCSNSREKIYNRSLGSTCHQCRQKTIDTKTNCRNPDCWGVRGQFCGPC
LRNRYGEEVRDALLDPNWHCPPCRGICNCSFCRQRDGRCATGVLVYLAKYHGFGNVHAYLKSLKQEFEMQA

FIGURE 287

GCTCCGGGAGACTTCCGGCAGGGCGGGCGCGGGGTCTTGGCGAACGGTCTTCGGAAGCGGCGGCGGCGCG**ATG**AC
CACGCTACGGGCCTTTACCTGCGACGACCTGTTCCGCTTCAACAACATTAACTTGGATCCACTTACAGAAACTTA
TGGGATTCCTTTCTACCTACAATACCTCGCCCACTGGCCAGAGTATTTCATTGTTGCAGAGGCACCTGGTGGAGA
ATTAATGGGTTATATTATGGGTAAAGCAGAAGGCTCAGTAGCTAGGGAAGAATGGCACGGGCACGTCACAGCTCT
GTCTGTTGCCCCAGAATTTCGACGCCTTGGTTTGGCTGCTAAACTTATGGAGTTACTAGAGGAGATTTCAGAAAG
AAAGGGTGGATTTTTTGTGGATCTCTTTGTAAGAGTATCTAACCAAGTTGCAGTTAACATGTACAAGCAGTTGGG
CTACAGTGTATATAGGACGGTCATAGAGTACTATTCGGCCAGCAACGGGGAGCCTGATGAGGACGCTTATGATAT
GAGGAAAGCACTTTCCAGGGATACTGAGAAGAAATCCATCATACCATTACCTCATCCTGTGAGGCCTGAAGACAT
TGAA**TAA**CCCTGGGCAGTGGTTCTTAGGCAGATACTCTAGATGCTTTATGGACAATATTATTTTCATTGGATGAT
TCTGGAGCTCTATTAGGAGAAAAGTAATCATTTTAGGTCTTAAAGACTTCAAGAAAATACAGGTTATCAATTTAT
TTTAAATCTCATTGTTTCCAGTTAGCAATATCATACCTATTAAAGCTGTTCATTGTAACAAAATTCAATCAAAAA
GGCAGCTAGGTCAGAAGGAAACATACCACTCTCATGGTTCATAGTATTCACTGTATGTATGCTAGGGAAAAGACT
TGCTCCAGTCTCCTCCTCAGTTCTGTGCCTGAGAACCACTGCTGCATATATTTGTTTTTAAATTTTGTATTGAAC
TGTTAATTGAAGCTTTAAAAGCATATATGAAATGTATAAATCTAAGATGTATAATACATTATTGACTCTAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MTTLRAFTCDDLFRFNNINLDPLTETYGIPFYLQYLAHWPEYFIVAEAPGGELMGYIMGKAEGSVAREEWHGHVT
ALSVAPEFRRLGLAAKLMELLEEISERKGGFFVDLFVRVSNQVAVNMYKQLGYSVYRTVIEYYSASNGEPDEDAY
DMRKALSRDTEKKSIIPLPHPVRPEDIE

FIGURE 289

GTGCTCGGCGTTGAGCTCCTGCAGCCGCCGCCGCTGCAGTGGTCGTCCCTGCCCTCCCCGGCCCCGGGGTGCACC
CCGCAAGGCTCCCGCTGGTGTCCCTGGAGCATGGGAGGCTGCTGAGCGTGAGTGGCGGTGTCTGGCAGGAGCTGC
GTGGCAGGGAGGGCGTCC**ATG**GCTGCAGCCAACAAGGGCAACAAGCCCAGAGTCCGGGGTATCCGCTTTGCGGCA
GGCCACGATGCAGAAGGATCCCACAGCCACGTCCACTTTGATGAGAAGCTGCATGACTCGGTGGTCATGGTCACC
CAGGAGAGTGACAGCAGCTTTCTGGTCAAGGTTGGCTTCCTGAAGATCCTGCACAGGTATGAGATTACCTTCACT
CTGCCCCCAGTGCACAGGCTGAGCAAGGATGTCCGCGAGGCACCTGTCCCCAGCCTGCACCTCAAGCTCCTCAGC
GTGGTGCCCGTCCCTGAAGGTTATAGTGTCAAGTGTGAGTACTCGGCGCACAAAGAGGGCGTCCTCAAAGAGGAG
ATACTGCTAGCCTGCGAAGGTGGCACTGGCACCTGTGTGCGCGTGACGGTGCAGGCCCGCGTCATGGACCGGCAC
CACGGCACGCCCATGCTGCTGGATGGTGTCAAGTGTGTGGGCGCCGAGCTGGAATACGACTCAGAGCACAGCGAC
TGGCACGGCTTTGAC**TGA**GGCCCGAGGCCCCGCCTGCCCCGGGCCCCTCAGCCTTAAACCCCGCCTTGTCCCCCC
GACATGCTGCGTGATGGTGTGGCTTCCTCGCCCCTCTCTGGGGTGGGTGTGGGGGTGGAGTGGCCTTGCCCACGC
CTCTCACCTCTGCCTTCATTTGTGCTGCCACCCTGCCCCTCCCTCGTCCTCCTCTCCCACTTCCTCCTCTCTGTG
TGCCTCAGTCTCCTGCCGGAAGAAATGGGTTGATCCCGAAAGGAGGCTGTCTGAGGAAGGGAGAGGGAGGGCCTG
GGGTGGGTCCCCCACTCCCCACCCCAAGCCACAGGGACTCCCACCAGGGTCTGGGAGAGGACGGAGCTGGCTCTG
TGGCGTCGTGGCCCCATTACTGCTGCCTTGCTTCAGCCACCTCTCCTGCCCCTCCCTAGTCCCCACTGCTGTCCA
CCATGAGTAGGAGGGAGGTGCAGTCCCCAGCCCCCACCCCTCAGGTCTGTGTTACTTGGTTTTTAAGCGACTGGT
TGGGATAGAACCCTAAAGAAATAAACTTCCAGTGGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

FIGURE 290

MAAANKGNKPRVRGIRFAAGHDAEGSHSHVHFDEKLHDSVVMVTQESDSSFLVKVGFLKILHRYEITFTLPPVHR
LSKDVREAPVPSLHLKLLSVVPVPEGYSVKCEYSAHKEGVLKEEILLACEGGTGTCVRVTVQARVMDRHHGTPML
LDGVKCVGAELEYDSEHSDWHGFD

FIGURE 291

CTGAGCGGCGGGGGGCAGTGTCGCCTCGGTCTAGGCACGGCGGCGGAGTCGGTGGTCCCTGCGCGATGGCCACCT
CGGTGTTGTGCTGCCTGCGGTGCTGCAGAGACGGGGGGACTGGCCACATCCCTCTGAAGGAGATGCCGGCCGTGC
AGCTGGACACGCAGCACATGGGAACAGATGTTGTTATTGTAAAGAATGGAAGAAGAATATGTGGAACAGGAGGTT
GTTTAGCCAGCGCACCTTTACATCAAAACAAAAGCTATTTTGAATTCAAAATCCAGTCCACAGGAATCTGGGGTA
TTGGTGTTGCAACTCAGAAGGTTAACTTGAATCAGATTCCTCTTGGCCGAGATATGCACAGTCTGGTGATGAGAA
ATGATGGAGCCCTTTACCACAACAATGAAGAGAAAAATAGGCTGCCAGCAAACAGTCTTCCGCAGGAAGGAGATG
TGGTGGGTATTACTTATGACCATGTCGAATTAAATGTATACTTGAATGGAAAAAACATGCATTGTCCAGCATCAG
GTATACGAGGGACAGTGTATCCAGTTGTTTATGTTGATGACAGTGCAATTTTGGATTGCCAGTTCAGTGAGTTTT
ATCATACGCCTCCACCTGGTTTTGAAAAAATATTATTTGAACAGCAAATCTTC**TGA**ATGTATTTGTTTTTAAAAC
TTGTATTTCTGCACTGTTAAAAAATGTTCATCATTTAATAAAACTTTACCTGGCCTATAGATGAAAATATATTCT
TAAAAATATGCTTGTTGATGCCGTCTAAGGAACCAATGTATTCAGTATACCACCCTGAAGTTGTGATTTAAAATA
CTTTATGTTTTGTGAAATGAAAATAAGCATTTGGGCAGTTTATTTAATTCTTATTTAAATAAATAGAATTATGGG
TTTAATTAACAGTATAACATGACTATATATACATATATATTTAAAGGGAATTCTTTCTTACATAATATATTTGTT
TTGATAGAGATGTAGAGTTGGGTGGGTGTTTTTGTCACTCTGAAGTTTAGACCTCATTAAATATTTGACATCTAC
AGTTGGATAATTTTGCCGCTTAGTGTCCTTTTTTATATACAATATAACAAAGTGAGAGAAATTTATATTACTGGC
AATTTCATTTTTGGCAGTCTATTTCTGTATCATGTACCGCTTTTCTTAAAACTTAAATTGCTTATTTTGTTGTGT
AATGTCATTGCTTTTGATTTGCTTTGTGAAAGGAGATAAACGTTTCAGTAATTGTCAGAGCATTTTGTTGCCTCA
GGCTGTGTTACCTCAATTTCAGAGTAAGTAGTGGTTGATTAGTAATGTAGTATACACTGGCAGACATCTAGAATA
GTATGATGCTTTACATTTAAATGAGGTTATTCTTTTAAGGACTTTTATTTGTATGTTTTCTGTAAGGAATAATAA
AATAATTGTAATTAAGGAATATACCATACTATATTAAACACATTCTTCCTAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 292

ERRGAVSPRSRHGGGVGGPCAMATSVLCCLRCCRDGGTGHIPLKEMPAVQLDTQHMGTDVVIVKNGRRICGTGGC
LASAPLHQNKSYFEFKIQSTGIWGIGVATQKVNLNQIPLGRDMHSLVMRNDGALYHNNEEKNRLPANSLPQEGDV
VGITYDHVELNVYLNGKNMHCPASGIRGTVYPVVYVDDSAILDCQFSEFYHTPPPGFEKILFEQQIF

FIGURE 293

AAGAATGTCTCAGGAGGAAGCATGACAGAGATGTTTGTCCAGTTAAAACTGGGAGATCAGAGGTATAAAAGTAAG
G**ATG**GGCATTTTGGACATTGAAGTGTGGGGAAAGGACAACAAAAAGCATGAGGAACGTCTGGGCACGTGTAAAGT
GGATATCTCGGCACTCCCTCTGAAGCAAGCCAACTGCCTGGAGCTGCCACTGGACAGCTGTCTGGGGGCTCTCCT
TATGTTGGTCACACTTACACCCTGTGCGGGGGTCTCCGTCTCTGATCTGTGTGTCTGCCCCTTAGCAGACCTCAG
CGAAAGAAAGCAGATTACCCAGCGATATTGCTTACAGAACTCCCTGAAAGATGTGAAAGACGTCGGCATTCTACA
AGTGAAGGTTTTAAAGGCAGCAGATCTCTTAGCGGCAGATTTCTCAGGGAAGAGTGACCCATTTTGCTTGTTGGA
GTTAGGCAATGACCGACTTCAGACGCATACCGTCTACAAAAACCTCAACCCTGAATGGAACAAAGTTTTTACATT
TCCCATTAAAGATATCCATGATGTTTTGGAAGTGACAGTGTTTGATGAAGATGGAGATAAACCCCCAGATTTTCT
TGGAAAAGTTGCCATTCCCTTGCTGTCCATTAGAGATGGACAACCGAATTGTTATGTACTAAAGAATAAAGATTT
AGAACAAGCTTTTAAAGGAGTTATTTACTTAGAGATGGACCTTATATATAATCCGGTGAAAGCAAGTATTAGGAC
TTTTACTCCCCGGGAAAAGCGCTTTGTTGAAGACAGCCGCAAGCTGTCCAAAAAGATCTTATCAAGAGATGTGGA
CCGTGTGAAAAGAATCACTATGGCAATATGGAATACAATGCAGTTCCTTAAAAGCTGCTTCCAGTGGGAATCCAC
ATTAAGAAGTACAATAGCATTCGCGGTATTTTTGATCACTGTCTGGAATTTTGAACTATATATGATCCCCTTGGC
ATTGTTGCTGATCTTTGTCTACAATTTCATCAGACCTGTGAAAGGCAAGGTCAGCAGCATCCAGGACAGCCAGGA
GAGCACAGACATAGATGACGAGGAGGATGAAGATGACAAGGAATCTGAGAAAAAGGGGTTGATTGAAAGAATCTA
TATGGTACAGGATATTGTTTCAACTGTTCAAAACGTCTTGGAGGAAATAGCTTCTTTTGGAGAAAGGATTAAGAA
CACATTTAACTGGACGGTCCCCTTCCTTTCATCTCTGGCCTGTTTGATTCTGGCAGCAGCCACCATCATTTTGTA
TTTCATTCCACTGCGGTACATCATTTTAATCTGGGGCATAAATAAATTTACTAAGAAGCTTCGAAATCCCTATTC
CATCGACAATAATGAGCTACTAGACTTCCTCTCTAGGGTACCGTCTGATGTTCAAAAGGTGCAGTATGCAGAATT
GAAACTCTGCAGCAGCCACAGCCCCCTGCGGAAGAAGCGCAGCGCTCTC**TAG**GGCACACACCGACTTTGGACAGC
AGCACCCAATATTGTGTTTGGTTGAGTAGACCAATGTTATGGCTGTTTCAGTGGTACCCAAGGTGTCCTTCTGAA
ATGCATGCCCTGTGGCACCCTCTGTATACTTCCTCCTCCTTCACGTGCACAGACATACACACATGTGCACACACC
CTCATGCATGGGTGTCCTAGTTGCGTAGAGGGTCAGCCCAGCGAAAAGCAACAACCCCAAGACTGTGAAAGACTA
ACATCCATTCTGAAATAGGAGATAACAAGGCTGCCATGGATCTGAACACCACCTTCCTTGAGAACAGCCAGGAGC
CCACTTGGATTCAAGAGTGACTTTGAACTTGTTTTCACACCTCCAACAGACTCTCATTAAGATTCAGTTATTTCC
GCTCCCCAGCCCCACACTCCTTTCAGATTATCGTTCATGGGCGTAAGTCTCTTCTCAGAGTTAACAAGTCTTTGG
TAGTCATCCTCTGTCCAAATATTGTATATTATTAAAAGGCATTTTTAATAATTACCAGAATTAGCTCAAACCTTT
AGGGATCTTTCAGCCATGATTATTAAGGATATGTATGTGAATTTTTGGGAAACCTCTCGGTGCTGGATGCCAGCC
TACAGCAGGGTCCATTGCTGGCAATGGATGGCCCAGGAAGGTCCCTAGAGATCACTCACTTGAAAAATGAGGGTC
CCATGAAAGTATTTGGTTGCCTTCTGATGCCACTTCTTCTCACTTTACTTTTTGCTTATTTTCAAAATATTATAA
AATGTCAACATATAATTTCAGAAAGGCAGGTGGGGGTAGGGGAGAAATGAATGAATAAATTCTCTAGGTATCTAG
AAAGATAAGAAACTGAAGACCGAGAGACTAATAAGGCTGCTTACCTAATTATTATAATCATTTCATTTGCCTGAA
TGTTTTAAGCAGGAAGTAGAAATACTTTGGCTGCCCAAATGTATCTTTTGTTCCTCTTAGAAGTAAAATAAGCTA
CATACAATAAAAATTTATTTCAGAACCCCATTTCTAGAAAATACCACCCCAGAGTCCTCATTTGATAGCATCTGT
CTCCTGCAGACCTCATCATTCCACAGTATTTCCCTGCCATGTAAAAATCCTGACTTTGTGCGTATATAAAATGTA
TGCAATTAAGTCTGTTTAAATGATATTTAAGTTTTAAAGACTGTATTTTGTTGACACATACTTTGTGCAGTTTTT
ATGTATGTATGTATTATAAAAAAAGTTAAGGTTAAAAAC

FIGURE 294

MGILDIEVWGKDNKKHEERLGTCKVDISALPLKQANCLELPLDSCLGALLMLVTLTPCAGVSVSDLCVCPLADLS
ERKQITQRYCLQNSLKDVKDVGILQVKVLKAADLLAADFSGKSDPFCLLELGNDRLQTHTVYKNLNPEWNKVFTF
PIKDIHDVLEVTVFDEDGDKPPDFLGKVAIPLLSIRDGQPNCYVLKNKDLEQAFKGVIYLEMDLIYNPVKASIRT
FTPREKRFVEDSRKLSKKILSRDVDRVKRITMAIWNTMQFLKSCFQWESTLRSTIAFAVFLITVWNFELYMIPLA
LLLIFVYNFIRPVKGKVSSIQDSQESTDIDDEEDEDDKESEKKGLIERIYMVQDIVSTVQNVLEEIASFGERIKN
TFNWTVPFLSSLACLILAAATIILYFIPLRYIIILIWGINKFTKKLRNPYSIDNNELLDFLSRVPSDVQKVQYAEL
KLCSSHSPLRKKRSAL

FIGURE 295

GCTGGGAGTACAGGCAACGGGAAGGATTATGGAAAAGACTACACACTTATTTTTCACTTGCAAAGAAAACCTAGG
CTGGAACTCCAAATCAAAGAAGTGGACGAATTTGGAAACTATAGTTGCCCTCATTACAAAGGCACCATTGTCGTT
TATAAAGTACCTAAAGGAAAGATAGTCCCCAACTTGAATCAATCTCTCGTAATTAATGAAAACCATTCTCAGTTG
CCAATTTGCAAATTACCATTGAAATTGCCAAAGCATAAGAAATTAATCAACCGTACACAGAGTACCAAAAGAGTT
TCTAAGGATCCTGTAGAAGCCCTTTGGGATAACTTGCTCCATTGGCTGGCTGAGGAGCTCTCAGAAGAAAATGCT
GAGTCTCTTTCCTCAACTCTCCCTCTGCGCCGTAGCACCATTCAGCTCATCAAACTCAAGAACCCTGATGATCTC
ACAGAACAGATCCACGAGTTTCTTTGCTTCTGGAAAAAATCGCTTCCAACTTTCACCGACAAACTTCGCCTCCTG
GCTCGACATCTCCGCAAGATTGGCAGGAGTGATCTTGCAGAAGAGCTCAAATTCAAGTGGGAAAATAAAGTGTTC
ACTGAACCACAGCAGTGTTTTGATGTAAA

FIGURE 296

AGSTGNGKDYGKDYTLIFHLQRKPRLELQIKEVDEFGNYSCPHYKGTIVVYKVPKGKIVPNLNQSLVINENHSQL
PICKLPLKLPKHKKLINRTQSTKRVSKDPVEALWDNLLHWLAEELSEENAESLSSTLPLRRSTIQLIKLKNPDDL
TEQIHEFLCFWKKSLPTFTDKLRLLARHLRKIGRSDLAEELKFKWENKVFTEPQQCFD

FIGURE 297

AGGTTCTCTTACATCGACCGCCTAAGAGTCGCGCTGTAAGAAGCAACAACCTCTCCTCTTCGTCTCCGCCATCAG
CTCGGCAGTCGCGAAGCAGCAACC**ATG**CGTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGC
AATGCCTGCTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATT
GGGGGAGGAGATGATTCCTTCAACACCTTCTTCAGTGAGACGGGGGCTGGCAAGCATGTGCCCCGGGCAGTGTTT
GTAGACTTGGAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAACTT
ATCACAGGCAAAGAAGATGCTGCCAATAACTATGCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTC
GTGTTGGACCGAATTCGCAAGCTGGCCGACCAGTGCACGGGTCTCCAGGGCTTCTTGGTTTTCCACAGCTTTGGT
GGGGGAACTGGTTCTGGGTTCACCTCGCTGCTCATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTG
GAGTTCTCTATTTACCCGGCGCCCCAGGTTTCCACAGCTGTAGTTGAGCCCTACAACTCCATCCTCACCACCCAC
ACCACCCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTCGTAGAAACCTC
GATATTGAGCGTCCAACCTATACTAACCTGAATAGGTTAATAGGTCAAATTGTGTCCTCCATCACTGCTTCCCTG
AGATTTGATGGAGCCCTGAATGTTGACCTGACAGAATTCCAGACCAACCTGGTGCCCTATCCCCGCATCCACTTC
CCTCTGGCCACATATGCCCCTGTCATCTCTGCTGAGAAAGCCTACCATGAACAGCTTTCTGTAGCAGAGATCACC
AATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTG
TTGTACCGTGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAGACCAAGCGTACCATCCAG
TTTGTGGATTGGTGCCCCACTGGCTTCAAGGTTGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGAC
CTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGCCTGGAC
CACAAGTTTGACCTGATGTATGCCAAACGTGCCTTTGTTCACTGGTACGTTGGGGAGGGGATGGAGGAAGGTGAG
TTTTCAGAGGCCCGTGAGGACATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGA
GAGGGTGAGGAAGAAGGAGAGGAATAC**TAA**AGTTAAAACGTCACAAAGGTGCTGCTTTTACAGGGAAGCTTATTC
TGTTTTAAACATTGAAAAGTTGTGGTCTGATCAGTTAATTTGTATGTAGCAGTGTATGCTCTCATATACAATTAC
TGACCTATGCTCTAAAACATGAATGCTTTGTTACAGACCCAAGCTGTCCATTTCTGTGATGGGTTTTGAATAAAG
TATTCCCTGTCTTAAAAAAAAAAAAAA

FIGURE 298

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVI
DEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLADQCTRLQGFLVFHSFGGGTGSGFT
SLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYT
NLNRLIGQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPGHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGVHSVEGEGEEEGEE
Y

FIGURE 299

CACGCTGCTACTTATTTTCTTGAATATGGATACACGGTACTGTTTATGTAATACTTATGTACTTATATAATATGT
AAAACACTGCATAACAGATAACATGAAAAAGAGCTCTGGTATAGTATGAAAC**<u>ATG</u>**ATTCCAAAACATGGTATCAA
GTATGATGGATTCATATTAGGTTATTGGAGAAAAGTAAAGTATTTTGAAACACACCTTTACATGTTTATCTTAGC
ATCTGGAAAGACAACCGTTATCTTCTTACAACATACTTCTTGGTACCAATTTCGGAGA**<u>TAA</u>**AATTCTAGATTGGC
TAGGCCACGGTTCTGACCCAGTGTGGAAATTCTTATGCCTTAAGGAACTAAACTTAAAATATAAAGGATTCACAG
ACTATTTATAAATTTACAAGAATATTTGCTTTGTTCGAATACCTGTTTTCATACAGGAATTTAATATAACATTAA
TATACTGGAGTCCACCAGCATTTTAGGAAACTTCTTTGAGATTTTGAAACTCCTTTGAAAACTTCTTGAGATTTT
GAAAATCAAAGAATTATTTGTGGAAAAGGGAAGAAAATGCCTTCATTCAACACGTTTATTGGACCCTGAATGTGT
GAGACATTGTTGTAGGTAGCGTAGATACAGATATGTGCTAAATAAATACATACATAAGACCATTATCCCTGGAGA
GCTTTTGATCTGCTGTGGGAGAGAAAGTTTGTAGTGTGATGCAGAGGTGTGACTAAACTGCCATGGAGATGGGAT
GGAGTAGCTGACCTTTGAAATCAAGGATGAATTCTAGTTTTACAGGATGAAGGGCACGGGTGGCAGGAAGACATT
CCAGGCATATAGTATAGTGTATT

FIGURE 300

MIPKHGIKYDGFILGYWRKVKYFETHLYMFILASGKTTVIFLQHTSWYQFRR

FIGURE 301

TTTTCCCGCGAAACTCGGCGGCTGAGCGTGGAGGTTCTTGTCTCCCCTGGTTTGTGAAGTGCGGAAAACCAGAGG
CGCAGTC**ATG**TCGGGATTCGACGATCCTGGCATTTTCTACAGCGACAGCTTCGGGGGCGACGCCCAGGCCGACGA
GGGGCAGGCCCGCAAATCGCAGCTGCAGAGGCGCTTCAAGGAGTTCCTGCGGCAGTACCGAGTGGGCACCGACCG
CACGGGCTTCACCTTCAAATACAGGGATGAACTCAAGCGGCATTACAACCTGGGGGAGTACTGGATTGAGGTGGA
GATGGAGGATCTGGCCAGCTTTGATGAGGACCTGGCCGACTACTTGTACAAGCAGCCAGCCGAGCACCTGCAGCT
GCTGGAGGAAGCTGCCAAGGAGGTAGCTGATGAGGTGACCCGGCCCCGGCCTTCTGGGGAGGAGGTGCTCCAGGA
CATCCAGGTCATGCTCAAGTCGGACGCCAGCCCTTCCAGCATTCGTAGCCTGAAGTCGGACATGATGTCACACCT
GGTGAAGATCCCTGGCATCATCATCGCGGCCTCTGCGGTCCGTGCCAAGGCCACCCGCATCTCTATCCAGTGCCG
CAGCTGCCGCAACACCCTCACCAACATTGCCATGCGCCCTGGCCTCGAGGGCTATGCCCTGCCCAGGAAGTGCAA
CACAGATCAGGCTGGACGCCCCAAATGCCCATTGGACCCGTACTTCATCATGCCCGACAAATGCAAATGCGTGGA
CTTCCAGACCCTGAAGCTGCAGGAGCTGCCTGATGCAGTCCCCCACGGGGAGATGCCCAGACACATGCAGCTCTA
CTGCGACAGGTACCTGTGTGACAAGGTCGTCCCTGGGAACAGGGTTACCATCATGGGCATCTACTCCATCAAGAA
GTTTGGCCTGACTACCAGCAGGGGCCGTGACAGGGTGGGCGTGGGCATCCGAAGCTCCTACATCCGTGTCCTGGG
CATCCAGGTGGACACAGATGGCTCTGGCCGCAGCTTTGCTGGGGCCGTGAGCCCCCAGGAGGAGGAGGAGTTCCG
TCGCCTGGCTGCCCTCCCAAATGTCTATGAGGTCATCTCCAAGAGCATCGCCCCCTCCATCTTTGGGGGCACAGA
CATGAAGAAGGCCATTGCCTGCCTGCTCTTTGGGGGCTCCCGAAAGAGGCTCCCTGATGGACTTACTCGCCGAGG
AGACATCAACCTGCTGATGCTAGGGGACCCTGGGACAGCCAAGTCCCAGCTTCTGAAGTTTGTGGAGAAGTGTTC
TCCCATTGGGGTATACACGTCTGGGAAAGGCAGCAGCGCAGCTGGACTGACAGCCTCGGTGATGAGGGACCCTTC
GTCCCGGAATTTCATCATGGAGGGCGGAGCCATGGTCCTGGCCGATGGTGGGGTCGTCTGTATTGACGAGTTTGA
CAAGATGCGAGAAGATGACCGTGTGGCAATCCACGAAGCCATGGAGCAGCAGACCATCTCTATCGCCAAGGCTGG
GATCACCACCACCCTGAACTCCCGCTGCTCCGTCCTGGCTGCTGCCAACTCAGTGTTCGGCCGCTGGGATGAGAC
GAAGGGGGAGGACAACATTGACTTCATGCCCACCATCTTGTCGCGCTTCGACATGATCTTCATCGTCAAGGATGA
GCACAATGAGGTGAGGGATGTGATGCTGGCCAAGCATGTCATCACTCTGCACGTGAGTGCACTGACACAGACACA
GGCTGTGGAGGGCGAGATTGACCTGGCCAAGCTGAAGAAGTTTATTGCCTACTGCCGAGTGAAGTGTGGCCCCCG
GCTGTCAGCAGAGGCTGCAGAGAAACTGAAGAACCGCTACATCATCATGCGGACGGGGCCCGTCAGCACGAGAGG
GACAGTGACCGCGTCCAGCATCCCCATCACTGTGCGGCAGTTGGAGGCCATTGTGCGCATCGCGGAAGCCCTCAG
CAAGATGAAGCTGCAGCCCTTCGCCACAGAGGCAGATGTGGAGGAGGCCCTGCGGCTCTTCCAAGTGTCCACGTT
GGATGCTGCCTTGTCCGGTACCCTGTCAGGGGTGGAGGGCTTCACCAGCCAGGAGGACCAGGAGATGCTGAGCCG
CATCGAGAAGCAGCTCAAGCGCCGCTTTGCCATTGGCTCCCAGGTGTCTGAGCACAGCATCATCAAGGACTTCAC
CAAGCAGAAATACCCGGAGCACGCCATCCACAAGGTGCTGCAGCTCATGCTGCGGCGCGGCGAGATCCAGCATCG
CATGCAGCGCAAGGTTCTCTACCGCCTCAAG**TGA**GTCGCGCCGCTCACTGGACTCATGGACTCGCCACGCTCGCC
CTCCTTGCCGCTGCCTGCCATTGACAATGTTGCTGGGACCTCTGCCTCCCCACTGCAGCCCTCGAACTTCCCAGG
CACCCTCCTTTCTGCCCCAGAGGAAGGAGCTGTAGTGTCCTGCTGCCTCTGGGCGCCCGCTCTAGCGGGTTCTGG
GAAGTGTGCTTTTGGCATCCGTTAATAATAAAGCCACGGTGTGTTCAGGT

FIGURE 302

MSGFDDPGIFYSDSFGGDAQADEGQARKSQLQRRFKEFLRQYRVGTDRTGFTFKYRDELKRHYNLGEYWIEVEME
DLASFDEDLADYLYKQPAEHLQLLEEAAKEVADEVTRPRPSGEEVLQDIQVMLKSDASPSSIRSLKSDMMSHLVK
IPGIIIAASAVRAKATRISIQCRSCRNTLTNIAMRPGLEGYALPRKCNTDQAGRPKCPLDPYFIMPDKCKCVDFQ
TLKLQELPDAVPHGEMPRHMQLYCDRYLCDKVVPGNRVTIMGIYSIKKFGLTTSRGRDRVGVGIRSSYIRVLGIQ
VDTDGSGRSFAGAVSPQEEEEFRRLAALPNVYEVISKSIAPSIFGGTDMKKAIACLLFGGSRKRLPDGLTRRGDI
NLLMLGDPGTAKSQLLKFVEKCSPIGVYTSGKGSSAAGLTASVMRDPSSRNFIMEGGAMVLADGGVVCIDEFDKM
REDDRVAIHEAMEQQTISIAKAGITTTLNSRCSVLAAANSVFGRWDETKGEDNIDFMPTILSRFDMIFIVKDEHN
EVRDVMLAKHVITLHVSALTQTQAVEGEIDLAKLKKFIAYCRVKCGPRLSAEAAEKLKNRYIIMRTGPVSTRGTV
TASSIPITVRQLEAIVRIAEALSKMKLQPFATEADVEEALRLFQVSTLDAALSGTLSGVEGFTSQEDQEMLSRIE
KQLKRRFAIGSQVSEHSIIKDFTKQKYPEHAIHKVLQLMLRRGEIQHRMQRKVLYRLK

FIGURE 303A

CCACGCGTCCGGGGAAGATGCCCAGGGGACAGGATTGATGCATATTCCTGATCTTCCACAGGAGTGGTCCCGTAG
GCCTCACCCTCTCCGTCCACCATCTCTACTGCCCGCTCTGCTGGTTGGGCCTCTGGTGT**ATG**GACTTGTACATGA
TGAACTGTGAACTTCTAGCCACGTGTAGCGCCCTTGGGTACTTGGAAGGAGGGACTTACCACAAGGAGCCGGATT
GCCTGGAGAGTGTGAAGGATTTGATCCGATACCTGAGGCACGAGGATGAGACCCGAGATGTGCGGCAGCAGCTGG
GAGCTGCACAGATCCTGCAGAGCGACCTCCTGCCAATCCTCACGCAGCATCGCCAGGACAAGCCTCTCTTCGATG
CCGTGATCAGGCTGATGGTAAATTTGACACAGCCAGCCTTGCTCTGTTTTGGCAGCGTGCCTAAGGACTCCAGTG
TACGGCACCATTTTCTGCAGGTTCTAACGTACCTGCAAGCCTACAAAGAGGCCTTTGCCAGTGAGAAGGCATTTG
GAGTCCTCAGCGAGACCTTGTATGAATTGCTACAGCTGGGCTGGGAGGATCGGCAAGAAGAAGACAACTTGCTGA
TCGAGCGGATCCTTCTGCTGGTCAGAAATATTCTCCATGTCCCGGCCAACCTTGAGCAGGAGAAGAGTATCGATG
ATGATGCCAGCATCCACGACCGTCTCCTTTGGGCAATTCACCTCAGTGGCATGGACGACTTGCTCCTCTTCCTGT
CCAGCTCATCCGCCGAGCAGCAGTGGAGCCTCCATGTGCTGGAGATCATCTCCCTCATGTTCCGAGACCAGACCC
CTGAGCAGCTAGCGGGAGTAGGGCAGGGACGCTTGGCTCAGGAGCGAAGCACGGATGTGGCAGAATTGGAGGTGC
TGCGCCAACGGGAGATGGCGGAGAAGAGAGCTCGGGCCCTCCAGCGAGGAAACAGGCACTCTCGATTTGGGGGCT
CCTACATTGTCCAGGGGTTGAAATCTATTGGGGAGAAGGATGTCGTCTTTCACAAAGGCCTTCACAATCTCCAGA
ACTACAGCTCAGATCTGGGAAAGCAGCCCAGGAGGGTGCCCAAGCGTCGTCAGGCTGCCCAGGAGCTGTCTGTCC
ATCGCCGCTCTGTCCTGAATGTGAGACTCTTCCTCAGAGACTTCTGCTCTGAGTTCCTGGAGAACTGCTACAACC
CGCTCATGGGCGCGGTCAAGGATCATCTGCTTCGGGAGAGAGCGCAGCAGCATGACGAGACTTACTACATGTGGG
CAATGGCTTTCTTCATGGCCTTCAACCGAGCTGCCACCTTCCGCCCCGGCCTTGTTTCTGAGACCCTCAGTATCC
GTACCTTTCACTTTGTGGAGCAGAACCTCACCAACTACTACGAGATGATGCTGACAGACCGCAAGGAGGCCGCCT
CCTGGGCGCGCAGGATGCACCTGGCCCTGAAGGCCTACCAGGAGCTGCTGGCCACGGTGAACGAGATGGACATGT
GCCCAGATGAGGCTGTTAGGGAGAGCAGTCGTATCATCAAAAACAACATTTTCTATATGATGGAGTACCGAGAAC
TATTCCTGGCGCTCTTTCGAAAGTTTGATGAGAGATACCATCCACGCTCATTCCTTCGAGACCTGGTGGAAACCA
CCCACCTCTTCCTCAAAATGTTGGAGCGCTTTTGCCGGAGCCGCGGGAACCTGATGGTGCAGAACAAAAGAAAAA
AGAGGAAAAAGAAAAAGAAGGTTCAGGACCAGGGTGTTGCTTTCTCACAAAGCCCCGGGGAGCTGGAGGCCATGT
GGCCAGCCCTGGCAGAGCAGCTGCTGCAGTGTGCCCAGGACCCTGAGCTCAGTGTGGACCCCGTCGTTCCCTTTG
ATGCGGCCTCAGAGGTGCCAGTGGAGGAGCAGCGGGTAGAAGCCATGGTGAGGATCCAAGACTGCCTTACGGCTG
GCCAGGCCCCGCAAGCCCTGGCCCTCCTGCGGTCTGCCCGGGAAGTGTGGCCTGAAGGAAATGCGTTTGGCTCTC
CAGTCATTTCCCCAGGGGAAGAAATGCAGTTGCTGAAACAAATCCTCTCCACGCCCCTTCCCCGGCAGCAGGAGC
CAGAAGAAGGAGATGCAGAGGAGGAAGAGGAAGAGGAGGAGGAAGAGGAGTTACAGGTGGTCCAGGTGTCAGAGA
AGGAGTTTAACTTTCTGGAATACCTGAAACGCTTCGCATCCTCAACCATCGTGCGGGCCTACGTGCTTCTCCTGC
GGAGCTACAGGCAGAACAGTGCTCACACCAACCACTGCATCGCCAAGATGCTGCACCGGCTGGCCCATGGCCTGG
GGATGGAAGCCCTGCTTTTCCAGCTGTCCCTGTTCTGCCTCTTCAATCGGCTGCTTAGTGACCCAGCTGCTGCGG
CCTACAAAGAGCTAGTGACTTTTGCCAAATACATCATTGGCAAGTTCTTTGCGTTGGCTGCCGTGAACCAGAAAG
CGTTTGTGGAGCTGCTATTCTGGAAGAACACCGCAGTGGTTCGGGAAATGACCCAGGGATATGGCTCCCTCGACA
GTGGGTCTTCCAGCCACAGAGCTCCTCTGTGGAGCCCTGAGGAAGAGGCCCAGCTTCAGGAACTATACCTCGCCC
ACAAGGATGTGGAAGGTCAAGATGTAGTGGAAACCATATTGGCGCACCTGAAAGTCGTTCCTCGAACACGCAAGC
AGGTCATCCACCACCTGGTCCGGATGGGCCTGGCCGACAGCGTCAAGGAGTTCCAGAAGAGGAAAGGGACCCAGA
TTGTCTTGTGGACGGAGGACCAGGAGCTGGAGTTACAGCGGCTCTTTGAGGAGTTCCGGGACTCTGATGATGTTC
TTGGTCAAATCATGAAGAATATCACAGCCAAACGTTCACGGGCTCGAGTAGTGGACAAACTGTTGGCCCTGGGGT
TGGTGTCTGAGCGGAGGCAGCTATACAAGAAACGGAGAAAGAAGCTGGCGCCTTCTTGCATGCAGAATGGAGAAA
AGTCCCCGAGAGACCCCTGGCAGGAAGATCCGGAAGAGGAAGACGAACACTTGCCAGAGGACGAAAGTGAAGATG
AGGAGAGTGAGGAAGGCTTGCCATCAGGACAGGGTCAGGGCAGCTCATCTCTCTCTGCTGAAAACCTCGGTGAGA
GCCTTCGTCAGGAAGGCCTCTCTGCTCCCCTCCTGTGGCTCCAGAGCTCCCTGATCCGAGCAGCAAATGACCGAG
AAGAGGATGGCTGCTCCCAGGCAATCCCTCTGGTGCCTCTGACAGAGGAAAATGAGGAAGCAATGGAGAACGAAC
AGTTTCAGCATCTGCTACGCAAGCTAGGGATCCGGCCGCCCAGCTCAGGGCAGGAAACCTTCTGGAGAATTCCAG
CCAAACTGAGCTCCACCCAGCTTCGGAGGGTGGCTGCTTCTTTGAGTCAGCAAGAAAACGAGGAGGAAAGGGAAG
AGGAGCCAGAGCCAGGAGTCCCCGGAGAGCAGGGTCCCAGTGAGGAGCACCGGACAGAAGCCCTGAGAGCCCTTC
TGTCAGCCCGTAAGAGGAAAGCAGGCCTGGGGCCTACAGAAGAGGAGGCCACTGGGGAGGAAGAATGGAACTCAG

FIGURE 303B

CGCCCAAGAAGCGGCAACTGCTGGACAGCGACGAAGAGGAAGATGATGAGGGGAGGAGGCAAGCAGTGTCGGGAA
CGCCAAGAGTCCACAGGAAGAAACGGTTTCAGATTGAGGATGAGGATGAC**TGA**AAGCCAGATGTGTTTGACCGAT
GTGAGTTGGAGGCACAAAAGCTACTTTTGCCTGCGTTGGAAGCAATCTTCTCTACATTGACAGCCCAGGAATTTT
AGGCAGCAGTGTTGGGTGGAGTCTTTGCGGTCAGTCCTTGCCCCAGGTTCATCAGCGTGCACAGCCGGTCTCTGG
GTCCGTCTCGTAGCAAATGAAGAGTGGCGAAAGGTTCAAGGTGGCTTGTCCTCCTCTAAGGACTGCGTCTTGGCT
TCTGACGGGGAGCTTTATAACCCAGCACGGTTGTTCATTCTGTCCTCACAAAGCACTGGATTGCTCCCATTTTCT
TTCTTTCATCCCAGGACACATGATTGAACCCGTTTCTACAGTTGAGGGAGAGCTGGGATGCACCACTCTCAAGCT
GACAAGCATCCCTGATTTGTGTTTCATATTAAATGTGTACAATTAACAGTTGCTCATCTCAGAACGGCCAGCCAG
CCATCTGTTGTGTCTTCGGAAGAACTTTTAAGAGTAAAATTAAAAGACATGTCCTGAACTGAGCTTGGTAGTGTG
AGCTAATCCCATCGTGTGGGAGACAGAGGCAAGAGAATTGCCATGAGGGAGAGGAAAGAGTCATATAGCCCTACG
CGTGGGCCAATAAATGTAATTTAAAAAATCAGCTTGATAATAAATATAATTTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 304

MDLYMMNCELLATCSALGYLEGGTYHKEPDCLESVKDLIRYLRHEDETRDVRQQLGAAQILQSDLLPILTQHRQD
KPLFDAVIRLMVNLTQPALLCFGSVPKDSSVRHHFLQVLTYLQAYKEAFASEKAFGVLSETLYELLQLGWEDRQE
EDNLLIERILLLVRNILHVPANLEQEKSIDDDASIHDRLLWAIHLSGMDDLLLFLSSSSAEQQWSLHVLEIISLM
FRDQTPEQLAGVGQGRLAQERSTDVAELEVLRQREMAEKRARALQRGNRHSRFGGSYIVQGLKSIGEKDVVFHKG
LHNLQNYSSDLGKQPRRVPKRRQAAQELSVHRRSVLNVRLFLRDFCSEFLENCYNPLMGAVKDHLLRERAQQHDE
TYYMWAMAFFMAFNRAATFRPGLVSETLSIRTFHFVEQNLTNYYEMMLTDRKEAASWARRMHLALKAYQELLATV
NEMDMCPDEAVRESSRIIKNNIFYMMEYRELFLALFRKFDERYHPRSFLRDLVETTHLFLKMLERFCRSRGNLMV
QNKRKKRKKKKVQDQGVAFSQSPGELEAMWPALAEQLLQCAQDPELSVDPVVPFDAASEVPVEEQRVEAMVRIQ
DCLTAGQAPQALALLRSAREVWPEGNAFGSPVISPGEEMQLLKQILSTPLPRQQEPEEGDAEEEEEEEEEEELQV
VQVSEKEFNFLEYLKRFASSTIVRAYVLLLRSYRQNSAHTNHCIAKMLHRLAHGLGMEALLFQLSLFCLFNRLLS
DPAAAAYKELVTFAKYIIGKFFALAAVNQKAFVELLFWKNTAVVREMTQGYGSLDSGSSSHRAPLWSPEEEAQLQ
ELYLAHKDVEGQDVVETILAHLKVVPRTRKQVIHHLVRMGLADSVKEFQKRKGTQIVLWTEDQELELQRLFEEFR
DSDDVLGQIMKNITAKRSRARVVDKLLALGLVSERRQLYKKRRKKLAPSCMQNGEKSPRDPWQEDPEEEDEHLPE
DESEDEESEEGLPSGQGQGSSSLSAENLGESLRQEGLSAPLLWLQSSLIRAANDREEDGCSQAIPLVPLTEENEE
AMENEQFQHLLRKLGIRPPSSGQETFWRIPAKLSSTQLRRVAASLSQQENEEEREEEPEPGVPGEQGPSEEHRTE
ALRALLSARKRKAGLGPTEEEATGEEEWNSAPKKRQLLDSDEEEDDEGRRQAVSGTPRVHRKKRFQIEDEDD

FIGURE 305

ATCTGAACCCAGGAAAGAAACCCATTTGCCGACCCCCTCTTCCCTCTCCAGACAGGTGGAGAGCGGGTGAGGGTC
TCGCTCGGCTTTCCCCCTGCACCTTTCCCACCCTCCCGCCCGTCCCTGGGGGTCCTCCGTCACCGCGGCC**ATG**GC
CCAGAAGCCGAAGGTGGACCCCCACGTCGGGCGGCTGGGATACCTGCAGGCGCTGGTCACGGAATTCCAGGAGAC
CCAAAGCCAAGACGCCAAGGAGCAAGTCCTCGCCAACCTCGCCAACTTCGCTTATGACCCCAGCAACTACGAGTA
TCTGCGGCAGCTGCAGGTCCTGGATTTATTTCTCGATTCGCTGTCGGAGGAGAATGAGACCCTGGTGGAGTTTGC
TATTGGAGGCCTGTGCAACCTGTGCCCAGACAGGGCCAACAAGGAGCACATCCTGCACGCAGGAGGTGTCCCACT
CATCATCAACTGCCTATCCAGCCCCAATGAGGAGACGGTGCTGTCTGCCATCACCACGCTCATGCACCTGAGCCC
GCCGGGCCGCAGCTTTCTCCCAGAGCTGACCGCCACGCCCGTGGTGCAGTGCATGCTTCGCTTCTCCCTCTCGGC
CAGCGCCAGGCTCCGGAACCTGGCACAGATCTTCCTGGAGGACTTCTGCTCCCCCCGCCAGGTGGCCGAGGCCCG
CAGCCGGCAGGCGCACTCTGCCCTGGGTATCCCACTGCCGAGGAGCGTGGCCCCACGGCAGCGC**TGA**TCCATGGA
GACTGCGAGACCGTGGCACCCCTACTGCTGGGGACCACAGTCCTGATGTGGACGCAGGGAACGGGGAGCACATAC
TGCCCCATTGGTGCCTTTTCAGCCATCTGAAAGGCGGGTTCTTTCAGCAGGACAGGCATTTACACTGATGAAACG
CCACTGGGAGTGAGGAAGCCAGACTCCAGAGACACGGAGAAGATCAAACTGGAGCTGCGTTCATAGGCTGGCACT
CTCAATCCTACATCAGGTGCCACCACCAGACTCAGGCCCTGGTGTAAGAAGCGGCCAAGTGCCTGGACCCAG
AGGCTTTGCAGGACAGTGTTCTCAGGAGCTGGGCCTGAGGCTTAGGAGAGCTGCCTTCGCTGCAGGAAATCAGGG
ATTATCCCTTAACAGAAGTGTCTGGAGTAGTTTTCAGGTATAGGAATGAGATGCCTCGTGGTGAAAGGATCTCAC
CCTGGGAAGATGTGGTGCCCCCTCCAGGGCTCTGGAGGATGGATGCCTCCCCCAGGGGCTCTCCAAGCTGGGCAT
TTGGGCCTGGTGGATGCCAACCTGGATAACCTGTGGCCCAGCATTGACTGTCCACCCAGCCTTGCTGTTAGGCAC
CATGACTCCAAGATGAAGATGTGGTCCCTGCCTTTGAGTGACAGCCCAGGGACTTAATGTGGCCATCGGGCATCA
AGCACAAGGCCATGCAGGTGATGATACGTCGGAATAGAGGCACCAGCCCTGGTAACTGCATCTTCTCCCCTTGCC
ACCCCATGGCCCCGGCTGAAAGCTTCGGCCCTCCTCTGCTGTCACTCAATGATGGGGAGCCCTACCCCAGAAGTG
TATCCCACGAGGGCATCAGGGACGCAGTGAGTGTTGCTCAAGGGAGTCAGGAAGAGACGGCAACGTAAAGGATGT
GGCTCCATGTCCATGGTGCCCCCTGGTCAACATAAGGAGCGTGGGATCCGATGGAAAGGTGGAGCTCAGGGAAAA
TGGGGGTCCTTGCCTCTCGTGTACCCCCTCAAGGCTGACCCCTTAGATGGCCCAGGAATGGCAGGTGCTACAAAA
ATGGTACCCACGTGGGCATGGAAATGGGGCAGATTAGGGGACCACTGGACTCAGAGGGGAGGGAAGGGCTCATCA
GCACCCGCTCAGGGAGCCTGTCCCTTTATGTTCCCAAATAAAGGGTCCTAGAAGACTAAAAAAAAAAAAAAAAA

FIGURE 306

MAQKPKVDPHVGRLGYLQALVTEFQETQSQDAKEQVLANLANFAYDPSNYEYLRQLQVLDLFLDSLSEENETLVE
FAIGGLCNLCPDRANKEHILHAGGVPLIINCLSSPNEETVLSAITTLMHLSPPGRSFLPELTATPVVQCMLRFSL
SASARLRNLAQIFLEDFCSPRQVAEARSRQAHSALGIPLPRSVAPRQR

FIGURE 307

CGGCAGCCAGCCTATTCTTTGGCCGGGTCGGTGCGAGTGGTCGGCTGGGCAGAGTGCACGCTGCTTGGCGCCGCA
GGCTGATCCCGCCGTCCACTCCCGGGAGCAGTG**ATG**TTGGGCAACTCTGCGCCGGGGCCTGCGACCCGCGAGGCG
GGCTCGGCGCTGCTAGCATTGCAGCAGACGGCGCTCCAAGAGGACCAGGAGAATATCAACCCGGAAAAGGCAGCG
CCCGTCCAACAACCGCGGACCCGGGCCGCGCTGGCGGTACTGAAGTCCGGGAACCCGCGGGGTCTAGCGCAGCAG
CAGAGGCCGAAGACGAGACGGGTTGCACCCCTTAAGGATCTTCCTGTAAATGATGAGCATGTCACCGTTCCTCCT
TGGAAAGCAAACAGTAAACAGCCTGCGTTCACCATTCATGTGGATGAAGCAGAAAAAGAAGCTCAGAAGAAGCCA
GCTGAATCTCAAAAAATAGAGCGTGAAGATGCCCTGGCTTTTAATTCAGCCATTAGTTTACCTGGACCCAGAAAA
CCATTGGTCCCTCTTGATTATCCAATGGATGGTAGTTTTGAGTCACCACATACTATGGACATGTCAATTGTATTA
GAAGATGAAAAGCCAGTGAGTGTTAATGAAGTACCAGACTACCATGAGGATATTCACACATACCTTAGGGAAATG
GAGGTTAAATGTAAACCTAAAGTGGGTTACATGAAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCCTC
GTGGACTGGTTAGTTGAAGTAGGAGAAGAATATAAACTACAGAATGAGACCCTGCATTTGGCTGTGAACTACATT
GATAGGTTCCTGTCTTCCATGTCAGTGCTGAGAGGAAAACTTCAGCTTGTGGGCACTGCTGCTATGCTGTTAGCC
TCAAAGTTTGAAGAAATATACCCCCCAGAAGTAGCAGAGTTTGTGTACATTACAGATGATACCTACACCAAGAAA
CAAGTTCTGAGAATGGAGCATCTAGTTTTGAAAGTCCTTACTTTTGACTTAGCTGCTCCAACAGTAAATCAGTTT
CTTACCCAATACTTTCTGCATCAGCAGCCTGCAAACTGCAAAGTTGAAAGTTTAGCAATGTTTTTGGGAGAATTA
AGTTTGATAGATGCTGACCCATACCTCAAGTATTTGCCATCAGTTATTGCTGGAGCTGCCTTTCATTTAGCACTC
TACACAGTCACGGGACAAAGCTGGCCTGAATCATTAATACGAAAGACTGGATATACCCTGGAAAGTCTTAAGCCT
TGTCTCATGGACCTTCACCAGACCTACCTCAAAGCACCACAGCATGCACAACAGTCAATAAGAGAAAAGTACAAA
AATTCAAAGTATCATGGTGTTTCTCTCCTCAACCCACCAGAGACACTAAATCTG**TAA**CAATGAAAGACTGCCTTT
GTTTTCTAAGATGTAAATCACTCAAAGTATATGGTGTACAGTTTTTAACTTAGGTTTTAATTTTACAATCATTTC
TGAATACAGAAGTTGTGGCCAAGTACAAATTATGGTATCTATTACTTTTTAAATGGTTTTAATTTGTATATCTTT
TGTATATGTATCTGTCTTAGATATTTGGCTAATTTTAAGTGGTTTTGTTAAAGTATTAATGATGCCAGCTGTCAG
GATAATAAATTGATTTGGAAAACTTAAAAAAA

FIGURE 308

MLGNSAPGPATREAGSALLALQQTALQEDQENINPEKAAPVQQPRTRAALAVLKSGNPRGLAQQQRPKTRRVAPL
KDLPVNDEHVTVPPWKANSKQPAFTIHVDEAEKEAQKKPAESQKIEREDALAFNSAISLPGPRKPLVPLDYPMDG
SFESPHTMDMSIVLEDEKPVSVNEVPDYHEDIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEY
KLQNETLHLAVNYIDRFLSSMSVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRMEHLVLK
VLTFDLAAPTVNQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAGAAFHLALYTVTGQSWPES
LIRKTGYTLESLKPCLMDLHQTYLKAPQHAQQSIREKYKNSKYHGVSLLNPPETLNL

FIGURE 309

GGCCGGACAGTCCGCCGAGGTGCTCGGTGGAGTC**ATG**GCAGTGCCCTTTGTGGAAGACTGGGACTTGGTGCAAAC
CCTGGGAGAAGGTGCCTATGGAGAAGTTCAACTTGCTGTGAATAGAGTAACTGAAGAAGCAGTCGCAGTGAAGAT
TGTAGATATGAAGCGTGCCGTAGACTGTCCAGAAAATATTAAGAAAGAGATCTGTATCAATAAAATGCTAAATCA
TGAAAATGTAGTAAAATTCTATGGTCACAGGAGAGAAGGCAATATCCAATATTTATTTCTGGAGTACTGTAGTGG
AGGAGAGCTTTTTGACAGAATAGAGCCAGACATAGGCATGCCTGAACCAGATGCTCAGAGATTCTTCCATCAACT
CATGGCAGGGGTGGTTTATCTGCATGGTATTGGAATAACTCACAGGGATATTAAACCAGAAAATCTTCTGTTGGA
TGAAAGGGATAACCTCAAAATCTCAGACTTTGGCTTGGCAACAGTATTTCGGTATAATAATCGTGAGCGTTTGTT
GAACAAGATGTGTGGTACTTTACCATATGTTGCTCCAGAACTTCTGAAGAGAAGAGAATTTCATGCAGAACCAGT
TGATGTTTGGTCCTGTGGAATAGTACTTACTGCAATGCTCGCTGGAGAATTGCCATGGGACCAACCCAGTGACAG
CTGTCAGGAGTATTCTGACTGGAAAGAAAAAAAAACATACCTCAACCCTTGGAAAAAAATCGATTCTGCTCCTCT
AGCTCTGCTGCATAAAATCTTAGTTGAGAATCCATCAGCAAGAATTACCATTCCAGACATCAAAAAAGATAGATG
GTACAACAAACCCCTCAAGAAAGGGGCAAAAAGGCCCCGAGTCACTTCAGGTGGTGTGTCAGAGTCTCCCAGTGG
ATTTTCTAAGCACATTCAATCCAATTTGGACTTCTCTCCAGTAAACAGTGCTTCTAGTGAAGAAAATGTGAAGTA
CTCCAGTTCTCAGCCAGAACCCCGCACAGGTCTTTCCTTATGGGATACCAGCCCCTCATACATTGATAAATTGGT
ACAAGGGATCAGCTTTTCCCAGCCCACATGTCCTGATCATATGCTTTTGAATAGTCAGTTACTTGGCACCCCAGG
ATCCTCACAGAACCCCTGGCAGCGGTTGGTCAAAAGAATGACACGATTCTTTACCAAATTGGATGCAGACAAATC
TTATCAATGCCTGAAAGAGACTTGTGAGAAGTTGGGCTATCAATGGAAGAAAAGTTGTATGAATCAGGTTACTAT
ATCAACAACTGATAGGAGAAACAATAAACTCATTTTCAAAGTGAATTTGTTAGAAATGGATGATAAAATATTGGT
TGACTTCCGGCTTTCTAAGGGTGATGGATTGGAGTTCAAGAGACACTTCCTGAAGATTAAAGGGAAGCTGATTGA
TATTGTGAGCAGCCAGAAGGTTTGGCTTCCTGCCACA**TGA**TCGGACCATCGGCTCTGGGGAATCCTGGTGAATAT
AGTGCTGCTATGTTGACATTATTCTTCCTAGAGAAGATTATCCTGTCCTGCAAACTGCAAATAGTAGTTCCTGAA
GTGTTCACTTCCCTGTTTATCCAAACATCTTCCAATTTATTTTGTTTGTTCGGCATACAAATAATACCTATATCT
TAATTGTAAGCAAAACTTTGGGGAAAGGATGAATAGAATTCATTTGATTATTTCTTCATGTGTGTTTAGTATCTG
AATTTGAAACTCATCTGGTGGAAACCAAGTTTCAGGGGACATGAGTTTTCCAGCTTTTATACACACGTATCTCAT
TTTTATCAAAACATTTTGTTT

FIGURE 310

MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINKMLNHENVVKFYGHRR
EGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVYLHGIGITHRDIKPENLLLDERDNLKISDFG
LATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKK
TYLNPWKKIDSAPLALLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDF
SPVNSASSEENVKYSSSQPEPRTGLSLWDTSPSYIDKLVQGISFSQPTCPDHMLLNSQLLGTPGSSQNPWQRLVK
RMTRFFTKLDADKSYQCLKETCEKLGYQWKKSCMNQVTISTTDRRNNKLIFKVNLLEMDDKILVDFRLSKGDGLE
FKRHFLKIKGKLIDIVSSQKVWLPAT

FIGURE 311

GC**ATG**AGGAGAGTGTGTAGGGGCCGGGTTCCGTGGATGAACTCTCACCCGAGCGGTTTCTCTTTCCGGGACAACA
TGGCGCCGTCCACGCCGCTCTTGACAGTCCGAGGATCAGAAGGACTGTACATGGTGAATGGACCACCACATTTTA
CAGAAAGCACAGTGTTTCCAAGGGAATCTGGGAAGAATTGCAAAGTCTGTATCTTTAGTAAGGATGGGACCTTGT
TTGCCTGGGGCAATGGAGAAAAAGTAAATATTATCAGTGTCACTAACAAGGGACTACTGCACTCCTTCGATCTTC
TGAAGGCAGTTTGCCTTGAATTCTCACCCAAAAATACTGTCCTGGCAACGTGGCAGCCTTACAGTACTTCTAAAG
ATGGCACAGCTGGGATACCCAACCTACAACTTTATGATGTGAAAACTGGGACATGTTTGAAATCTTTCATCCAGA
AAAAAATGCAAAATTGGTGTCCATCCTGGTCAGAAGATGAAACTCTTTGTGCCCGCAATGTTAACAATGAAGTTC
ACTTCTTTGAAAACAACAATTTTAACACAATTGCAAATAAATTGCATTTGCAAAAAATTAATGATTTTGTATTAT
CACCTGGACCCCAACCATACAAGGTGGCTGTCTATGTTCCAGGAAGTAAAGGTGCACCTTCATTTGTTAGATTAT
ATCAGTACCCCAACTTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAGTTTCTTTAAGGCAGATAAAGTTACAA
TGCTGTGGAATAAAAAAGCTACTGCTGTGTTGGTAATAGCTAGCACAGATGTTGACAAGACAGGAGCTTCCTACT
ATGGAGAACAAACTCTACACTACATTGCAACAAATGGAGAAAGTGCTGTAGTGCAATTACCAAAAAATGGCCCCA
TTTATGATGTAGTTTGGAATTCTAGTTCTACTGAGTTTTGTGCTGTATATGGGTTTATGCCTGCCAAAGCGACAA
TTTTCAACTTGAAATGTGATCCTGTATTTGACTTTGGAACTGGTCCTCGTAATGCAGCCTACTATAGCCCTCATG
GACATATATTAGTATTAGCTGGATTTGGAAATCTGAGGGGACAAATGGAAGTGTGGGATGTGAAAAACTACAAAC
TTATTTCTAAACCGGTGGCTTCTGATTCTACATATTTTGCTTGGTGCCCGGATGGTGAGCATATTTTAACAGCTA
CATGTGCTCCCAGGTTACGGGTTAATAATGGATACAAAATTTGGCATTATACTGGCTCTATCTTGCACAAGTATG
ATGTGCCATCAAATGCAGAATTATGGCAGGTTTCTTGGCAGCCATTTTTGGATGGAATATTTCCAGCAAAAACAA
TAACTTACCAAGCAGTTCCAAGTGAAGTACCCAATGAGGAACCTAAAGTTGCAACAGCTTATAGACCCCCAGCTT
TAAGAAATAAACCAATCACCAATTCCAAATTGCATGAAGAGGAACCACCTCAGAATATGAAACCACAATCAGGAA
ACGATAAGCCATTATCAAAAACAGCTCTTAAAAATCAAAGGAAGCATGAAGCTAAGAAAGCTGCAAAGCAGGAAG
CAAGAAGTGACAAGAGTCCAGATTTGGCACCTACTCCTGCCCCACAGAGCACACCACGAAACACTGTCTCTCAGT
CAATTTCTGGGGACCCTGAGATAGACAAAAAAATCAAGAACCTAAAGAAGAAACTGAAAGCAATCGAACAACTGA
AAGAACAAGCAGCAACTGGAAAACAGCTAGAAAAAAATCAGTTGGAGAAAATTCAGAAAGAAACAGCCCTTCTCC
AGGAGCTGGAAGATTTGGAATTGGGTATT**TAA**AGATTCACGGAAAGCAAGTTGATGACCAGAAATCAGTGCAAAC
ACATCTTCTGTTAAACCCATTGGTATACACAGAATATTCCTGTGCCCACACTTAATGTCAATCTATAATTTTAAC
CATTTATCCAAGATTCTACTAAGTGTAAAATTATTTAATAATGTCTATTAAATTGATATTTATATCTTGCATCCT
ATATCATGTCAATATGTGATATAGAAAAGAGATACGTGAATTTTTTAGCTAAGCTTGACAGATTGAAAGACAAGT
GTCATTTTTTTTTGTAGAGGGTGATATATACCATGTAAATGAATAAAGACATTTTAAATTTAAAAAAAAAAAAAA
AAAA

FIGURE 312

MRRVCRGRVPWMNSHPSGFSFRDNMAPSTPLLTVRGSEGLYMVNGPPHFTESTVFPRESGKNCKVCIFSKDGTLF
AWGNGEKVNIISVTNKGLLHSFDLLKAVCLEFSPKNTVLATWQPYSTSKDGTAGIPNLQLYDVKTGTCLKSFIQK
KMQNWCPSWSEDETLCARNVNNEVHFFENNNFNTIANKLHLQKINDFVLSPGPQPYKVAVYVPGSKGAPSFVRLY
QYPNFAGPHAALANKSFFKADKVTMLWNKKATAVLVIASTDVDKTGASYYGEQTLHYIATNGESAVVQLPKNGPI
YDVVWNSSSTEFCAVYGFMPAKATIFNLKCDPVFDFGTGPRNAAYYSPHGHILVLAGFGNLRGQMEVWDVKNYKL
ISKPVASDSTYFAWCPDGEHILTATCAPRLRVNNGYKIWHYTGSILHKYDVPSNAELWQVSWQPFLDGIFPAKTI
TYQAVPSEVPNEEPKVATAYRPPALRNKPITNSKLHEEEPPQNMKPQSGNDKPLSKTALKNQRKHEAKKAAKQEA
RSDKSPDLAPTPAPQSTPRNTVSQSISGDPEIDKKIKNLKKKLKAIEQLKEQAATGKQLEKNQLEKIQKETALLQ
ELEDLELGI

FIGURE 313

AAAAAAAAAAAAGCATATCAAAACAAAATTTTAACTACTAATGGGAAGGTTAAAAAGCTGCCACGTATTTCTAGT
ACAATGTATCCAATAAGAGCAAGGACATTGTTAAATGGAACAAGACAGCTGGGAAAGGCCCCACTATCTCTAATA
GAATTGTGCTACTATAAAACA**TGA**AGATATCAGCAATTTGGCCACTTGCAGTTTTTTTCAGCATGTTAAAGCAAG
TGCTAAGTACTTTATTAGTACTTTATTTAGTACTTTATTTTAAAGGTCTAGAAAACAACAGTCTTCCTGGAGGCC
CCAGAATCCCTTTCATGGGATTCATAAGGGACTCAGGTATTCTTATTTTCTGCCAAAAGGTGTGCTTATTTAGGG
ACTCTTTTACGATACTTTGTTTCTGAAGTTAGGTAGATCTTGGTTTACTGTGCCAAGGTCCTACCTAGCATTCCC
TGTAGGAATATTTGAAATTCCACTAGCTAGTCTAAGAAGTCAAAGCACAAAATTAATTGTCAACGCTTCTCTCAT
ATTCTTAAAATTGAAGCAGTTTGCAGGGAAGAACAAGAATGAGGTGTCCCTGCCTTGGTAAAGCAACTGCCAAAT
TTTGTTCTAGAAAGAATCCCCAAGTGTGTGGATCTATTATAATTTCTTTATCTTTTATGAATGAGGGCATCTTTT
CTACTTGAGCAAGATCATGGTCCTTGACCAGTGGGCTTTTCCTTCATATCTGTCTTGTGTAGTTGTGCTTTTCCT
TTGGCTCGTTTTTGGTCTGTCAGGGTAACCAGCAGTGCACAATATGAGACAAATGCTCTTTAGAGAGAAATCTGG
TGAGACTGTAGAACCCAGAGCAAAACTGTTTTTTTTTCAGTCTCTGTTTTCTTTTCTAAATGCTATAGAAAATAA
AGGCACCTGAAAAGAAACTACTACTTTAACACTGCTGTGGAAGGCCTTTGCTTTATAAGAAAAATATTATTAGCT
ATGGGAAAGTAATGTTCTTTATGTAAAGACTTAAAAATAGACTAATAGTTTACAGAGTTATTATATAAAATACGA
TGTGAATTTATTTCAAACAAGTTGTGAAGGTACCAAAAACCACAATAAAAGTTAATATATATAAAAACTACTAGA
ACAAAAAAGCTTGAAGGTGTGGGGGTGGAGGGTATGGAAGACCAAAAGTAAATTTAAAAAAGAAATTTTTGAAAG
GAAACAGCTTTATCAGGGGAAGTTAAATATAACACTCCGTTTTTTTCTTCTTTCTAATAATGATATGGATCAACA
AATGCAATTTGAACTTTTTAAGATAACTCTAAATGTGTTTTGTTTCTTAAATGCACAATTGATTCTTCTATACTG
TAATGCTTCTTTGCTGACGCTGGAAAATGGTCAGACTGCTGACTTTGTGCCTTTAAAATGCATTCTGCTTTGACA
GTGGCAGACTTTTTGGTGCTGGAGAAGATTCACTAGCAGTCTTATATGTGCTTTTCAGGAAATATCTTTCTACTT
AAGGCCTTGAGAGATTCAAAGTGGCATGACTTAGGCTTGGACCAAATATAAGATCTTTTACATTGCAAACAAAAT
GTTGTATTGAATAAAAGGGTTAAAAAAATCATAATGACTAGTGGAAATTTTGATGGGTTGTTAATTATTTAAAAT
GTATTTGAAAGTATACAGACTGAAAATTTCAGTATGAATATCTTGAAAATTTTCAGCACTTTTCCTTGTTTACAA
AACATCTTTCTAACTTAAAAAAATGACTATTGCCTTAGAAAGTTTTAAAAGGCACAGTTACCCTTACATAACATA
TATAAGGAATTAAAATATTAATGCATTTGCTGAACTGTAAAAGAAAATTTTAAACCTTGATTTCAGAGTGAATTG
GATTGGCTTTCACTTGAGAGAGTCTTTACCTTATTCCCAAAGAAACTGCATTAAAAAGATGAAACTATTTCTTTA
GACTAAGTCTCTGCTACTCCAGCTCATATATATGTCAGATCTGCTCTGTAGTATTTCTGACATGGAGTTGTTATA
AGATATGTGAAATCACTTAGAAAATAAAATCAGATGTGAATAGTTTAGCAGGATGACCAAGCCAGATGCAGACTC
CTTGGCCTATGGCAAAGTTCTGTGCCAGTGATTTTATTTGGAGTCTGGGAACTGATAGCTTGATAAAATCACCTG
GTGTCAATTAAATATACAAATCTATCTTTTTTAATAGAATGAATCTTCTTTGTTTGTTCAATAATTGTAACTTAT
TATGTCAGGTACTAAATTAACATCCTTAAGGAGGTCACAATCTAGGAGGAACATGGGCAAACAGTTACTTATTTT
ATGGCATACGCTAACTCTGAAAGTTCAGCAATGATGTTTTAAAATGTTATTTTTTATTAAGGGAAAAGCAATTTT
AGGTAATCATTGGCTGTTATAAACGGAAATGTCACTGACAACAGGGATTAGAGTAAAAGTATCTCCAAACTAGAG
GGATCCCCTCCCCAACCAGGTCACATAGCATCTCTCTCAGGACCCCCTCTTACTGCAAAACCCAGCCTCTACTCA
ACAGTTCTGGTGATGGGGAGCATTTATTCCATAACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGTGTCTCT
TTTAAAGAAAACATACTTTATTTTGGTCTAAATTGTGAAAATACCCAAAACATTTGATAGAAATTGAACTCTGTC
AACAGTGTTATTTATACTAAGATCAGGACAGTTCCTTGAGATCATACTGTTTTATTACTAAGTTTGGCCTTTGTT
TTACAAATGTAATGTTCATATTTATTTGAATTTTAAGATTGGTTAAATGTTAATGAAAAGCAATCCAATTGTTAA
TTTTTAGTAGTGCCTTTTCTCTGTATGCCTTAATTTTATTTTATATTAATAATTCAAGTTACCCACCAAAATGAA
GATTTTTTCCAAAATCAGTAGGCTTCACAAGTTCATTTGGCCTTAGACTGTGTATTGGTCCTTAAATGTTTCTTA
ATGCCTGCCTCCTCCTACCCTTTTCTACCTCCTTTTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTTAGGAGAG
AAACATTAGGATTTGTCTGTGATAGACATGCTGCAGCTTCCACTAGACATGAATTCCCAACACAAGCATAGAAAG
AGGTATTCTCGTTCAGAAGAGACATGTAAATGTTTTCTGGGTTGAATATTCGATTTTCAATCACATTGGCACTGT
CCAAGTTCTTGGCATATTATAGTTCAGTTATGCCAA

FIGURE 314

KKKKAYQNKILTTNGKVKKLPRISSTMYPIRARTLLNGTRQLGKAPLSLIELCYYKT

FIGURE 315

ATGACGGTGGGCAAGAGCAGCAAGATGCTGCAGCATATTGATTACAGGATGAGGTGCATCCTGCAGGACGGCCGG
ATCTTCATTGGCACCTTCAAGGCTTTTGACAAGCACATGAATTTGATCCTCTGTGACTGTGATGAGTTCAGAAAG
ATCAAGCCAAAGAACTCCAAACAAGCAGAAAGGGAAGAGAAGCGAGTCCTCGGTCTGGTGCTGCTGCGAGGGGAG
AATCTGGTCTCAATGACAGTAGAGGGACCTCCTCCCAAAGATACTGGTATTGCTCGAGTTCCACTTGCTGGAGCT
GCCGGGGGGCCCAGGGATCGGCAGGGCTGCTGGCAGAGGAATCCCAGCTGGGGTTCCCATGCCCCAGGCTCCTGCA
GGACTTGCTGGGCCAGTCCGTGGGGTTGGCGGGCCATCCCAACAGGTGATGACCCCACAAGGAAGAGGTACTGTT
GCAGCCGCTGCAGCTGCTGCCACAGCCAGTATTGCCGGGGCTCCAACCCAGTACCCACCTGGCCGTGGGGGTCCT
CCCCCACCTATGGGCCGAGGAGCACCCCCTCCAGGCATGATGGGCCCACCTCCTGGTATGAGACCTCCTATGGGT
CCCCCAATGGGGATCCCCCCTGGAAGAGGGACTCCAATGGGCATGCCCCCTCCGGGAATGCGGCCTCCTCCCCCT
GGGATGCGAGGCCTTCTT**TGA**

FIGURE 316

MTVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVLGLVLLRGE
NLVSMTVEGPPPKDTGIARVPLAGAAGGPGIGRAAGRGIPAGVPMPQAPAGLAGPVRGVGGPSQQVMTPQGRGTV
AAAAAAATASIAGAPTQYPPGRGGPPPPMGRGAPPPGMMGPPPGMRPPMGPPMGIPPGRGTPMGMPPPGMRPPPP
GMRGLL

FIGURE 317

GGCACGAGGCCGGGCCGAGGCG**<u>ATG</u>**GCGCCCTGGGCGCTCCTCAGCCCTGGGGTCCTGGTGCGGACCGGGCACAC
CGTGCTGACCTGGGGAATCACGCTGGTGCTCTTCCTGCACGATACCGAGCTGCGGCAATGGGAGGAGCAGGGGGA
GCTGCTCCTGCCCCTCACCTTCCTGCTCCTGGTGCTGGGCTCCCTGCTGCTCTACCTCGCTGTGTCACTCATGGA
CCCTGGCTACGTGAATGTGCAGCCCCAGCCTCAGGAGGAGCTCAAAGAGGAGCAGACAGCCATGGTTCCTCCAGC
CATCCCTCTTCGGCGCTGCAGATACTGCCTGGTGCTGCAGCCCCTGAGGGCTCGGCACTGCCGTGAGTGCCGCCG
TTGCGTCCGCCGCTACGACCACCACTGCCCCTGGATGGAGAACTGTGTGGGAGAGCGCAACCACCCACTCTTTGT
GGTCTACCTGGCGCTGCAGCTGGTGGTGCTTCTGTGGGGCCTGTACCTGGCATGGTCAGGCCTCCGGTTCTTCCA
GCCCTGGGGTCTGTGGTTGCGGTCCAGCGGGCTCCTGTTCGCCACCTTCCTGCTGCTGTCCCTCTTCTCGTTGGT
GGCCAGCCTGCTCCTCGTCTCGCACCTCTACCTGGTGGCCAGCAACACCACCACCTGGGAATTCATCTCCTCACA
CCGCATCGCCTATCTCCGCCAGCGCCCCAGCAACCCCTTCGACCGAGGCCTGACCCGCAACCTGGCCCACTTCTT
CTGTGGATGGCCCTCAGGGTCCTGGGAGACCCTCTGGGCTGAGGAGGAGGAAGAGGGCAGCAGCCCAGCTGTT**<u>TA</u>**
<u>G</u>GGTTGCTGGAGGCCGGGCTACCGTCTTGTGCCTGAAAACCACGGGGCCTGTCCCCAGCTGGGGTGAGCGCTCAG
AGGGCCTGGGGCCCTCACTCCTGCCCACGCCTCCCAGACCCCAGAACGGAGCTTCAAGTCAGACAGATCCCTGCC
TTGGTGGGCAGTTCTGCCTTCCAAGGAAGAAGGGGAAGAAAAGGACCTGTGGGTGGCTCAGGCCCAAGCAGACCC
CGGGCTCCACCCCAGCCCCGCCCAGGCTGCTGCCAGTGCACACTTTTACAAATTTAATATAAAGCAAGTCCAGTC
TTAAAAGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 318

MAPWALLSPGVLVRTGHTVLTWGITLVLFLHDTELRQWEEQGELLLPLTFLLLVLGSLLLYLAVSLMDPGYVNVQ
PQPQEELKEEQTAMVPPAIPLRRCRYCLVLQPLRARHCRECRRCVRRYDHHCPWMENCVGERNHPLFVVYLALQL
VVLLWGLYLAWSGLRFFQPWGLWLRSSGLLFATFLLLSLFSLVASLLLVSHLYLVASNTTTWEFISSHRIAYLRQ
RPSNPFDRGLTRNLAHFFCGWPSGSWETLWAEEEEEGSSPAV

FIGURE 319

GATCTCAGGCTCGGCTCCCCGCCCGCCGCAGCCCACTGTTGACCCGGCCCGTACTGCGGCCCCGTGGCCACC**ATG**

TCCCTGCACGGCAAACGGAAGGAGATCTACAAGTATGAAGCGCCCTGGACAGTCTACGCGATGAACTGGAGTGTG
CGGCCCGATAAGCGCTTTCGCTTGGCGCTGGGCAGCTTCGTGGAGGAGTACAACAACAAGGTTCAGCTTGTTGGT
TTAGATGAGGAGAGTTCAGAGTTTATTTGCAGAAACACCTTTGACCACCCATACCCCACCACAAAGCTCATGTGG
ATCCCTGACACAAAAGGCGTCTATCCAGACCTACTGGCAACAAGCGGTGACTATCTCCGTGTGTGGAGGGTTGGT
GAAACAGAGACCAGGCTGGAGTGTTTGCTAAACAATAATAAGAACTCTGATTTCTGTGCTCCCCTGACCTCCTTT
GACTGGAATGAGGTGGATCCTTATCTTTTAGGTACCTCAAGCATTGATACGACATGCACCATCTGGGGGCTGGAG
ACAGGGCAGGTGTTAGGGCGAGTGAATCTCGTGTCTGGCCACGTGAAGACCCAGCTGATCGCCCATGACAAAGAG
GTCTATGATATTGCATTTAGCCGGGCCGGGGGTGGCAGGGACATGTTTGCCTCTGTGGGTGCTGATGGCTCGGTG
CGGATGTTTGACCTCCGCCATCTAGAACACAGCACCATCATTTACGAAGACCCACAGCATCACCCACTGCTTCGC
CTCTGCTGGAACAAGCAGGACCCTAACTACCTGGCCACCATGGCCATGGATGGAATGGAGGTGGTGATTCTAGAT
GTCCGGGTTCCCTGCACACCTGTCGCCAGGTTAAACAACCATCGAGCATGTGTCAATGGCATTGCTTGGGCCCCA
CATTCATCCTGCCACATCTGCACTGCAGCGGATGACCACCAGGCTCTCATCTGGGACATCCAGCAAATGCCCCGA
GCCATTGAGGACCCTATCCTGGCCTACACAGCTGAAGGAGAGATCAACAATGTGCAGTGGGCATCAACTCAGCCC
GACTGGATCGCCATCTGCTACAACAACTGCCTGGAGATACTCAGAGTG**TAG**TGTTGGTGGCGCTGTGCCCACGAG
GCAGGGGCTTTTGTATTTCCTGCCTCTGCCCCACCCCCAAAGTAAGAAGAAACATGTTTCCAGTGGCCAGTATGT
CTTTCATTGCTTTGCACCCACTGTTACCAGAAGCTGCTCTAGGAGTTCCTGGCCAGTCACCCCATCGCCCTCTGT
GGCAGACTCAGTGCTGTGTGGCGCCCTCCTAGCCCAGGGCTGAGTTTTAAGATTTTCTCTCCTTTCCTCTTCTCC
TTTGGTTCCTCAATTAA

FIGURE 320

MSLHGKRKEIYKYEAPWTVYAMNWSVRPDKRFRLALGSFVEEYNNKVQLVGLDEESSEFICRNTFDHPYPTTKLM
WIPDTKGVYPDLLATSGDYLRVWRVGETETRLECLLNNNKNSDFCAPLTSFDWNEVDPYLLGTSSIDTTCTIWGL
ETGQVLGRVNLVSGHVKTQLIAHDKEVYDIAFSRAGGGRDMFASVGADGSVRMFDLRHLEHSTIIYEDPQHHPLL
RLCWNKQDPNYLATMAMDGMEVVILDVRVPCTPVARLNNHRACVNGIAWAPHSSCHICTAADDHQALIWDIQQMP
RAIEDPILAYTAEGEINNVQWASTQPDWIAICYNNCLEILRV

FIGURE 321

TGGCAGTGATGTCATTCCTTACTAGGCTTCCAAAGCCACTGCTGTGGCCACAGCTTCCATGGAGACAGGCAAGC**T**
GAGCCTCTATGTGGCACCAATTCCTGCAGCTGTTTGTGTTGGAGGGAAAAAAATCCAAATGGACATCAACAGCTT
TCATCAACTAAATAACCACAGAAAATATTTATGAAGACTATAAAGCAATGATTACTTTTGAATTGGAAAGGAATC
ACTATTATTTGAAATGTTTCTTCAAAAGTGAGCATCCGGACAGGAACCATCATGGATGCTGAGGCCATGGATGAA
GGCCTACTCGGGAAGATGATATCCTTGCAGTCTCAAAACGGCACCCCACAAAGGTGATATCCTAATTTACAAAGG
GAAAAAGGTACCTTAATCTGAAATCTGGCAAATGCAGCCTCAACAGAAGTGACAGAATTGAACATCGCCAATAAT
GGGACACACAGACATCACATGCCCCCAGTCTGATGCACCACGGAGTCGTCTCTGATGTATTCTTGTCAAAAAATG
TTTGCCTGATTCTAATCATGAAAGAACAATTAGAAAAAATCCAAATTGACAGATATTCTGCAGAATAAATGGCCT
GACCTCATCAAAAACATCAATGTCATGAAAAACACAAAACATTGCAGATAGCGTGAAATTAAAGATTACAGAGAT
ATAACTTAATGCAAGATCTCTGACTGGATCCTAGACTGCAGGAAAAAGTCTGCTATAAAGAACATTTGGATCACT
TGTAGTAGCTGGGAAATAAAACAAAACATTATTTGTAAAAGGGGGGAAATCTGAACATGGGTCTTGCAGTATTTA
TGACAGTTTTTGCGGGGCAGAGATTTCTAGATTGACAGCTGTTTTAGTACTTTCAAGGTGATGCTCTGTCTGCTG
GTTTGCATTGTTTCTGTCTGAGTTAAGAGACTGGCAGAACACAGAGTTGCAGTAGCCAAACACTGGAGAAAGCTG
GGCCCTACAGAAACCTAACGCTGAAGAAACCTCAGGAGCCAAACTGGTGGAGAAAACAAAGAGTCCTCCCTCTCT
CCCTTTTCAAATAATGATCATACATCTTCAAGCTGTCTGAAATGGTTAAGGAGTTCAGTCTGTCGTCAGGCACAC
ACCAGAGCCAGCTAGCCCACACAGACCCCATCAGAGCAAAACAGACAAGAGAATTTAATTCATATCCACATAGAA
AGGACTTCTAGGTAGGAGGTAGACCCTTTAGCTCCCTTCCAATTAAAGGAGTCCCCAATTCTGGCACCTGAGAGT
CCCCTGGGTCTAACAGCTATGATATTTATGTAGTGTGTTGCTTACCTAAATGAATACAATTTCCTTCCAGACACG
TGACACTGATATTAAAGTGCTAATGAGAGGGATCTATTTCTTCTTGTACGCTAAAAGAGAAACAGTAGTTCAGAT
TTCCCATCAGAAGTCCGAGGACTTTGTTCTTGATAACTACTACCAATAAAAATTGAGTATTTGAAAAATTCCTTT
GTATTTTCCATCCATACACATTTTTTTTTAAAGCATTTTAGGAAGTCCTCTAATTATATAGTAAAAATTGTCAGC
AATGGCCTGCTAGTTTTCTATTTGACCTAATCACAACCATCCTCGTTAGGTCCTGAGGTCTGCTCTGCTGCTTGG
CCAAAACCAAATGGTGCCAGGTCACAAAGCACTTGCACATGTGAATCCTGCATCCATTCTACAATGGGTCACTAT
TGACTGAAATACTTTAATAAAAATGATAGAGCACATAAAGCTTGCTGTTGACAGAAACTTCCGTGCTCAAGCAAG
GCAGTGCTATACATGGTGAGACCTTGCACAAAGTCAGTTAACTAACAGATGATCTAGAAGCAGGTGACACAATGA
AATACCCTTTGGAGCTGTTGCCTATGTCTGTGGATAGGCTCTTTGTAGCTAGGTTAGGCTTCTGTGTTAAAGTGT
GTTAGAAGAAAGCATCACATAAGGAAAATAGAACTCTATTCGTATGTTTTTTCAAAACAGAAGTCAAGTCACATT
CAGGCAAACCAAATCTGTAACATTCAAGAAGATGCAGTGACTCTTCCGCATCTTAGAGCCACGGTGTCTGAGGTG
GCTGGCATGGCTCCAACACGCTGGCTTCCCTGTCAGTGGATCATTTACAATATGGTGCATTTCAAATTACTGGTG
AATTCACTGAATACTGGCTGTTTTTTTTTTTTTAGGGGTAATCTTATACATAAAATTTAGGAAAAGAAAGAGAAA
AAAGCAAAAATGACAGAAATAACTCAAAAGTTCCTAAAATTTATGTGTATCTTTTCGTACCTGTGAACTCCTGAA
TAAGTATTTATATCTGACAGGTACAAATACAATAATTATATTTTTAAGTAAAACCTATTTAATAATATGAAGTAT
GGTGTTAAATACATGTATTAAAAGATAAGTAACTTCAGAAGTCTTCTGACTTTTTAATTGTAAAATAAGTGAAAA
CTGTTTTGTGCTTTTTTATTTACTGTATGC

FIGURE 322

AVMSFLTRLPKPLLWPQLPWRQAS

FIGURE 323A

CGGCGCGGGTGTTGAGAGCGGTGTGGTAGGTGTTGTAGCCGCTATGGTGAAGTTCGCTTTGTAGCGGCCCCGGCT
AGAGAGTTGGCCTGTTCCCTGCCTTTGTGACCCGGAGGAGCTTTTGGGGGTGCGTCAAGCCCCTGGCCTGAGGCA
GCGAACTGGTTTGTGGCCTGTTTGATTCCTGTCAGAGGTTTGCTGACCCAAGACAGTATCGAAA**ATG**CATATTAA
GTCAATTATTCTAGAGGGATTCAAGTCCTATGCTCAGAGGACCGAAGTCAATGGTTTTGACCCCCTCTTCAATGC
TATCACTGGCTTAAATGGTAGTGGAAATCCAACATATTGGACTCCATCTGCTTTTTACTGGGCATCTCCAACCT
GTCTCAGGTTCGGGCTTCTAATTTACAAGATTTAGTTTACAAAAATGGGCAGGCTGGTATTACCAAAGCCTCTGT
GTCAATCACTTTTGATAATTCTGACAAAAAGCAAAGTCCTTTAGGATTTGAGGTTCATGATGAAATCACAGTAAC
AAGGCAGGTGGTTATTGGTGGTAGAAATAAATATTTAATCAATGGAGTCAATGCCAACAACACCAGAGTACAGGA
TCTCTTCTGTTCTGTTGGCCTTAATGTTAACAACCCTCACTTTCTCATCATGCAGGGCCGAATTACAAAAGTATT
GAATATGAAACCACCAGAGATTTTATCCATGATAGAAGAAGCAGCTGGAACCAGGATGTATGAATACAAAAAAAT
AGCTGCACAGAAAACTATAGAAAAAAAGGAGGCTAAGCTGAAAGAAATTAAGACGATACTTGAAGAAGAGATTAC
TCCAACCATTCAAAAATTAAAAGAGGAAAGATCGTCCTACTTGGAGTACCAAAAAGTAATGAGAGAAATAGAACA
TTTGAGTCGTTTATATATTGCTTATCAGTTTTTGCTGGCTGAAGATACCAAAGTACGCTCAGCTGAGGAATTAAA
AGAAATGCAAGATAAAGTTATAAAGCTTCAGGAAGAATTGTCTGAGAATGATAAAAAAATAAAAGCACTTAATCA
TGAAATAGAAGAATTGGAAAAAAGAAAAGATAAGGAAACTGGAGTTATACTTCGATCTTTAGAAGATGCTCTTGC
AGAGGCTCAGCGAGTTAATACTAAATCTCAAAGCGCATTTGATCTCAAGAAGAAAAATCTGGCATGTGAGGAAAG
CAAACGCAAAGAGCTGGAAAAAAATATGGTTGAGGACTCAAAAACTTTAGCAGCAAAGGAAAAAGAGGTTAAAAA
GATAACAGATGGACTGCATGCCCTTCAAGAAGCAAGTAATAAAGATGCTGAAGCTCTGGCAGCTGCACAGCAGCA
CTTCAATGCTGTTTCCGCTGGCCTGTCCAGTAATGAAGATGGAGCAGAAGCAACTCTTGCTGGTCAAATGATGGC
CTGTAAAAATGATATAAGTAAAGCTCAGACAGAAGCCAAACAGGCTCAGATGAAGTTGAAGCATGCTCAACAGGA
ATTAAAGAATAAACAAGCTGAAGTTAAGAAGATGGATAGTGGCTACAGGAAGGATCAAGAAGCTCTAGAAGCTGT
AAAAAGACTTAAAGAAAAACTTGAAGCTGAAATGAAAAAGCTAAATTATGAAGAAAATAAAGAGGAAAGCCTTTT
GGAAAAGCGCAGGCAGCTGTCTCGTGATATTGGTAGATTGAAAGAAACATATGAAGCTCTATTAGCCAGATTTCC
CAATCTTCGATTTGCATACAAGGATCCAGAGAAGAACTGGAATAGAAATTGTGTGAAAGGACTTGTGGCTTCTCT
GATTAGTGTGAAAGACACTTCTGCAACCACAGCTTTAGAATTAGTGGCTGGAGAACGACTCTACAATGTTGTAGT
AGACACAGAAGTTACTGGTAAAAAGCTACTAGAAAGGGGGGAACTGAAACGTCGATACACTATAATTCCACTCAA
TAAAATTTCAGCCAGATGTATTGCACCAGAAACTCTGAGAGTTGCTCAGAATCTTGTTGGCCCTGACAACGTTCA
TGTGGCTCTTTCCTTGGTTGAATATAAACCAGAACTTCAGAAAGCAATGGAGTTTGTCTTTGGAACAACATTTGT
TTGTGACAATATGGATAATGCCAAAAAAGTGGCCTTTGATAAGAGGATAATGACTAGAACTGTAACTCTCGGAGG
TGATGTGTTTGATCCTCATGGGACATTGAGTGGAGGTGCTCGATCCCAGGCAGCTTCCATTTTAACCAAGTTTCA
AGAACTCAAAGATGTTCAGGATGAACTGAGAATCAAAGAGAATGAGCTGCGGGCTCTAGAAGAGGAATTAGCAGG
TCTTAAAAACACTGCTGAAAAGTATCGCCAACTAAAACAGCAGTGGGAGATGAAAACTGAAGAGGCAGATTTATT
ACAAACCAAGCTCCAGCAAAGCTCATATCACAAGCAACAAGAAGAATTAGATGCCCTTAAAAAAACCATTGAGGA
AAGTGAGGAGACTTTGAAAAACACTAAAGAAATCCAAAGAAAAGCAGAAGAAAAATATGAAGTATTGGAAAATAA
AATGAAAAATGCAGAAGCTGAAAGAGAGCGAGAACTGAAAGATGCTCAGAAAAAACTGGATTGTGCCAAAACAAA
GGCAGATGCATCTAGCAAGAAGATGAAAGAAAAACAACAGGAAGTTGAAGCTATCACTCTGGAACTGGAAGAGCT
CAAGAGAGAGCATACATCTTACAAACAACAGCTTGAAGCTGTAAATGAAGCTATCAAATCCTATGAAAGTCAGAT
TGAAGTAATGGCAGCTGAGGTGGCTAAAAATAAGGAGTCAGTAAATAAAGCTCAAGAAGAGGTGACCAAGCAAAA
AGAGGTGATAACAGCCCAAGACACTGTAATTAAGCTAAATATGCAGAAGTGGCAAAACACAAGGAGCAAAACAAT
GATTCTCAGCCTTAAAATTAAGGAATTAGACCACCACATCAGCAAACATAAACGGGAGGCTGAAGATGGTGCTGC
AAAGGTATCCAAAATGTTGAAAGATTATGACTGGATTAATGCAGAGAGACACCTCTTTGGCCAACCCAATAGTGC
CTATGATTTCAAAACTAACAACCCTAAAGAAGCTGGTCAGAGACTTCAGAAGTTGCAAGAAATGAAGGAGAAACT
AGGAAGAAATGTCAATATGAGAGCTATGAATGTATTGACAGAAGCTGAAGAGCGATGCAATGACTTGATGAAGAA
GAAGAGAATTGTAGAAAATGACAAATCCAAAATTCTTACAACTATAGAAGACCTTGACCAGAAGAAAAACCAAGC
CCTAAATATTGCATGGCAAAAGGTGAACAAGGACTTTGGGTCTATTTTTTCTACTCTTTTGCCTGGTGCTAATGC
TATGCTTGCACCACCAGAGGGTCAAACTGTTTTGGATGGTCTGGAGTTCAAGGTTGCCTTAGGAAATACCTGGAA
AGAAAACCTAACTGAACTTAGTGGTGGTCAGAGGTCTTTAGTGGCCTTGTCATTAATACTGTCCATGCTTCTCTT
CAAACCTGCTCCAATTTATATCCTTGATGAGGTAGATGCAGCCTTGGATCTTTCTCATACCCAAAACATTGGACA

FIGURE 323B

GATGCTGCGTACTCATTTCACACATTCTCAGTTCATTGTGGTGTCACTAAAAGAAGGTATGTTCAACAATGCAAA
CGTTCTTTTCAAAACCAAGTTTGTGGATGGTGTTTCTACAGTAGCCAGATTTACTCAATGTCAAAATGGAAAGAT
TTCAAAGGAAGCAAAATCCAAGGCAAAACCACCCAAAGGAGCACATGTGGAAGTT**TAA**ACTACAAAGTTATTTCT
TCATCTTGACCTGTTTTTTTAAATGTAAACTTTTAAGGACTTGAGATAACTAATTTGTTTATATACAAAAATTAA
TGTTACTGTGTTACTTAACCCATGTTTTCTCTTTATATAATCACTTATCGCTTACAAATGAGCATATATTCCTCA
TCTCTTAACTAGTCTAATTATGGTCCAATTATTGTGGTTGTGATTTTATGCATATCCATCAAAATGTTTTTTTTC
TTATGCGGGTCTTTTATATATTAGGGATCCTGAGATACCCGATTCTATATGTAAAAGCTAATATACAAAAAAGCA
GATTAAATTACATGATAAATGTAGCTGAAAAAAAAAAAAAA

FIGURE 324

MHIKSIILEGFKSYAQRTEVNGFDPLFNAITGLNGSGKSNILDSICFLLGISNLSQVRASNLQDLVYKNGQAGIT
KASVSITFDNSDKKQSPLGFEVHDEITVTRQVVIGGRNKYLINGVNANNTRVQDLFCSVGLNVNNPHFLIMQGRI
TKVLNMKPPEILSMIEEAAGTRMYEYKKIAAQKTIEKKEAKLKEIKTILEEEITPTIQKLKEERSSYLEYQKVMR
EIEHLSRLYIAYQFLLAEDTKVRSAEELKEMQDKVIKLQEELSENDKKIKALNHEIEELEKRKDKETGVILRSLE
DALAEAQRVNTKSQSAFDLKKKNLACEESKRKELEKNMVEDSKTLAAKEKEVKKITDGLHALQEASNKDAEALAA
AQQHFNAVSAGLSSNEDGAEATLAGQMMACKNDISKAQTEAKQAQMKLKHAQQELKNKQAEVKKMDSGYRKDQEA
LEAVKRLKEKLEAEMKKLNYEENKEESLLEKRRQLSRDIGRLKETYEALLARFPNLRFAYKDPEKNWNRNCVKGL
VASLISVKDTSATTALELVAGERLYNVVVDTEVTGKKLLERGELKRRYTIIPLNKISARCIAPETLRVAQNLVGP
DNVHVALSLVEYKPELQKAMEFVFGTTFVCDNMDNAKKVAFDKRIMTRTVTLGGDVFDPHGTLSGGARSQAASIL
TKFQELKDVQDELRIKENELRALEEELAGLKNTAEKYRQLKQQWEMKTEEADLLQTKLQQSSYHKQQEELDALKK
TIEESEETLKNTKEIQRKAEEKYEVLENKMKNAEAERERELKDAQKKLDCAKTKADASSKKMKEKQQEVEAITLE
LEELKREHTSYKQQLEAVNEAIKSYESQIEVMAAEVAKNKESVNKAQEEVTKQKEVITAQDTVIKLNMQKWQNTR
SKTMILSLKIKELDHHISKHKREAEDGAAKVSKMLKDYDWINAERHLFGQPNSAYDFKTNNPKEAGQRLQKLQEM
KEKLGRNVNMRAMNVLTEAEERCNDLMKKKRIVENDKSKILTTIEDLDQKKNQALNIAWQKVNKDFGSIFSTLLP
GANAMLAPPEGQTVLDGLEFKVALGNTWKENLTELSGGQRSLVALSLILSMLLFKPAPIYILDEVDAALDLSHTQ
NIGQMLRTHFTHSQFIVVSLKEGMFNNANVLFKTKFVDGVSTVARFTQCQNGKISKEAKSKAKPPKGAHVEV

FIGURE 325

AGCA**ATG**GCGGTTCCCGGCGTGGGGCTCTTGACCCGTTTGAACCTGTGTGCCCGGAGAAGAACTCGAGTCCAGCG
GCCTATCGTCAGGCTTTTGAGTTGCCCAGGAACTGTGGCCAAAGACCTTAGGAGAGACGAGCAGCCTTCAGGGAG
CGTGGAGACAGGCTTTGAAGACAAGATTCCCAAAAGGAGATTCTCTGAGATGCAAAATGAAAGACGAGAACAGGC
ACAGCGGACTGTTTTAATACATTGCCCAGAGAAAATCAGTGAAAACAAGTTTCTTAAATATTTATCCCAATTTGG
ACCTATTAATAATCATTTCTTCTATGAAAGCTTTGGTCTCTATGCTGTCGTAGAATTTTGCCAAAAGGAAAGCAT
AGGTTCACTGCAGAATGGGACTCATACTCCAAGCACGGCCATGGAGACTGCAATTCCATTCAGATCACGTTTCTT
CAATCTGAAGTTGAAAAACCAGACTTCTGAACGGTCACGCGTACGGTCAAGTAATCAGTTGCCACGTTCAAACAA
GCAGCTTTTTGAATTACTTTGTTATGCAGAAAGTATAGACGATCAGCTGAACACTCTCTTGAAGGAGTTCCAGCT
AACAGAGGAGAACACTAAGCTCCGATATCTCACCTGTTCTCTTATTGAAGACATGGCCGCCGCGTATTTTCCAGA
CTGCATAGTCAGACCCTTTGGCTCCTCAGTCAACACTTTTGGGAAGTTAGGATGTGATTTGGACATGTTTTTGGA
TCTAGATGAAACCAGAAACCTCAGCGCTCACAAGATCTCAGGAAATTTTCTGATGGAATTTCAAGTGAAAAATGT
TCCTTCAGAAAGAATTGCAACTCAGAAGATCCTGTCTGTGTTAGGAGAGTGCCTTGACCACTTTGGCCCTGGCTG
TGTGGGTGTGCAAAAAATATTAAATGCCCGGTGTCCGCTCGTGAGGTTCTCACACCAGGCCTCCGGATTTCAGTG
TGATTTGACTACGAACAATAGGATTGCCTTGACAAGTTCCGAACTCCTTTATATATATGGTGCCCTAGACTCAAG
AGTGAGAGCCTTGGTGTTCAGTGTACGGTGCTGGGCTCGAGCACATTCACTAACAAGTAGTATTCCTGGTGCATG
GATTACAAATTTCTCCCTTACAATGATGGTCATCTTTTTTCTCCAGAGAAGATCACCCCCTATTCTTCCAACACT
AGATTCCTTAAAAACCCTAGCAGATGCAGAAGATAAATGTGTAATAGAAGGCAACAACTGCACATTTGTTCGTGA
CTTGAGTAGAATTAAACCTTCACAGAACACAGAAACATTAGAATTACTACTGAAGGAATTTTTTGAGTATTTTGG
CAATTTTGCTTTCGATAAAAATTCCATAAATATTCGACAGGGAAGGGAGCAAAACAAACCTGATTCTTCTCCTCT
GTACATTCAGAATCCATTTGAAACTTCTCTCAACATAAGCAAAAATGTAAGTCAAAGCCAGCTGCAAAAATTTGT
AGATTTGGCCCGAGAAAGTGCCTGGATTTTACAACAGGAAGATACAGATCGACCTTCCATATCAAGTAATCGGCC
CTGGGGGCTGGTATCCCTATTGCTACCATCTGCTCCAAACAGAAAGTCCTTTACCAAGAAGAAAAGCAATAAGTT
TGCAATTGAAACAGTCAAAAACTTGCTAGAATCTTTAAAAGGTAACAGAACAGAAAATTTCACAAAAACCAGTGG
GAAGAGAACAATTAGTACTCAGACA**TGA**TGGCTGCTACATTGTGTAAAGAACTGGGCTTAGCCTATCAAATGGTC
TGTGGACTTACTTGGAAAAACTGATTTGAAACTTTCACAGATCTCAGCTTTCATCTGATGTCACTTTTCATGATC
TTCTCATTGGCCCCCTTAACCTGGTCTGAAGTTCTGGGATGTTTTCAGTTTGATCAGTCTGATACTCAGTGGCAC
TTTATTAAAACATCAGCTGTGGAGTGTGGCGGTGCACACCTGTAGTCCCAGCTGCTCAGGAGGCTGAGGCAGGAG
GATCTCTTGAGCCCAGGATTTTGAATCCATCGTGGACAACATAGCAAGATTCCATCTCT

FIGURE 326

MAVPGVGLLTRLNLCARRRTRVQRPIVRLLSCPGTVAKDLRRDEQPSGSVETGFEDKIPKRRFSEMQNERREQAQ
RTVLIHCPEKISENKFLKYLSQFGPINNHFFYESFGLYAVVEFCQKESIGSLQNGTHTPSTAMETAIPFRSRFFN
LKLKNQTSERSRVRSSNQLPRSNKQLFELLCYAESIDDQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDC
IVRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQVKNVPSERIATQKILSVLGECLDHFGPGCV
GVQKILNARCPLVRFSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVRCWARAHSLTSSIPGAWI
TNFSLTMMVIFFLQRRSPPILPTLDSLKTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFEYFGN
FAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNVSQSQLQKFVDLARESAWILQQEDTDRPSISSNRPW
GLVSLLLPSAPNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTISTQT

FIGURE 327

TTCTGCTTATC**ATG**GTTACCAACAAAATGACTGCTGCCTTTAGAAACCCTAGTGGGAAACAGGTGGCGACAGACA
AAGTTGCAGAAAAGCTGAGCTCTACTCTCTCATGGGTGAAGAACACAGTATCGCATACAGTCAGTCAGATGGCCA
GTCAGGTGGCAAGTCCATCTACTTCATTACATACCACATCCTCATCTACCACACTATCAACACCAGCCCTTTCAC
CATCTTCCCCATCACAGTTGAGTCCAGACGTCTTAGAACTCCTGGCTAAACTGGAAGAACAGAATATATTGTTAG
AAACGGATAGTAAGTCTTTAAGATCTGTAAATGGGTCAAGAAGAAACAGTGGCTCTTCTCTTGTGTCGAGTTCAT
CAGCCTCTAGCAACCTCAGTCACCTTGAAGAAGATTCTTGGATTCTTTGGGGAAGAATTGTTAATGAATGGGAAG
ATGTACGCAAAAAGAAGGAAAAGCAAGTTAAGGAACTTGTTCATAAAGGGATACCCCATCACTTTAGAGCAATAG
TTTGGCAACTTTTATGCAGTGCACAAAGTATGCCAATTAAGGATCAGTATTCAGAACTCCTGAAAATGACCTCGC
CTTGTGAAAAATTGATCCGAAGGGACATTGCTAGAACTTACCCTGAACACAACTTTTTTAAGGAAAAAGATAGCC
TTGGACAGGAGGTTTTATTTAATGTAATGAAGGCTTACTCTTTAGTAGATCGTGAGGTTGGTTACTGTCAAGGAA
GTGCTTTTATAGTTGGATTGTTGCTTATGCAGATGCCAGAAGAAGAAGCTTTCTGTGTATTTGTTAAATTAATGC
AAGATTATAGACTTCGTGAACTTTTTAAACCAAGTATGGCAGAATTGGGCCTTTGTATGTACCAGTTTGAATGTA
TGATACAGGAGCATCTTCCAGAGCTCTTTGTACATTTTCAATCTCAGAGTTTTCATACCTCAATGTATGCATCAT
CCTGGTTTCTGACTATCTTTCTTACAACTTTTCCACTACCAGTTGCAACAAGGATATTTGATATCTTTATGTCTG
AGGGTTTAGAAATAGTGTTTCGTGTAGGATTAGCACTTCTTCAGATGAATCAGGCAGAACTGATGCAACTTGACA
TGGAAGGGATGTTACAGCACTTTCAAAAGGTCATTCCACATCAGTTTGATGGTGTCCCAGACAAGCTAATCCAAG
CAGCTTACCAAGTCCAATACAATTCAAAAAAAATGAAAAAGCTTGAAAAGGAATACACTACAATAAAAACGAAAG
AAATGGAAGAGCAAGTTGAAATTAAAAGGTTACGCACAGAAAATAGACTTTTAAAACAGCGCATCGAGACATTAG
AAAAACATAAATGCAGTTCCAACTACAACGAAGATTTTGTGCTACAGCTAGAGAAGGAATTGGTCCAAGCCCGAC
TGAGTGAAGCTGAGTCTCAGTGTGCATTAAAAGAGATGCAGGATAAAGTCTTGGATATAGAGAAGAGGAATAACT
CCCTTCCTGATGAGAATAATATTGCAAGGCTTCAGGAAGAACTCATTGCTGTGAAACTTAGAGAAGCAGAAGCCA
TTATGGGTTTGAAAGAACTTAGACAGCAAGTCAAGGATTTAGAGGAACACTGGCAGCGCCACTTAGCTCGTACTA
CTGGGAGATGGAAAGACCCACCCAAGAAAAATGCTATGAATGAGTTACAGGATGAACTGATGACCATTCGACTTA
GAGAAGCTGAAACACAAGCAGAAATAAGAGAAATAAAACAAAGGATGATGGAAATGGAAACACAGTTGGTTGAAT
CCGCAGATGTGGAGCCTGCATATATGAAGGGC**TGA**CCGTATACTCTCTGCTCCTTCCAGAGTATCTGGCATGTGA
TGAGCTCGCCACAAACATTTAGTGATTCGAGTAAGGCTCTGGTTGATTTACAGTTTCTACTTTCCTGACACTCTG
TTGCTGGTTTGAATAAAAATTTCTTCCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 328

MVTNKMTAAFRNPSGKQVATDKVAEKLSSTLSWVKNTVSHTVSQMASQVASPSTSLHTTSSSTTLSTPALSPSSP
SQLSPDVLELLAKLEEQNILLETDSKSLRSVNGSRRNSGSSLVSSSSASSNLSHLEEDSWILWGRIVNEWEDVRK
KKEKQVKELVHKGIPHHFRAIVWQLLCSAQSMPIKDQYSELLKMTSPCEKLIRRDIARTYPEHNFFKEKDSLGQE
VLFNVMKAYSLVDREVGYCQGSAFIVGLLLMQMPEEEAFCVFVKLMQDYRLRELFKPSMAELGLCMYQFECMIQE
HLPELFVHFQSQSFHTSMYASSWFLTIFLTTFPLPVATRIFDIFMSEGLEIVFRVGLALLQMNQAELMQLDMEGM
LQHFQKVIPHQFDGVPDKLIQAAYQVQYNSKKMKKLEKEYTTIKTKEMEEQVEIKRLRTENRLLKQRIETLEKHK
CSSNYNEDFVLQLEKELVQARLSEAESQCALKEMQDKVLDIEKRNNSLPDENNIARLQEELIAVKLREAEAIMGL
KELRQQVKDLEEHWQRHLARTTGRWKDPPKKNAMNELQDELMTIRLREAETQAEIREIKQRMMEMETQLVESADV
EPAYMKG

FIGURE 329

TGGTGAAAACATGATCTTGCTATGTTGCTCAGGCTGGTTGTCTGGCATTTTCTTTGTCCTTTATTCTTTATAC**TA**
GCTAAACCCTGGAGTATCCTTGAAGCCTTTACTGGCATACAGAGTACCTGAATCTTACTTTGGAGCCTAGCATGG
GTCATAAATATATCTGATTCATTAACCTGTGAGACAGCTGAGAGAACACAGACTCCTTACCTGTATCTCCAGGCA
TATCTGGTTTTTCTCTGCCTAATAGATTTTCCTGCTTTCTAGTTAGTAATATTGAGAAAGAAGAAAGGCTTATTT
ATCATTTGCTTTTTTTCCACTGTGAATCATCTGTTCTTTCCATGAACATTCTGGGGAGCACCTCCTGATTAAACT
CCTGTCTCCCTGACCACTATCCTGCTGTCATTGGACTTCTTGAAGCACATGGGCTACTGCCCCAGGACACTGGGA
TTTGAGAGGAGTTTAGTGGTAATTGTCAGGTCTTTCAAAGCATTTATTATTCCTTTTATACGGAGATTTCAGTAT
TGAGACTTAAAATGAACTGAAAAATGAGATTGAACATTTAATATTTTGGATGTAACTTTTGAAGAAAGTATGCTT
TGGTGCTTAAAATTGTATATGATTTTAGGTAAGAAACTTTGATAATATTGGCATAANNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTCAAATTAGCATGATAGATCAG
GCTACTTAGATTCAGCTTTCTGAGATGTTATTTGTTAACATTAAGGCTAATTTATTATAATGAAAATGTAAACTT
TGAGGTATGTTAATATATAAACATCTTTTTCCTTTGGCCTAAAAGGTCTTTAGTATTCAGCACACTGGGTAAAGT
TCAGTTTAGACACAATCAAATTGGCATCTTTTAAACATAAGTGAAATATAGAGAGCTTGAACTTGAGTTACTTAA
AGAAGATACAGTATAATTAATTATACAGAACAAAACAAAGATGTGTTTAGAGTGACTCTGGCCTGACTCTTGTCC
ATCAGCCCCTAGTAGCCTATCTTCAGCCTTTGGGAAGTCTTAACTTCCCAGGTTAAACTAGAATATTCTGGAACT
GAGCTGTCCAAATTTCATCTTAAAGTGGATCATTTGACTCTGAAACACGATTCTCATGGCAGAAAAAGCCCTGGT
GTTTCCTTGGAGCTGGGGATAAAGGCCAGTGAGCCAGCCTGTGATGAGAGCTGCCCCTGGCACTATCTGAGTGGA
AAGCTCATTGGGACAGCCATGCAGCTATCAGAGCCGACTGAAGCCCTGTCCCTTACCCCTCAGGCACCTGATGCT
TAACTTGCCTCCTGGGAAATAATGATCTAGCATTTACTTGGAACAATGATTAATCATGTTCTTTAATAATTGCTG
ACATTTGTATTTTAAGCTGTATACCAATGTTCGTATTTGACATTGATTTTCTAACCATTAGAGATATTTAATTAA
AACTTGGAAATGAAAGAAACAAAATGA

FIGURE 330

GENMILLLCCSGWLSGIFFVLYSLY

FIGURE 331

GGGAGCAGAGTCGACTGGGAGCGACCGAGCGGGCCGCCGCCGCCGCC**ATG**AACCCCGAATATGACTACCTGTTTA
AGCTGCTTTTGATTGGCGACTCAGGCGTGGGCAAGTCATGCCTGCTCCTGCGGTTTGCTGATGACACGTACACAG
AGAGCTACATCAGCACCATCGGGGTGGACTTCAAGATCCGAACCATCGAGCTGGATGGCAAAACTATCAAACTTC
AGATCTGGGACACAGCGGGCCAGGAACGGTTCCGGACCATCACTTCCAGCTACTACCGGGGGGCTCATGGCATCA
TCGTGGTGTATGACGTCACTGACCAGGAATCCTACGCCAACGTGAAGCAGTGGCTGCAGGAGATTGACCGCTATG
CCAGCGAGAACGTCAATAAGCTCCTGGTGGGCAACAAGAGCGACCTCACCACCAAGAAGGTGGTGGACAACACCA
CAGCCAAGGAGTTTGCAGACTCTCTGGGCATCCCCTTCTTGGAGACGAGCGCCAAGAATGCCACCAATGTCGAGC
AGGCGTTCATGACCATGGCTGCTGAAATCAAAAAGCGGATGGGGCCTGGAGCAGCCTCTGGGGGCGAGCGGCCCA
ATCTCAAGATCGACAGCACCCCTGTAAAGCCGGCTGGCGGTGGCTGTTGC**TAG**GAGGGGCACATGGAGTGGGACA
GGAGGGGGCACCTTCTCCAGATGATGTCCCTGGAGGGGGGAGGAGGTACCTCCCTCTCCCTCTCCTGGGGCATTT
GAGTCTGTGGCTTTGGGGTGTCCTGGGCTCCCCATCTCCTTCTGGCCCATCTGCCTGCTGCCCTGAGCCCCGGTT
CTGTCAGGGTCCCTAAGGGAGGACACTCAGGGCCTGTGGCCAGGCAGGGCGGAGGCCTGCTGTGCAGTTGCCTCT
AGGTGACTTTCCAAGATGCCCCCCTACACACCTTTCTTTGGAACGAGGGCTCTTCTGTCGGTGTCCCTCCCACCC
CCATGTATGCTGCACTGGGTTCTCTCCTTCTTCTTCCTGCTGTCCTGCCCAAGAACTGAGGGTCTCCCCGGCCTC
TACTGCCCTGGCTGCAGTCAGTGCCCAGGGCGAGGAATGTGGCCAGGGGATCCAGGACCTGGGATCCAGGGCCCT
GGGCTGGACCTCAGGACAGGCATGGAGGCCACAGGGGCCCAGCAGCCCACCCTTTCCTCTCCCCACTGCCTCCTC
TCCCTTCCTACACTCCCAGCTCGAGCCGTCCAGCTGCGGTGGGATCTGAGTATATCTAGGGCGGGTGGGCGGGTA
GCAGTGCTGGGCCTGTGTCTTGAGCCTGGAGGGAGACTGCTCCTGCCGCCCTCTGCCCTGCCGGAGACAGACCCA
TGCGCTGCCTGCCCACCGTGCCCCTTTGTCCCCATGTCAGGCGGAGGCGGAAGGCCCACCGTGCCAGAGGCTGGG
CACCAGCCTTAACCCTCACTCTGCTAGCACCTCCTCCCTTTCCCCAAGGTAGCACATCTGGCTCACTCCCCACTC
CGTCTCTGGAGCCCACCAGGGAAGGCCCTCATCCCCTGCCGCTACTTCTCTGGGGAATGTGGGTTCCATCCAGGA
TTGGGGGCCTCTCTGCTCACCCACTCTGCACCCAGGATCCTAGTCCCCTGCCCTCTGGCACAGCTGCTTCCTGCA
AGAAAGCAAGTCTTTGGTCTCCCTGAGAAGCCATGTCCCTCGTGCTGTCTCTTGCCTGTCCCACCTGTGCCCTGC
CCTCCAGCTTGTATTTAAGTCCCTGGGCTGCCCCCTTGGGGTGCCCCCCGCTCCCAGGTTCCCCTCTGGTGTCAT
GTCAGGCATTTTGCAAGGAAAAGCCACTTGGGGAAAGATGGAAAAGGACAAAAAAAATTAATAAATTTCCATTGG
CCCTCGGGTGAGCTGAGGGTTTTTGCAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAGAAAAAAAAAAAAAAAAAAA

FIGURE 332

MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQIWDTAGQERFRTITS
SYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVGNKSDLTTKKVVDNTTAKEFADSLGIPFLET
SAKNATNVEQAFMTMAAEIKKRMGPGAASGGERPNLKIDSTPVKPAGGGCC

FIGURE 333

GCGCGACACTGACCTTCAGCGCCTCGGCTCGGCC**ATG**GCGCCCTCCAGGAAGTTCTTCGTTGGGGGAAACTGGAA
GATGAACGGGCGGAAGCAGAGTCTGGGGGAGCTCATCGGCACTCTGAACGCGGCCAAGGTGCCGGCCGACACCGA
GGTGGTTTGTGCTCCCCCTACTGCCTATATCGACTTCGCCCGGCAGAAGCTAGATCCCAAGATTGCTGTGGCTGC
GCAGAACTGCTACAAAGTGACTAATGGGGCTTTTACTGGGGAGATCAGCCCTGGCATGATCAAAGACTGCGGAGC
CACGTGGGTGGTCCTGGGACACTCAGAGAGAAGGCATGTCTTTGGGGAGTCAGATGAGCTGATTGGGCAGAAAGT
GGCCCATGCTCTGGCAGAGGGACTCGGAGTAATCGCCTGCATTGGGGAGAAGCTAGATGAAAGGGAAGCTGGCAT
CACTGAGAAGGTTGTTTTCGAGCAGACAAAGGTCATCGCAGATAACGTGAAGGACTGGAGCAAGGTCGTCCTCGC
CTATGAGCCTGTGTGGGCCATTGGTACTGGCAAGACTGCAACACCCCAACAGGCCCAGGAAGTACACGAGAAGCT
CCGAGGATGGCTGAAGTCCAACGTCTCTGATGCGGTGGCTCAGAGCACCCGTATCATTTATGGAGGCTCTGTGAC
TGGGGCAACCTGCAAGGAGCTGGCCAGCCAGCCTGATGTGGATGGCTTCCTTGTGGGTGGTGCTTCCCTCAAGCC
CGAATTCGTGGACATCATCAATGCCAAACAA**TGA**GCCCCATCCATCTTCCCTACCCTTCCTGCCAAGCCAGGGAC
TAAGCAGCCCAGAAGCCCAGTAACTGCCCTTTCCCTGCATATGCTTCTGATGGTGTCATCTGCTCCTTCCTGTGG
CCTCATCCAAACTGTATCTTCCTTTACTGTTTATATCTTCACCCTGTAATGGTTGGGACCAGGCCAATCCCTTCT
CCACTTACTATAATGGTTGGAACTAAACGTCACCAAGGTGGCTTCTCCTTGGCTGAGAGATGGAAGGCGTGGTGG
GATTTGCTCCTGGGTTCCCTAGGCCCTAGTGAGGGCAGAAGAGAAACCATCCTCTCCCTTCTTACACCGTGAGGC
CAAGATCCCCTCAGAAGGCAGGAGTGCTGCCCTCTCCCATGGTGCCCGTGCCTCTGTGCTGTGTATGTGAACCAC
CCATGTGAGGGAATAAACCTAGCACTAGG

FIGURE 334

MAPSRKFFVGGNWKMNGRKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQKLDPKIAVAAQNCYKVTNGAF
TGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVFEQTKV
IADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKSNVSDAVAQSTRIIYGGSVTGATCKELASQP
DVDGFLVGGASLKPEFVDIINAKQ

FIGURE 335

GTGCGGGAATCACACACATACCTCAGA**ATG**CCGGGTCTAAGTTGTAGATTTTATCAACACAAATTTCCTGAGGTG
GAAGATGTAGTGATGGTGAATGTCAGATCCATTGCTGAAATGGGGGCTTATGTCAGCTTGCTGGAATACAACAAC
ATTGAAGGCATGATTCTTCTTAGTGAATTATCCAGAAGGCGTATCCGTTCTATCAACAAACTCATCCGAATTGGC
AGGAATGAGTGTGTGGTTGTCATTAGGGTGGACAAAGAAAAAGGATATATTGATTTGTCAAAAAGAAGAGTTTCT
CCAGAGGAAGCAATCAAATGTGAAGACAAATTCACAAAATCCAAAACTGTTTATAGCATTCTTCGTCATGTTGCT
GAGGTGTTAGAATACACCAAGGATGAGCAGCTGGAAAGCCTATTCCAGAGGACTGCCTGGGTCTTTGATGACAAG
TACAAGAGACCTGGATATGGTGCCTATGATGCATTTAAGCATGCAGTCTCAGACCCATCTATTTTGGATAGTTTA
GATTTGAATGAAGATGAACGGGAAGTACTCATTAATAATATTAATAGGCGCTTGACCCCACAGGCTGTCAAAATT
CGAGCAGATATTGAAGTGGCTTGTTATGGTTATGAAGGCATTGATGCTGTAAAAGAAGCCCTAAGAGCAGGTTTG
AATTGTTCTACAGAAAACATGCCCATTAAGATTAATCTAATAGCTCCTCCTCGGTATGTAATGACTACGACAACC
CTGGAGAGAACAGAAGGCCTTTCTGTCCTCAGTCAAGCTATGGCTGTTATCAAAGAGAAGATTGAGGAAAAGAGG
GGTGTGTTCAATGTTCAAATGGAGCCCAAAGTGGTCACAGATACAGATGAGACTGAACTTGCGAGGCAGATGGAG
AGGCTTGAAAGAGAAAATGCCGAAGTGGATGGAGATGATGATGCAGAAGAAATGGAAGCCAAAGCTGAAGAT**TAA**

CTTTGTGGGAAACAGAGTCCAATTTAAGGAACACAGAGCAGCGCTTCCTGGCTGTAAATCCTAGACTTGAAAGTT
TTCCAGTATTGAAAACTTCAAAGCTGAATATTTTTTATTTCTAAGTATTTAAATGTTCTAACAGATCAGAACATG
AAATGCCCTCCTAAATGTCAGCTGTTGTCACACAGTAGCTCCAACACTTTGAGCATTTTTAAGGGAGTGGCCTCA
TTTCACTAGAGACAAATCTTTAAGAATAGTTCTAAAATTGGGCTTGTGATTTCCATTTCTGATGTCTCCAGATTG
GCACCCCTTTCTAGTTCAATGCCTCACGAGATTTGCCAGGGGCATCCAAGGCAAACAATCCCAATCTTTCTATAT
AAAATGTATTCAAGCAAACATCAAATAAATTTCTGGGATATTT

FIGURE 336

MPGLSCRFYQHKFPEVEDVVMVNVRSIAEMGAYVSLLEYNNIEGMILLSELSRRRIRSINKLIRIGRNECVVVIR
VDKEKGYIDLSKRRVSPEEAIKCEDKFTKSKTVYSILRHVAEVLEYTKDEQLESLFQRTAWVFDDKYKRPGYGAY
DAFKHAVSDPSILDSLDLNEDEREVLINNINRRLTPQAVKIRADIEVACYGYEGIDAVKEALRAGLNCSTENMPI
KINLIAPPRYVMTTTTLERTEGLSVLSQAMAVIKEKIEEKRGVFNVQMEPKVVTDTDETELARQMERLERENAEV
DGDDDAEEMEAKAED

FIGURE 337

GGGGGCCAGTTACCATATTGTCCGGAGTGGGTCCTTGACATTCAGGAAAGATACATCCTCAGACCTTTCAAAATT
TGTCATGCCTCTCTAACCTAAAACAGCCCTCATTAAATGCACTTTAATCCGAGCACTGTATGGCTTGGAAAGAAT
T**ATG**AGTGAGGAGAGGAGCCTTTCCTTATTGGCCAAAGCCGTGGATCCCAGACACCCCAATATGATGACAGATGT
GGTTAAACTTCTCTCTGCGGTATGCATTGTAGGGGAAGAAAGCATCCTTGAAGAAGTTTTAGAAGCTTTAACTTC
AGCTGGTGAAGAAAAAAAAATTGACAGATTTTTTTGTATTGTGGAAGGCCTCCGGCACAATTCAGTTCAACTGCA
AGTAGCTTGTATGCAGCTCATCAATGCCCTGGTTACATCTCCTGATGATTTGGATTTCAGGCTTCACATCAGAAA
TGAATTTATGCGTTGTGGATTGAAAGAGATATTGCCAAATTTAAAATGCATTAAGAATGATGGCCTGGATATCCA
ACTTAAAGTCTTTGATGAGCATAAAGAAGAAGATTTGTTTGAGTTATCCCATCGCCTTGAAGATATTAGAGCTGA
ACTTGATGAAGCATATGATGTTTACAACATGGTGTGGAGCACAGTTAAAGAAACTAGAGCAGAGGGATATTTTAT
TTCTATTCTTCAGCATCTTTTGCTGATTCGAAATGATTATTTTATAAGGCAACAATACTTCAAATTAATTGATGA
GTGTGTATCCCAGATTGTATTGCATAGAGATGGAATGGATCCAGACTTCACATATCGAAAAAGACTAGATTTAGA
TTTAACCCAGTTTGTAGACATTTGCATAGATCAAGCAAAACTAGAAGAGTTTGAAGAGAAAGCATCAGAACTTTA
CAAGAAATTTGAAAAAGAGTTTACCGACCACCAAGAAACTCAGGCTGAATTGCAGAAAAAAGAGGCAAAGATTAA
TGAGCTTCAAGCAGAGCTACAAGCTTTTAAGTCTCAGTTTGGTGCCTTGCCAGCTGATTGTAATATTCCTTTGCC
TCCCTCTAAAGAAGGTGGAACTGGCCACTCAGCACTTCCTCCTCCGCCTCCACTGCCTTCTGGTGGAGGGGTGCC
GCCTCCACCTCCTCCCCCACCACCTCCTCCACTTCCAGGAATGCGGATGCCATTCAGTGGTCCTGTGCCTCCACC
ACCTCCCCTGGGATTCCTTGGAGGACAAAATTCTCCTCCTCTACCAATCCTGCCATTTGGGTTGAAACCAAAGAA
AGAATTTAAACCTGAAATCAGCATGAGAAGATTGAATTGGTTAAAGATCAGACCTCATGAAATGACTGAAAACTG
TTTCTGGATAAAAGTAAATGAAAATAAGTATGAAAACGTGGATTTGCTTTGTAAACTTGAGAATACATTTTGTTG
CCAACAAAAAGAGAGAAGAGAAGAGGAAGATATTGAAGAGAAGAAATCGATTAAGAAAAAAATTAAAGAACTTAA
GTTTTTAGATTCTAAAATTGCCCAGAACCTTTCAATCTTCCTGAGCTCTTTTCGGGTGCCATATGAGGAAATCAG
AATGATGATATTGGAAGTAGATGAAACACGGTTGGCAGAGTCTATGATTCAGAACTTAATAAAGCATCTTCCTGA
TCAAGAGCAATTAAATTCATTGTCTCAGTTCAAGAGTGAATATAGCAACTTATGTGAACCTGAGCAGTTTGTGGT
TGTGATGAGCAATGTGAAGAGACTACGGCCACGGCTCAGTGCTATTCTCTTTAAGCTTCAGTTTGAAGAGCAGGT
GAACAACATCAAACCTGACATCATGGCTGTCAGTACTGCCTGCGAAGAGATAAAGAAGAGCAAAAGCTTTAGCAA
GTTGCTGGAACTTGTATTGCTAATGGGAAACTACATGAATGCTGGCTCCCGGAATGCTCAAACCTTCGGATTTAA
CCTTAGCTCTCTCTGTAAACTAAAGGACACAAAATCAGCAGATCAGAAAACAACGCTACTTCATTTCCTGGTAGA
AATATGTGAAGAGAAGTACCCTGATATACTGAATTTTGTGGATGATTTGGAACCTTTAGACAAAGCTAGTAAAGG
TTTGTGCCTTTTTAAGAAACATTTCATGGCTCTGATCTTCAGTGCTAAAAGACTGAAAATTATACCTTTTATTTG
TATGTACTTTCCACTTTCTCACAGTGTTTTCATACCCAATATCTCATTT**TAA**AAATAAAGAGAGTTGTAGGATAT
TAAAAAAAAAAAAAAAAAAAAAG

FIGURE 338

MSEERSLSLLAKAVDPRHPNMMTDVVKLLSAVCIVGEESILEEVLEALTSAGEEKKIDRFFCIVEGLRHNSVQLQ
VACMQLINALVTSPDDLDFRLHIRNEFMRCGLKEILPNLKCIKNDGLDIQLKVFDEHKEEDLFELSHRLEDIRAE
LDEAYDVYNMVWSTVKETRAEGYFISILQHLLLIRNDYFIRQQYFKLIDECVSQIVLHRDGMDPDFTYRKRLDLD
LTQFVDICIDQAKLEEFEEKASELYKKFEKEFTDHQETQAELQKKEAKINELQAELQAFKSQFGALPADCNIPLP
PSKEGGTGHSALPPPPPLPSGGGVPPPPPPPPPPPLPGMRMPFSGPVPPPPPLGFLGGQNSPPLPILPFGLKPKK
EFKPEISMRRLNWLKIRPHEMTENCFWIKVNENKYENVDLLCKLENTFCCQQKERREEEDIEEKKSIKKKIKELK
FLDSKIAQNLSIFLSSFRVPYEEIRMMILEVDETRLAESMIQNLIKHLPDQEQLNSLSQFKSEYSNLCEPEQFVV
VMSNVKRLRPRLSAILFKLQFEEQVNNIKPDIMAVSTACEEIKKSKSFSKLLELVLLMGNYMNAGSRNAQTFGFN
LSSLCKLKDTKSADQKTTLLHFLVEICEEKYPDILNFVDDLEPLDKASKGLCLFKKHFMALIFSAKRLKIIPFIC
MYFPLSHSVFIPNISF

FIGURE 339

AAGAGCAAGGGATCACTGTGCTGGGTTTAAATGCGGTATTTGACATCTTGGTGATAGGCAAATTCAATGTTCTGG
AAATTGTCCAGAAGGTACTACATAAGGACAAGTCATTAGAGAATCTCGGC**ATG**CTCAGGAACGGGGGCCTCCTCT
TCAGAATGACCCTGCTCACCTCTGGAGGGGCTGGGATGCTCTACGTGCGCTGGAGGATCATGGGCACGGGCCCGC
CGGCCTTCACCGAGGTGGACAACCCGGCCTCCTTTGCTGACAGCATGCTGGTGAGGGCCGTAAACTACAATTACT
ACTATTCATTGAATGCCTGGCTGCTGCTGTGTCCCTGGTGGCTGTGTTTTGATTGGTCAATGGGCTGCATCCCCC
TCATTAAGTCCATCAGCGACTGGAGGGTAATTGCACTTGCAGCACTCTGGTTCTGCCTAATTGGCCTGATATGCC
AAGCCCTGTGCTCTGAAGACGGCCACAAGAGAAGGATCCTTACTCTGGGCCTGGGATTTCTCGTTATCCCATTTC
TCCCCGCGAGTAACCTGTTCTTCCGAGTGGGCTTCGTGGTCGCGGAGCGTGTCCTCTACCTCCCCAGCGTTGGGT
ACTGTGTGCTGCTGACTTTTGGATTCGGAGCCCTGAGCAAACATACCAAGAAAAAGAAACCCATTGCCGCTGTCG
TGCTGGGAATCTTATTCATCAACACGCTGAGATGTGTGCTGCGCAGCGGCGAGTGGCGGAGTGAGGAACAGCTTT
TCAGAAGTGCTCTGTCTGTGTGTCCCCTCAATGCTAAGGTTCACTACAACATTGGCAAAAACCTGGCTGATAAAG
GCAACCAGACAGCTGCCATCAGAAACTACCGGGAAGCTGTAAGATTAAATCCCAAGTATGTTCATGCCATGAATA
ATCTTGGAAATATCTTAAAAGAAAGGAATGAGCTACAGGAAGCTGAGGAGCTGCTGTCTTTGGCTGTTCAAATAC
AGCCAGACTTTGCCGCTGCGTGGATGAATCTAGGCATAGTGCAGAATAGCCTGAAACGGTTTGAAGCAGCAGAGC
AAAGTTACCGGACAGCAATTAAACACAGAAGGAAATACCCAGACTGTTACTACAACCTCGGGCGTCTGTATGCAG
ATCTCAATCGCCACGTGGATGCCTTGAATGCGTGGAGAAATGCCACCGTGCTGAAACCAGAGCACAGCCTGGCCT
GGAACAACATGATTATACTCCTCGACAATACAGGTAATTTAGCCCAAGCTGAAGCAGTTGGAAGAGAGGCACTGG
AATTAATACCTAATGATCACTCTCTCATGTTCTCGTTGGCAAACGTGCTGGGGAAATCCCAGGAATACAAGGAAT
CTGAAGCTTTATTCCTCAAGGCAATTAAAGCAAATCCAAATGCTGCAAGTTACCATGGTAATTTGGCTGTGCTTT
ATCATCGTTGGGGACATCTAGACTTGGCCAAGAAACACTATGAAATCTCCTTGCAGCTTGACCCCACGGCATCAG
GAACTAAGGAGAATTACGGTCTGCTGAGAAGAAAGCTAGAACTAATGCAAAAGAAAGCTGTC**TGA**TCCTGTTTCC
TTCATGTTTTGAGTTTGAGTGTGTGTGCATGAGGCATATCATTAATAGTATGTGGTTACATTTAACCATTTAAAA
GTCTTAGACATGTTATTTTACTGATTTTTTTCTATGAAAACAAAGACATGCAAAAAGATTATAGCACCAGCAATA
TACTCTTGAATGCGTGATATGATTTTTCATTGAAATTGTATTTTTTCAGACAACTCAAATGTAATTCTAAAATTC
CAAAAATGTCTTTTTTAATTAAACAGAAAAAGAGAAAAAATTATCTTGAGCAACTTTTAGTAGAATTGAGCTTAC
ATTTGGGATCTGAGCCTTGTCGTGTATGGACTAGCACTATTAAACTTCAATTATGACCAAGAAAGGATACACTGG
CCCCTACAATTTGTATAAATATTGAACATGTCTATATATTAGCATTTTTATTTAATGACAAAGCAAATTAAGTTT
TTTTATCTCTTTTTTTTAAAACAACATACTGTGAACTTTGTAAGGAAATATTTATTTGTATTTTTATGTTTTGAA
TAGGGCAAATAATCGAATGAGGAATGGAAGTTTTAACATAGTATATCTATATGCTTTTCCCCATAGGAAGAAATT
GACTCTTGCAGTTTTTGGATGCTCTGACTTGTGCAATTTCAATACACAGGAGATTATGTAATGTAATATTTTTCA
TAAGCGGTTACTATCAATTGAAAGTTCAAGCCATGCTTTAGGCAAGAGCAGGCAGCCTCACATCTTTATTTTTGT
TACATCCAAGGTGAAGAGGGCAACACATCTGTGTAAGCTGCTTTTTAGTGTGTTTATCTGAAGGCCGTTTTCCAT
TTTGCTTAATGTAACTACAGACATTATCCAGAAAATGCAAAATTTTCTATCAAATGGAGCCACATTCGGGGAATT
CGTGGTATTTTTAAGAATTGAGTTGTTCCTGCTGTTTTTTATTTGATCCAAACAATGTTTTGTTTTGTTCTTCTC
TGTATGCTGTTGACCTAATGATTTATGCAATCTCTGTAATTTCTTATGCAGTAAAATTACTACACAAACTAG

FIGURE 340

MLRNGGLLFRMTLLTSGGAGMLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNAWLLLCPWWLCF
DWSMGCIPLIKSISDWRVIALAALWFCLIGLICQALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAER
VLYLPSVGYCVLLTFGFGALSKHTKKKKPIAAVVLGILFINTLRCVLRSGEWRSEEQLFRSALSVCPLNAKVHYN
IGKNLADKGNQTAAIRNYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQPDFAAAWMNLGIVQNS
LKRFEAAEQSYRTAIKHRRKYPDCYYNLGRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNLAQA
EAVGREALELIPNDHSLMFSLANVLGKSQEYKESEALFLKAIKANPNAASYHGNLAVLYHRWGHLDLAKKHYEIS
LQLDPTASGTKENYGLLRRKLELMQKKAV

FIGURE 341

ATGAGTTGGAGCTTTCTGACTCGCCTGCTAGAGGAGATTCACAACCATTCCACATTTGTGGGGAAGATCTGGCTC
ACTGTTCTGATTGTCTTCCGGATCGTCCTTACAGCTGTAGGAGGAGAATCCATCTATTACGATGAGCAAAGCAAA
TTTGTGTGCAACACAGAACAGCCGGGCTGTGAGAATGTCTGTTATGATGCGTTTGCACCTCTCTCCCATGTACGC
TTCTGGGTGTTCCAGATCATCCTGGTGGCAACTCCCTCTGTGATGTACCTGGGCTATGCTATCCACAAGATTGCC
AAAATGGAGCACGGTGAAGCAGACAAGAAGGCAGCTCGGAGCAAGCCCTATGCAATGCGCTGGAAACAACACCGG
GCTCTGGAAGAAACGGAGGAGGACAACGAAGAGGATCCTATGATGTATCCAGAGATGGAGTTAGAAAGTGATAAG
GAAAATAAAGAGCAGAGCCAACCCAAACCTAAGCATGATGGCCGACGACGGATTCGGGAAGATGGGCTCATGAAA
ATCTATGTGCTGCAGTTGCTGGCAAGGACCGTGTTTGAGGTGGGTTTTCTGATAGGGCAGTATTTTCTGTATGGC
TTCCAAGTCCACCCGTTTTATGTGTGCAGCAGACTTCCTTGTCCTCATAAGATAGACTGCTTTATTTCTAGACCC
ACTGAAAAGACCATCTTCCTTCTGATAATGTATGGTGTTACAGGCCTTTGCCTCTTGCTTAACATTTGGGAGATG
CTTCATTTAGGGTTTGGGACCATTCGAGACTCACTAAACAGTAAAAGGAGGGAACTTGAGGATCCGGGTGCTTAT
AATTATCCTTTCACTTGGAATACACCATCTGCTCCCCCTGGCTATAACATTGCTGTCAAACCAGATCAAATCCAG
TACACCGAACTGTCCAATGCTAAGATCGCCTACAAGCAAAACAAGGCCAACACAGCCCAGGAACAGCAGTATGGC
AGCCATGAGGAGAACCTCCCAGCTGACCTGGAGGCTCTGCAGCGGGAGATCAGGATGGCTCAGGAACGCTTGGAT
CTGGCAGTTCAGGCCTACAGTCACCAAAACAACCCTCATGGTCCCCGGGAGAAGAAGGCCAAAGTGGGGTCCAAA
GCTGGGTCCAACAAAAGCACTGCCAGTAGCAAATCAGGGGATGGAAGAACTCTGTCTGGATT**TAA**

FIGURE 342

MSWSFLTRLLEEIHNHSTFVGKIWLTVLIVFRIVLTAVGGESIYYDEQSKFVCNTEQPGCENVCYDAFAPLSHVR
FWVFQIILVATPSVMYLGYAIHKIAKMEHGEADKKAARSKPYAMRWKQHRALEETEEDNEEDPMMYPEMELESDK
ENKEQSQPKPKHDGRRRIREDGLMKIYVLQLLARTVFEVGFLIGQYFLYGFQVHPFYVCSRLPCPHKIDCFISRP
TEKTIFLLIMYGVTGLCLLLNIWEMLHLGFGTIRDSLNSKRRELEDPGAYNYPFTWNTPSAPPGYNIAVKPDQIQ
YTELSNAKIAYKQNKANTAQEQQYGSHEENLPADLEALQREIRMAQERLDLAVQAYSHQNNPHGPREKKAKVGSK
AGSNKSTASSKSGDGKNSVWI

FIGURE 343

CTCGAGATTTACCGGGGGCCTGGCTGCACGTTCCCTGTCGGCGTTCTGCGGCACGGGCCGGTGGGACGTTGGTGG
GGTTGCGCTGCGGGGAGGAAGAGGCGACTTTCCACCTTCTAAGCCCGCCTCGGGTCGCG**ATG**TCGTCCGGGGCCG
GGTCTCGGCGGCCGCGGGAGCCGCCGGAGCACGAGCTGCAGCGGCGGCGGGAGCAGAAACGGCGGCGGCACGACG
CGCAGCAGCTGCAGCAGCTCAAGCACCTGGAGTCCTTTTATGAGAAACCTCCTCCTGGGTTTATAAAGGAGGACG
AGACGAAGCCAGAAGACTGTATACCAGATGTGCCCGGCAATGAACATGCCAGGGAGTTTCTGGCTCACGCTCCGA
CTAAAGGACTGTGGATGCCCCTGGGGAGAGAGGTCAAAGTTATGCAATGTTGGCGTTGCAAACGGTATGGCCATC
GAACAGGCGACAAAGAATGCCCTTTCTTTATCAAAGGCAACCAGAAGTTAGAACAGTTCCGAGTCGCACATGAAG
ATCCTATGTACGACATCATTCGCGAGAATAAAAGACATGAAAAGGATGTAAGGATCCAGCAGTTAAAGCAGTTAC
TGGAGGACTCCACCTCAGATGACGACGGGAGCAGCTCCAGCTCCTCGGGGGACAGAGAGAAGCGCAAGAAAAGGA
AGAAAAAAGAAAAGCACAAGAAACGCAAGAAGGAGAAGAAAAAGAAGAAGAAACGGAAGCACAAGGCTTCCAAGT
CCAGTGAGAGCTCTGACTCAGAG**TGA**CAGCACCACCCACAGGCCAAAGGACAGAGCCGCCGCCGAGAGTGAGAGA
CTGGACATCTAGCACAGCCCTGGGCCCTCACCGCCTCCTGGTGCCAAGTGACCACTGCAGAGCAGGTGGGCTCCT
GCGACACCTGTGTCCTCTACCTTATGGTCACCGTGTCTGTGACTGCTTCAGTAGGCCGCTGCAGTGGGAGGTGAT
GAGAAGACACTGAAGGGGCAGACACTCTAGGGCACTGCCACGGCGGCGTTTGCCCTCCATGGTGTGGTAACTCAT
TTTCCATGAACTTAAGGCTTCACCCTTCTTTGTGGTTTGGGATAAGGTAAATCTCGAG

FIGURE 344

MSSGAGSRRPREPPEHELQRRREQKRRRHDAQQLQQLKHLESFYEKPPPGFIKEDETKPEDCIPDVPGNEHAREF
LAHAPTKGLWMPLGREVKVMQCWRCKRYGHRTGDKECPFFIKGNQKLEQFRVAHEDPMYDIIRENKRHEKDVRIQ
QLKQLLEDSTSDDDGSSSSSSGDREKRKKRKKKEKHKKRKKEKKKKKKRKHKASKSSESSDSE

FIGURE 345A

ATGGCCTCAGGAGCCGGAGGAGTCGGAGGGGGCGGTGGCGGCAAGATCCGGACGCGGCGTTGCCACCAGGGGCCA
ATTAAGCCTTACCAGCAGGGGCGACAACAGCATCAGGGCATTCTTAGCAGGGTTACAGAATCTGTTAAGAATATT
GTGCCAGGGTGGTTACAAAGATACTTCAACAAGAATGAAGATGTATGCAGCTGTTCAACAGACACAAGCGAGGTT
CCACGCTGGCCAGAAAATAAAGAGGACCATCTGGTATATGCCGATGAGGAGAGCTCTAATATTACTGATGGGAGA
ATCACACCTGAGCCAGCAGTCAGTAATACAGAAGAACCTTCAACAACTAGTACTGCTTCAAATTATCCAGATGTG
TTAACAAGGCCTTCTCTTCATCGGAGCCATCTGAATTTTTCCATGTTGGAATCCCCTGCATTACACTGTCAGCCA
TCTACATCCTCGGCATTCCCAATTGGCAGTTCGGGATTTTCCCTTGTAAAGGAAATTAAAGATTCTACCTCTCAG
CATGATGATGATAACATCTCAACTACCAGTGGTTTTTCTTCAAGAGCTTCTGATAAAGATATAACTGTTTCAAAG
AACACTTCATTGCCACCTCTGTGGTCCCCAGAAGCTGAACGTTCTCACTCACTCTCACAGCACACTGCCACCAGC
TCAAAAAAACCAGCATTCAACTTGTCTGCCTTTGGAACACTTTCCCCTTCACTTGGGAATTCTTCAATCCTTAAA
ACCAGTCAGCTTGGAGATTCTCCTTTTTATCCTGGAAAAACAACATACGGTGGGGCAGCAGCTGCTGTAAGACAG
TCTAAACTACGAAATACACCTTATCAGGCACCAGTTAGAAGACAAATGAAAGCTAAGCAACTCAGTGCACAATCT
TACGGTGTGACCAGTTCAACAGCTCGGCGAATATTGCAGTCTTTAGAGAAGATGTCAAGCCCTTTAGCGGATGCA
AAAAGAATTCCATCCATTGTTTCTTCTCCTCTGAATTCTCCTCTTGATAGGAGTGGGATAGATATCACAGATTTT
CAGGCCAAAAGAGAAAAGGTGGATTCTCAATATCCTCCTGTTCAGAGACTTATGACCCCAAAGCCAGTTTCCATA
GCAACAAATCGAAGTGTTTATTTTAAACCATCTCTGACTCCTTCTGGTGAATTCAGGAAGACTAATCAAAGAATA
GATAACAAGTGCAGTACTGGATATGAAAAAAATATGACACCCGGACAAAATAGAGAACAACGAGAAAGTGGCTTT
TCATATCCAAATTTCAGTTTGCCTGCAGCCAATGGTTTATCTTCTGGAGTAGGTGGTGGAGGTGGCAAGATGAGA
CGAGAAAGACACGCCTTTGTTGCTTCTAAACCTCTGGAGGAGGAGGAAATGGAAGTTCCAGTATTACCGAAAATC
TCTCTACCGATCACCAGTTCTTCACTGCCTACCTTTAATTTTAGTTCCCCTGAGATCACAACTTCCTCTCCATCA
CCCATCAATTCGTCTCAAGCATTAACAAACAAGGTACAAATGACCTCTCCGAGCAGCACTGGCAGTCCCATGTTT
AAATTTTCATCTCCAATCGTAAAATCTACTGAGGCAAATGTACTACCTCCATCATCTATTGGATTTACATTTAGT
GTGCCTGTTGCAAAAACAGCAGAACTTTCTGGTTCTAGTAGTACTTTAGAACCAATTATAAGTAGTTCAGCTCAT
CATGTCACTACAGTGAACAGTACAAATTGTAAGAAGACACCACCTGAAGATTGTGAGGGTCCTTTTAGACCTGCA
GAAATCCTGAAAGAAGGAAGTGTTCTAGATATTCTGAAAAGCCCTGGTTTCGCATCGCCGAAGATAGATTCTGTT
GCTGCTCAGCCCACCGCAACAAGCCCAGTAGTTTATACAAGACCAGCAATAAGTAGCTTTTCTTCTAGTGGAATT
GGGTTTGGGGAGAGTTTAAAAGCTGGGTCATCATGGCAGTGTGATACATGTCTACTCCAGAACAAAGTTACAGAC
AACAAATGCATAGCCTGTCAAGCAGCAAAATTGTCACCCAGAGATACTGCTAAACAGACTGGAATTGAAACACCA
AATAAAAGTGGCAAAACAACTCTTTCTGCATCAGGGACAGGCTTTGGAGACAAATTTAAACCAGTGATAGGCACT
TGGGATTGTGATACCTGTTTAGTGCAAAATAAACCTGAAGCAATAAAATGTGTAGCCTGTGAAACACCGAAACCT
GGAACTTGTGTGAAGCGAGCCCTTACATTGACAGTGGTTTCGGAAAGTGCTGAGACTATGACTGCTTCATCTTCC
AGCTGCACTGTAACCACTGGTACCTTAGGATTTGGAGATAAATTCAAAAGGCCCATTGGATCTTGGGAGTGTTCA
GTATGCTGTGTTTCTAATAATGCAGAAGACAATAAGTGTGTGTCCTGTATGTCTGAGAAACCAGGAAGTTCAGTA
CCTGCTTCAAGTAGCAGCACTGTACCTGTCTCTCTGCCTTCTGGAGGCTCTCTAGGATTGGAAAAGTTCAAGAAA
CCCGAGGGAAGCTGGGACTGTGAATTGTGCCTAGTGCAGAATAAGGCAGACTCTACCAAATGTTTGGCATGTGAA
AGTGCAAAGCCAGGCACAAAATCTGGGTTTAAAGGCTTTGACACATCTTCCTCATCTTCGAACTCAGCAGCCTCC
TCATCCTTCAAATTTGGTGTCTCATCATCCTCTTCTGGGCCTTCTCAGACTTTAACAAGCACTGGAAATTTTAAA
TTTGGAGATCAGGGAGGATTCAAAATAGGTGTGTCATCTGATTCTGGGTCTATAAACCCCATGAGTGAAGGCTTT
AAATTTTCTAAACCAATAGGAGATTTTAAATTTGGAGTTTCATCTGAATCTAAGCCCGAAGAAGTTAAAAAAGAT
AGTAAGAATGATAATTTTAAGTTTGGACTTTCTTCTGGTTTAAGCAACCCAGTTTCTTTAACTCCATTTCAATTT
GGGGTATCTAATCTTGGACAGGAAGAAAAGAAAGAGGAACTGCCCAAATCTTCCTCTGCAGGTTTTAGCTTTGGT
ACAGGTGTTATTAACTCCACCCCTGCTCCTGCTAACACCATAGTGACCTCTGAGAACAAGAGCAGCTTCAACCTT
GGAACCATAGAAACCAAGAGTGCTTCAGTGGCTCCTTTCACATGTAAGACATCAGAAGCTAAAAAAGAAGAAATG
CCTGCCACCAAAGGAGGATTCTCTTTTGGCAACGTGGAGCCTGCCTCTCTGCCATCTGCCTCAGTGTTTGTTTTG
GGAAGGACAGAAGAGAAACAGCAAGAGCCTGTCACTTCTACTTCCCTAGTTTTTGGGAAGAAAGCTGACAATGAA
GAGCCAAAGTGTCAACCAGTGTTTTCCTTTGGGAATTCAGAGCAAACCAAAGATGAGAATTCTTCAAAGTCCACA
TTTAGTTTTAGTATGACAAAACCATCTGAGAAGGAATCTGAACAGCCAGCAAAAGCCACTTTTGCCTTTGGAGCT
CAAACTAGTACTACAGCTGATCAAGGTGCAGCAAAGCCAGTTTTTAGTTTCTTGAACAACAGTTCCTCTAGTTCA

FIGURE 345B

AGTACACCAGCCACTTCTGCTGGTGGTGGCATATTTGGTAGTTCCACCTCTTCCTCCAATCCACCTGTGGCTACC
TTTGTGTTTGGACAGTCCAGCAATCCTGTGAGCAGCTCTGCCTTTGGTAACACTGCTGAATCCAGCACCTCTCAG
TCTTTGCTATTTTCTCAAGATAGCAAACTAGCAACCACATCCAGCACAGGTACAGCTGTCACCCCATTTGTCTTT
GGTCCAGGAGCCAGCAGTAATAATACTACCACCTCTGGTTTCGGCTTTGGAGCCACAACCACATCTAGCTCTGCA
GGATCCTCCTTTGTATTTGGAACTGGACCCTCAGCACCATCTGCCAGTCCAGCATTTGGTGCTAACCAGACCCCA
ACATTTGGACAAAGTCAAGGTGCCAGCCAGCCCAATCCCCCAGGCTTTGGATCTATATCATCTTCCACAGCATTA
TTTCCCACTGGTTCTCAGCCTGCACCACCTACTTTTGGGACAGTGTCAAGCAGTAGCCAGCCCCCTGTGTTTGGA
CAGCAACCTAGTCAGTCTGCATTTGGCTCTGGAACAACTCCTAATTCTAGTTCGGCTTTCCAGTTTGGCAGCAGC
ACTACAAATTTCAACTTCACAAACAACAGTCCATCAGGAGTGTTCACATTTGGTGCAAATTCTAGCACACCTGCA
GCCTCAGCCCAGCCTTCAGGCTCGGGGGGCTTTCCATTTAACCAGTCTCCAGCAGCATTTACAGTGGGGTCAAAT
GGGAAAAATGTGTTCTCTTCTTCTGGAACTTCATTCTCTGGTCGCAAGATAAAGACTGCTGTTAGACGCAGGAAA
TAAAGGTCACATTGGTGTTGTACTCAATTTTAACAACAGCTGGTGCCCTGCTTTCAGATACTGGATTGTACTTTG
TGCTGGGGTTATCTGAAGTCAGATCTGCCTAAGGACTTCTTTAATTTTGGAATTTTCCTCCTTTCTCTTTCGTTA
CAGAAGCCCCACCCTGCCTCACCCACCCTTTTTTAAATAAATAAATAGCTAGACTGGTGACTGATTCTTCAGCAA
AAATATTTTATGATCCAGCAGATTATTCACTGATTTGACATAGTCTGGCTGTACCCAGGAATGGAGCCTGCACGG
TGAATGGCTTTGTATAGAACCTCTTTGTCTACACCATTATGTGCGCTGATAACGTTCATGGAACGCGTTGAAATT
GTAATTATATCTGAGGAATTCTGTATAGATTAGAATTCTGTATAGATTAGAGAGTGTTGAAACGGATGATTTCTA
TGCTGAGTTTGTGCTGGTGTATGTGTGAAGTGAGTGAGTTGGGTGTATTGTGCGCTAAACTTTTCTGATAGAGGA
AGCCTGATTAAAGAATGGTCCGTGCTAAGGACTTGTTAGATCTAGTTCACTCTCCATTTAATAATTATATGCTAT
TTCTATATTTTCATTCTCCTATCACCTGTCTTGCCTTTTTCATTATTTTATTATGAAACTTGTGTAAATACAATT
TTGTTTCTGTACTTTTTGGCATAACATAAATCTGTGAACTTGAAATTTGAATTTTGTGTTAGAGATTTTTTTGTT
GTTTGTTTAGTCTTGTCTCAGATTTTATTATGTAAATCCCATTATTCAAAGTTGCCTAAATCCATTTGGAAATCT
TTAAAAAAAAAATTGGGGATTCTTAAAGTTGAATTTATTGGCTTTTCTGATCCAGTTTTGTTTGGACCAAAAACC
AGTATTGTACAAAGTATTAAGCATATATTTTTATATTTACTAAAATGGTCTGTGGTGACTTTTGGATAATAAGGA
AAAGTTTAATATTAAAGCCATGTTTATTACAGTATAATTAACATGTTAAACCATGGGATAAATGCCATCAATAAA
AAATTATGACAT

FIGURE 346

MASGAGGVGGGGGGKIRTRRCHQGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVCSCSTDTSEV
PRWPENKEDHLVYADEESSNITDGRITPEPAVSNTEEPSTTSTASNYPDVLTRPSLHRSHLNFSMLESPALHCQP
STSSAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDITVSKNTSLPPLWSPEAERSHSLSQHTATS
SKKPAFNLSAFGTLSPSLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQAPVRRQMKAKQLSAQS
YGVTSSTARRILQSLEKMSSPLADAKRIPSIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPVSI
ATNRSVYFKPSLTPSGEFRKTNQRIDNKCSTGYEKNMTPGQNREQRESGFSYPNFSLPAANGLSSGVGGGGGKMR
RERHAFVASKPLEEEEMEVPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSSQALTNKVQMTSPSSTGSPMF
KFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDCEGPFRPA
EILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVYTRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTD
NKCIACQAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGTWDCDTCLVQNKPEAIKCVACETPKP
GTCVKRALTLTVVSESAETMTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKCVSCMSEKPGSSV
PASSSSTVPVSLPSGGSLGLEKFKKPEGSWDCELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAAS
SSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGSINPMSEGFKFSKPIGDFKFGVSSESKPEEVKKD
SKNDNFKFGLSSGLSNPVSLTPFQFGVSNLGQEEKKEELPKSSSAGFSFGTGVINSTPAPANTIVTSENKSSFNL
GTIETKSASVAPFTCKTSEAKKEEMPATKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGKKADNE
EPKCQPVFSFGNSEQTKDENSSKSTFSFSMTKPSEKESEQPAKATFAFGAQTSTTADQGAAKPVFSFLNNSSSSS
STPATSAGGGIFGSSTSSSNPPVATFVFGQSSNPVSSSAFGNTAESSTSQSLLFSQDSKLATTSSTGTAVTPFVF
GPGASSNNTTTSGFGFGATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQPNPPGFGSISSSTAL
FPTGSQPAPPTFGTVSSSSQPPVFGQQPSQSAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTPA
ASAQPSGSGGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIKTAVRRRK

FIGURE 347

CCTTCACACAGCTCTTTCACC**ATG**CCTGGATCACTTCCTTTGAATGCAGAAGCTTGCTGGCCAAAAGATGTTGGG
ATTGTTGCCCTTGAGATCTATTTTCCTTCTCAATATGTTGATCAAGCAGAGTTGGAAAAATATGATGGTGTAGAT
GCTGGGAAGTATACCATTGGCTTGGGCCAGGCCAAGATGGGCTTCTGCACAGATAGAGAAGATATTAACTCTCTT
TGCATGACTGTGGTTCAGAATCTTATGGAGAGAAATAACCTTTCCTATGATTGCATTGGGCGGCTGGAAGTTGGA
ACAGAGACAATCATCGACAAATCAAAGTCTGTGAAGACTAATTTGATGCAGCTGTTTGAAGAGTCTGGGAATACA
GATATAGAAGGAATCGACACAACTAATGCATGCTATGGAGGCACAGCTGCTGTCTTCAATGCTGTTAACTGGATT
GAGTCCAGCTCTTGGGATGGACGGTATGCCCTGGTAGTTGCAGGAGATATTGCTGTATATGCCACAGGAAATGCT
AGACCTACAGGTGGAGTTGGAGCAGTAGCTCTGCTAATTGGGCCAAATGCTCCTTTAATTTTTGAACGAGGGCTT
CGTGGGACACATATGCAACATGCCTATGATTTTTACAAGCCTGATATGCTATCTGAATATCCTATAGTAGATGGG
AAACTCTCCATACAGTGCTACCTCAGTGCATTAGACCGCTGCTATTCTGTCTACTGCAAAAAGATCCATGCCCAG
TGGCAGAAAGAGGGAAATGATAAAGATTTTACCTTGAATGATTTTGGCTTCATGATCTTTCACTCACCATATTGT
AAACTGGTTCAGAAATCTCTAGCTCGGATGTTGCTGAATGACTTCCTTAATGACCAGAATAGAGATAAAAATAGT
ATCTATAGTGGCCTGGAAGCCTTTGGGGATGTTAAATTAGAAGACACCTACTTTGATAGAGATGTGGAGAAGGCA
TTTATGAAGGCTAGCTCTGAACTCTTCAGTCAGAAAACAAAGGCATCTTTACTTGTATCAAATCAAAATGGAAAT
ATGTACACATCTTCAGTATATGGTTCCCTTGCATCTGTTCTAGCACAGTACTCACCTCAGCAATTAGCAGGGAAG
AGAATTGGAGTGTTTTCTTATGGTTCTGGTTTGGCTGCCACTCTGTACTCTCTTAAAGTCACACAAGATGCTACA
CCGGGGTCTGCTCTTGATAAAATAACAGCAAGTTTATGTGATCTTAAATCAAGGCTTGATTCAAGAACTGGTGTG
GCACCAGATGTCTTCGCTGAAAACATGAAGCTCAGAGAGGACACCCATCATTTGGTCAACTATATTCCCCAGGGT
TCAATAGATTCACTCTTTGAAGGAACGTGGTACTTAGTTAGGGTGGATGAAAAGCACAGAAGAACTTACGCTCGG
CGTCCCACTCCAAATGATGACACTTTGGATGAAGGAGTAGGACTTGTGCATTCAAACATAGCAACTGAGCATATT
CCAAGCCCTGCCAAGAAAGTACCAAGACTCCCTGCCACAGCAGCAGAACCTGAAGCAGCTGTCATTAGTAATGGG
GAACAT**TAA**GATACTCTGTGAGGTGCAAGACTTCAGGGTGGGGTGGGCATGGGGTGGGGGTATGGGAACAGTTGG

FIGURE 348

MPGSLPLNAEACWPKDVGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQN
LMERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTNACYGGTAAVFNAVNWIESSSWDG
RYALVVAGDIAVYATGNARPTGGVGAVALLIGPNAPLIFERGLRGTHMQHAYDFYKPDMLSEYPIVDGKLSIQCY
LSALDRCYSVYCKKIHAQWQKEGNDKDFTLNDFGFMIFHSPYCKLVQKSLARMLLNDFLNDQNRDKNSIYSGLEA
FGDVKLEDTYFDRDVEKAFMKASSELFSQKTKASLLVSNQNGNMYTSSVYGSLASVLAQYSPQQLAGKRIGVFSY
GSGLAATLYSLKVTQDATPGSALDKITASLCDLKSRLDSRTGVAPDVFAENMKLREDTHHLVNYIPQGSIDSLFE
GTWYLVRVDEKHRRTYARRPTPNDDTLDEGVGLVHSNIATEHIPSPAKKVPRLPATAAEPEAAVISNGEH

FIGURE 349

<u>ATG</u>GCTGCTGAGAAGCAGGTCCCAGGCGGCGGCGGCGGCGGCGGCAGTGGCGGCGGCGGTGGACGTGGTGCC
GGAGGGGAAGAAAATAAAGAAAACGAACGCCCTTCGGCCGGATCGAAGGCAAACAAAGAATTTGGGGATAGCCTG
AGTTTGGAGATTCTTCAGATTATTAAGGAATCCCAGCAGCAGCATGGTTTACGGCATGGAGATTTTCAGAGGTAC
AGGGGCTACTGTTCCCGTAGACAAAGACGTCTTCGAAAAACACTCAACTTCAAGATGGGTAACAGACACAAATTC
ACAGGGAAGAAAGTGACTGAAGAGCTTCTGACCGATAATAGATACTTGCTTCTGGTTCTGATGGATGCTGAAAGA
GCCTGGAGCTACGCCATGCAGCTGAAACAGGAAGCCAACACTGAACCCCGAAAACGGTTTCACTTGTTATCTCGC
CTACGCAAAGCCGTGAAGCATGCAGAGGAATTGGAACGCTTGTGTAAGAGCAATCGCGTGGATGCCAAGACCAAA
TTAGAGGCTCAGGCTTACACAGCTTACCTCTCAGGAATGCTACGTTTTGAACATCAAGAATGGAAAGCTGCCATT
GAGGCTTTTAACAAATGCAAAACTATCTATGAGAAGCTAGCCAGTGCTTTCACAGAGGAGCAGGCTGTGCTGTAT
AACCAACGTGTGGAAGAGATTTCACCCAACATCCGCTATTGTGCATATAATATTGGGGACCAGTCAGCCATCAAT
GAACTCATGCAGATGAGATTGAGGTCTGGGGGCACTGAGGGTCTCTTGGCTGAAAAATTGGAGGCTTTGATCACT
CAGACTCGAGCCAAACAGGCAGCTACCATGAGTGAAGTGGAGTGGAGAGGGAGAACGGTTCCAGTGAAGATTGAC
AAAGTGCGCATTTTCTTATTAGGACTGGCTGATAACGAAGCAGCTATTGTCCAGGCTGAAAGCGAAGAAACTAAG
GAGCGCCTGTTTGAATCAATGCTCAGCGAGTGTCGGGACGCCATCCAGGTGGTTCGGGAGGAGCTCAAGCCAGAT
CAGAAACAGAGAGATTATATCCTTGAAGGAGAGCCAGGGAAGGTGTCTAATCTTCAATACTTGCATAGCTACCTG
ACTTACATCAAGCTATCAACGGCAATCAAGCGTAATGAGAACATGGCCAAAGGTCTGCAGAGGGCTCTGCTGCAG
CAGCAGCCAGAGGATGACAGCAAGCGCTCACCCCGGCCCCAGGACCTGATCCGACTCTATGACATCATCTTACAG
AATCTGGTGGAATTGCTCCAGCTTCCTGGTTTAGAGGAAGACAAAGCCTTCCAGAAAGAGATAGGCCTCAAGACT
CTGGTGTTCAAAGCTTACAGGTGTTTTTTCATTGCTCAGTCCTATGTGCTGGTGAAGAAGTGGAGCGAAGCCCTT
GTCCTGTATGACAGAGTCCTGAAATATGCAAATGAAGTAAATTCTGATGCTGGCGCCTTCAAGAACAGCCTAAAG
GACCTGCCTGATGTGCAAGAGCTCATCACTCAAGTGCGGTCAGAGAAGTGCTCCCTGCAGGCCGCAGCCATCCTT
GAGTCAAACGACGCTCATCAAACAGAGACCTCCTCCTCCCAAGTCAAGGACAATAAGCCTCTGGTTGAACGGTTT
GAGACATTCTGCCTGGACCCTTCCCTTGTCACCAAGCAAGCCAACCTTGTGCACTTCCCACCAGGCTTCCAGCCC
ATTCCCTGCAAGCCTTTGTTCTTTGACCTGGCCCTCAACCATGTGGCTTTCCCACCCCTTGAGGACAAGTTGGAA
CAGAAGACCAAGAGTGGCCTCACTGGATACATCAAGGGCATCTTTGGATTCAGGAGC**<u>TAA</u>**

FIGURE 350

MAAEKQVPGGGGGGGGSGGGGGRGAGGEENKENERPSAGSKANKEFGDSLSLEILQIIKESQQQHGLRHGDFQRY
RGYCSRRQRRLRKTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAMQLKQEANTEPRKRFHLLSR
LRKAVKHAEELERLCKSNRVDAKTKLEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTEEQAVLY
NQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTEGLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKID
KVRIFLLGLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQKQRDYILEGEPGKVSNLQYLHSYL
TYIKLSTAIKRNENMAKGLQRALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEEDKAFQKEIGLKT
LVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLKYANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAIL
ESNDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPPGFQPIPCKPLFFDLALNHVAFPPLEDKLE
QKTKSGLTGYIKGIFGFRS

FIGURE 351

CCTAGTACACCGCAATC**ATG**TCTATTATGTCCTATAACGGAGGGGCCGTCATGGCCATGAAGGGGAAGAACTGTG
TGGCCATCGCTGCAGACAGGCGCTTCGGGATCCAGGCCCAGTTGGTGACCACGGACTTCCAGAAGATCTTTCCCA
TGGGTGACCGGCTGTACATCGGTCTGGCCGGGCTCGCCACTGACGTCCAGACAGTTGCCCAGCGCCTCAAGTTCC
GGCTGAACCTGTATGAGTTGAAGGAAGGTCGGCAGATCAAACCTTATACCCTCATGAGCATGGTGGCCAACCTCT
TGTATGAGAAACGGTTTGGCCCTTACTACACTGAGCCAGTCATTGCCGGGTTGGACCCGAAGACCTTTAAGCCCT
TCATTTGCTCTCTAGACCTCATCGGCTGCCCCATGGTGACTGATGACTTTGTGGTCAGTGGCACCTGCGCCGAAC
AAATGTACGGAATGTGTGAGTCCCTCTGGGAGCCCAACATGGATCCGGATCACCTGTTTGAAACCATCTCCCAAG
CCATGCTGAATGCTGTGGACCGGGATGCAGTGTCAGGCATGGGAGTCATTGTCCACATCATCGAGAAGGACAAAA
TCACCACCAGGACACTGAAGGCCCGAATGGAC**TAA**CCCTGTTCCCAGAGCCCACTTTTTTTTCTTTTTTTGAAAT
AAAATAGCCTGTCTTTC

FIGURE 352

MSIMSYNGGAVMAMKGKNCVAIAADRRFGIQAQLVTTDFQKIFPMGDRLYIGLAGLATDVQTVAQRLKFRLNLYE
LKEGRQIKPYTLMSMVANLLYEKRFGPYYTEPVIAGLDPKTFKPFICSLDLIGCPMVTDDFVVSGTCAEQMYGMC
ESLWEPNMDPDHLFETISQAMLNAVDRDAVSGMGVIVHIIEKDKITTRTLKARMD

FIGURE 353

GAAAGTCAGTGAGCAAATCGCGGACCACCGGGGCTGCCAGCTCGCCTGACTCCCGGCCTCTTGCGCTCCTAGGGG
CGGAGAAGGGTGCGGGCTCTTCGCCCTTTGTGTCCTCCTTCTTTCACTAACTTCTGGACTTTCCAGCTCTTCCGA
AGTTCGTTCTTGCGCAAAGCCCAAAGGCTGGAAAACCGTCCACG**ATG**ACCAGCATGACTCAGTCTCTGCGGGAGG
TGATAAAGGCCATGACCAAGGCTCGCAATTTTGAGAGAGTTTTGGGAAAGATTACTCTTGTCTCTGCTGCTCCTG
GGAAAGTGATTTGTGAAATGAAAGTAGAAGAAGAGCATACCAATGCAATAGGCACTCTCCACGGCGGTTTGACAG
CCACGTTAGTAGATAACATATCAACAATGGCTCTGCTATGCACGGAAAGGGGAGCACCCGGAGTCAGTGTCGATA
TGAACATAACGTACATGTCACCTGCAAAATTAGGAGAAGATATAGTGATTACAGCACATGTTCTGAAGCAAGGAA
AAACACTTGCATTTACCTCTGTGGATCTGACCAACAAGGCCACAGGAAAATTAATAGCACAAGGAAGACACACAA
AACACCTGGGAAAC**TGA**GAGAACAGCAGAATGACCTAAAGAAACCCAACAATGAATATCAAGTATAGATTTGACT
CAAACAATTGTAATTTTTGAAATAAACTAGCAAAACCAGAAAAAAAAAAAAAAAAAAA

FIGURE 354

MTSMTQSLREVIKAMTKARNFERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVDNISTMALLCT
ERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQGKTLAFTSVDLTNKATGKLIAQGRHTKHLGN

FIGURE 355A

TTCCGGCGGGGGAGGCGCCGGGAAGTCGATGGCGCCGGCGGCTCCTGCAGGAGGCCACTGTCTGCAGCTCCCGTG
AAG**ATG**TCCACTCCAGACCCACCCCTGGGCGGAACTCCTCGGCCAGGTCCTTCCCCGGGCCCTGGCCCTTCCCCT
GGAGCCATGCTGGGCCCTAGCCCGGGTCCCTCGCCGGGCTCCGCCCACAGCATGATGGGGCCCAGCCCAGGGCCG
CCCTCAGCAGGACACCCCATCCCCACCCAGGGGCCTGGAGGGTACCCTCAGGACAACATGCACCAGATGCACAAG
CCCATGGAGTCCATGCATGAGAAGGGCATGTCGGACGACCCGCGCTACAACCAGATGAAAGGAATGGGGATGCGG
TCAGGGGGCCATGCTGGGATGGGGCCCCCGCCCAGCCCCATGGACCAGCACTCCCAAGGTTACCCCTCGCCCCTG
GGTGGCTCTGAGCATGCCTCTAGTCCAGTTCCAGCCAGTGGCCCGTCTTCGGGGCCCCAGATGTCTTCCGGGCCA
GGAGGTGCCCCGCTGGATGGTGCTGACCCCCAGGCCTTGGGGCAGCAGAACCGGGGCCCAACCCCATTTAACCAG
AACCAGCTGCACCAGCTCAGAGCTCAGATCATGGCCTACAAGATGCTGGCCAGGGGGCAGCCCCTCCCCGACCAC
CTGCAGATGGCGGTGCAGGGCAAGCGGCCGATGCCCGGGATGCAGCAGCAGATGCCAACGCTACCTCCACCCTCG
GTGTCCGCAACAGGACCCGGCCCTGGCCCTGGCCCTGGCCCCGGCCCGGGTCCCGGCCCGGCACCTCCAAATTAC
AGCAGGCCTCATGGTATGGGAGGGCCCAACATGCCTCCCCCAGGACCCTCGGGCGTGCCCCCCGGGATGCCAGGC
CAGCCTCCTGGAGGGCCTCCCAAGCCCTGGCCTGAAGGACCCATGGCGAATGCTGCTGCCCCCACGAGCACCCCT
CAGAAGCTGATTCCCCCGCAGCCAACGGGCCGCCCTTCCCCCGCGCCCCCTGCCGTCCCACCCGCCGCCTCGCCC
GTGATGCCACCGCAGACCCAGTCCCCCGGGCAGCCGGCCCAGCCCGCGCCCATGGTGCCACTGCACCAGAAGCAG
AGCCGCATCACCCCCATCCAGAAGCCGCGGGGCCTCGACCCTGTGGAGATCCTGCAGGAGCGCGAGTACAGGCTG
CAGGCTCGCATCGCACACCGAATTCAGGAACTTGAAAACCTTCCCGGGTCCCTGGCCGGGGATTTGCGAACCAAA
GCGACCATTGAGCTCAAGGCCCTCAGGCTGCTGAACTTCCAGAGGCAGCTGCGCCAGGAGGTGGTGGTGTGCATG
CGGAGGGACACAGCGCTGGAGACAGCCCTCAATGCTAAGGCCTACAAGCGCAGCAAGCGCCAGTCCCTGCGCGAG
GCCCGCATCACTGAGAAGCTGGAGAAGCAGCAGAAGATCGAGCAGGAGCGCAAGCGCCGGCAGAAGCACCAGGAA
TACCTCAATAGCATTCTCCAGCATGCCAAGGATTTCAAGGAATATCACAGATCCGTCACAGGCAAAATCCAGAAG
CTGACCAAGGCAGTGGCCACGTACCATGCCAACACGGAGCGGGAGCAGAAGAAAGAGAACGAGCGGATCGAGAAG
GAGCGCATGCGGAGGCTCATGGCTGAAGATGAGGAGGGGTACCGCAAGCTCATCGACCAGAAGAAGGACAAGCGC
CTGGCCTACCTCTTGCAGCAGACAGACGAGTACGTGGCTAACCTCACGGAGCTGGTGCCGCAGCACAAGGCTGCC
CAGGTCGCCAAGGAGAAAAAGAAGAAAAAGAAAAAGAAGAAGGCAGAAAATGCAGAAGGACAGACGCCTGCCATT
GGGCCGGATGGCGAGCCTCTAGACGAGACCAGCCAGATGAGCGACCTCCCGGTGAAGGTGATCCACGTGGAGAGT
GGGAAGATCCTCACAGGCACAGATGCCCCCAAAGCCGGGCAGCTGGAGGCCTGGCTCGAGATGAACCCGGGGTAT
GAAGTAGCTCCGAGGTCTGATAGTGAAGAAAGTGGCTCAGAAGAAGAGGAAGAGGAGGAGGAGGAAGAGCAGCCG
CAGGCAGCACAGCCTCCCACCCTGCCCGTGGAGGAGAAGAAGAAGATTCCAGATCCAGACAGCGATGACGTCTCT
GAGGTGGACGCGCGGCACATCATTGAGAATGCCAAGCAAGATGTCGATGATGAATATGGCGTGTCCCAGGCCCTT
GCACGTGGCCTGCAGTCCTACTATGCCGTGGCCCATGCTGTCACTGAGAGAGTGGACAAGCAGTCAGCGCTTATG
GTCAATGGTGTCCTCAAACAGTACCAGATCAAAGGTTTGGAGTGGCTGGTGTCCCTGTACAACAACAACCTGAAC
GGCATCCTGGCCGACGAGATGGGCCTGGGGAAGACCATCCAGACCATCGCGCTCATCACGTACCTCATGGAGCAC
AAACGCATCAATGGGCCCTTCCTCATCATCGTGCCTCTCTCAACGCTGTCCAACTGGGCGTACGAGTTTGACAAG
TGGGCCCCCTCCGTGGTGAAGGTGTCTTACAAGGGATCCCCAGCAGCAAGACGGGCCTTTGTCCCCCAGCTCCGG
AGTGGGAAGTTCAACGTCTTGCTGACGACGTACGAGTACATCATCAAAGACAAGCACATCCTCGCCAAGATCCGT
TGGAAGTACATGATTGTGGACGAAGGTCACCGCATGAAGAACCACCACTGCAAGCTGACGCAGGTGCTCAACACG
CACTATGTGGCACCCCGCCGCCTGCTGCTGACGGGCACACCGCTGCAGAACAAGCTTCCCGAGCTCTGGGCGCTG
CTCAACTTCCTGCTGCCCACCATCTTCAAGAGCTGCAGCACCTTCGAGCAGTGGTTTAACGCACCCTTTGCCATG
ACCGGGGAAAAGGTGGACCTGAATGAGGAGGAAACCATTCTCATCATCCGGCGTCTCCACAAAGTGCTGCGGCCC
TTCTTGCTCCGACGACTCAAGAAGGAAGTCGAGGCCCAGTTGCCCGAAAAGGTGGAGTACGTCATCAAGTGCGAC
ATGTCTGCGCTGCAGCGAGTGCTCTACCGCCACATGCAGGCCAAGGGCGTGCTGCTGACTGATGGCTCCGAGAAG
GACAAGAAGGGCAAAGGCGGCACCAAGACCCTGATGAACACCATCATGCAGCTGCGGAAGATCTGCAACCACCCC
TACATGTTCCAGCACATCGAGGAGTCCTTTTCCGAGCACTTGGGGTTCACTGGCGGCATTGTCCAAGGGCTGGAC
CTGTACCGAGCCTCGGGTAAATTTGAGCTTCTTGATAGAATTCTTCCCAAACTCCGAGCAACCAACCACAAAGTG
CTGCTGTTCTGCCAAATGACCTCCCTCATGACCATCATGGAAGATTACTTTGCGTATCGCGGCTTTAAATACCTC
AGGCTTGATGGAACCACGAAGGCGGAGGACCGGGGCATGCTGCTGAAAACCTTCAACGAGCCCGGCTCTGAGTAC
TTCATCTTCCTGCTCAGCACCCGGGCTGGGGGGCTCGGCCTGAACCTCCAGTCGGCAGACACTGTGATCATTTTT

FIGURE 355B

GACAGCGACTGGAATCCTCACCAGGACCTGCAAGCGCAGGACCGAGCCCACCGCATCGGGCAGCAGAACGAGGTG
CGTGTGCTCCGCCTCTGCACCGTCAACAGCGTGGAGGAGAAGATCCTAGCTGCAGCCAAGTACAAGCTCAACGTG
GACCAGAAGGTGATCCAGGCCGGCATGTTCGACCAGAAGTCCTCCAGCCATGAGCGGCGCGCCTTCCTGCAGGCC
ATCCTGGAGCACGAGGAGCAGGATGAGAGCAGACACTGCAGCACGGGCAGCGGCAGTGCCAGCTTCGCCCACACT
GCCCCTCCGCCAGCGGGCGTCAACCCCGACTTGGAGGAGCCACCTCTAAAGGAGGAAGACGAGGTGCCCGACGAC
GAGACCGTCAACCAGATGATCGCCCGGCACGAGGAGGAGTTTGATCTGTTCATGCGCATGGACCTGGACCGCAGG
CGCGAGGAGGCCCGCAACCCCAAGCGGAAGCCGCGCCTCATGGAGGAGGACGAGCTCCCCTCGTGGATCATCAAG
GACGACGCGGAGGTGGAGCGGCTGACCTGTGAGGAGGAGGAGGAGAAGATGTTCGGCCGTGGCTCCCGCCACCGC
AAGGAGGTGGACTACAGCGACTCACTGACGGAGAAGCAGTGGCTCAAGGCCATCGAGGAGGGCACGCTGGAGGAG
ATCGAAGAGGAGGTCCGGCAGAAGAAATCATCACGGAAGCGCAAGCGAGACAGCGACGCCGGCTCCTCCACCCCG
ACCACCAGCACCCGCAGCCGCGACAAGGACGACGAGAGCAAGAAGCAGAAGAAGCGCGGGCGGCCGCCTGCCGAG
AAACTCTCCCCTAACCCACCCAACCTCACCAAGAAGATGAAGAAGATTGTGGATGCCGTGATCAAGTACAAGGAC
AGCAGCAGTGGACGTCAGCTCAGCGAGGTCTTCATCCAGCTGCCCTCGCGAAAGGAGCTGCCCGAGTACTACGAG
CTCATCCGCAAGCCCGTGGACTTCAAGAAGATAAAGGAGCGCATTCGCAACCACAAGTACCGCAGCCTCAACGAC
CTAGAGAAGGACGTCATGCTCCTGTGCCAGAACGCACAGACCTTCAACCTGGAGGGCTCCCTGATCTATGAAGAC
TCCATCGTCTTGCAGTCGGTCTTCACCAGCGTGCGGCAGAAAATCGAGAAGGAGGATGACAGTGAAGGCGAGGAG
AGTGAGGAGGAGGAAGAGGGCGAGGAGGAAGGCTCCGAATCCGAATCTCGGTCCGTCAAAGTGAAGATCAAGCTT
GGCCGGAAGGAGAAGGCACAGGACCGGCTGAAGGGCGGCCGGCGGCGGCCGAGCCGAGGGTCCCGAGCCAAGCCG
GTCGTGAGTGACGATGACAGTGAGGAGGAACAAGAGGAGGACCGCTCAGGAAGTGGCAGCGAAGAAGAC**TGA**GCC
CCGACATTCCAGTCTCGACCCCGAGCCCCTCGTTCCAGAGCTGAGATGGCATAGGCCTTAGCAGTAACGGGTAGC
AGCAGATGTAGTTTCAGACTTGGAGTAAAACTGTATAAACAAAAGAATCTTCCATATTTATACAGCAGAGAAGCT
GTAGGACTGTTTGTGACTGGCCCTGTCCTGGCATCAGTAGCATCTGTAACAGCATTAACTGTCTTAAAGAGA

FIGURE 356

MSTPDPPLGGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIPTQGPGGYPQDNMHQMHKP
MESMHEKGMSDDPRYNQMKGMGMRSGGHAGMGPPPSPMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPG
GAPLDGADPQALGQQNRGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQGKRPMPGMQQQMPTLPPPSV
SATGPGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGMPGQPPGGPPKPWPEGPMANAAAPTSTPQ
KLIPPQPTGRPSPAPPAVPPAASPVMPPQTQSPGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQ
ARIAHRIQELENLPGSLAGDLRTKATIELKALRLLNFQRQLRQEVVVCMRRDTALETALNAKAYKRSKRQSLREA
RITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVTGKIQKLTKAVATYHANTEREQKKENERIEKE
RMRRLMAEDEEGYRKLIDQKKDKRLAYLLQQTDEYVANLTELVPQHKAAQVAKEKKKKKKKKKAENAEGQTPAIG
PDGEPLDETSQMSDLPVKVIHVESGKILTGTDAPKAGQLEAWLEMNPGYEVAPRSDSEESGSEEEEEEEEEEQPQ
AAQPPTLPVEEKKKIPDPDSDDVSEVDARHIIENAKQDVDDEYGVSQALARGLQSYYAVAHAVTERVDKQSALMV
NGVLKQYQIKGLEWLVSLYNNNLNGILADEMGLGKTIQTIALITYLMEHKRINGPFLIIVPLSTLSNWAYEFDKW
APSVVKVSYKGSPAARRAFVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLNTH
YVAPRRLLLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEKVDLNEEETILIIRRLHKVLRPF
LLRRLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQAKGVLLTDGSEKDKKGKGGTKTLMNTIMQLRKICNHPY
MFQHIEESFSEHLGFTGGIVQGLDLYRASGKFELLDRILPKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLR
LDGTTKAEDRGMLLKTFNEPGSEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDLQAQDRAHRIGQQNEVR
VLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAFLQAILEHEEQDESRHCSTGSGSASFAHTA
PPPAGVNPDLEEPPLKEEDEVPDDETVNQMIARHEEEFDLFMRMDLDRRREEARNPKRKPRLMEEDELPSWIIKD
DAEVERLTCEEEEEKMFGRGSRHRKEVDYSDSLTEKQWLKAIEEGTLEEIEEEVRQKKSSRKRKRDSDAGSSTPT
TSTRSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIVDAVIKYKDSSSGRQLSEVFIQLPSRKELPEYYEL
IRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNAQTFNLEGSLIYEDSIVLQSVFTSVRQKIEKEDDSEGEES
EEEEEGEEEGSESESRSVKVKIKLGRKEKAQDRLKGGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSGSEED

FIGURE 357

AGCAACGGGGTGCGGCAGGGTGGGGAACGCGGGAGCGGGGCCAGCTCCCAGGAAAGCTGGTCTGCGAGCGGCCCC
TGCCCGGCTCCCAGGTCCCTGCGCGACCCCGCCCTTCCCGAGACCCCAGCCGGGCTGCCGCCCGCGTCCCGGAAG
CTCCAGCCTGAACC**ATG**TTTTTCACTTGTGGCCCAAATGAGGCCATGGTGGTCTCCGGGTTCTGCCGAAGCCCCC
CAGTCATGGTGGCTGGAGGGCGTGTCTTTGTCCTGCCCTGCATCCAACAGATCCAGAGGATCTCTCTCAACACAC
TGACCCTCAATGTCAAGAGTGAAAAGGTTTACACTCGCCATGGGGTCCCCATCTCAGTCACTGGCATTGCCCAGG
TAAAAATCCAGGGGCAGAACAAGGAGATGTTGGCGGCCGCCTGTCAGATGTTCCTGGGGAAGACGGAGGCTGAGA
TTGCCCACATTGCCCTGGAGACGTTAGAGGGCCACCAGAGGGCCATCATGGCCCACATGACTGTGGAGGAGATCT
ATAAGGACAGGCAGAAATTCTCAGAACAGGTTTTCAAAGTGGCCTCCTCAGACCTGGTCAACATGGGCATCAGTG
TGGTTAGCTACACTCTGAAGGACATTCACGATGACCAGGACTATTTGCACTCTTTGGGGAAGGCTCGAACAGCTC
AAGTCCAAAAAGATGCACGGATTGGAGAAGCAGAGGCCAAGAGAGATGCTGGGATCCGGGAAGCTAAAGCCAAGC
AGGAAAAGGTGTCTGCTCAGTACCTGAGTGAGATCGAGATGGCCAAGGCACAGAGAGATTACGAACTGAAGAAGG
CCGCCTATGACATCGAGGTCAACACCCGCCGAGCACAGGCTGACCTGGCCTATCAGCTTCAGGTGGCCAAGACTA
AGCAGCAGATTGAGGAGCAGCGGGTGCAGGTGCAGGTGGTGGAGCGGGCCCAGCAGGTGGCAGTGCAGGAGCAGG
AGATCGCCCGGCGGGAGAAGGAGCTGGAGGCCCGGGTGCGGAAGCCAGCGGAAGCGGAGCGCTACAAGCTGGAGC
GCCTAGCCGAGGCAGAGAAGTCCCAACTAATTATGCAGGCGGAGGCAGAAGCCGCGTCTGTGCGGATGCGTGGGG
AAGCTGAGGCCTTTGCCATAGGGGCCCGAGCCCGAGCCGAGGCTGAGCAGATGGCCAAGAAGGCAGAAGCCTTCC
AGCTGTACCAAGAGGCTGCTCAGCTGGACATGCTGCTAGAGAAGCTGCCCCAGGTGGCAGAGGAGATCAGTGGTC
CCTTGACTTCAGCCAATAAGATCACACTGGTGTCCAGCGGCAGTGGGACCATGGGGGCAGCCAAAGTGACTGGGG
AAGTACTGGACATTCTAACTCGCCTGCCAGAGAGTGTGGAAAGACTCACAGGCGTGAGCATCTCCCAGGTGAATC
ACAAGCCTTTGAGAACAGCC**TGA**GCCTTCAGCCCTCACAGATGCCCAGCCTCATAGCTGAAGTTGCCTGAATGAT
CCTCCTGTTGCATGTAACCCACTGGCCTCCCTGAGCATGTCCATTGACAGTGAGGTCCCACCCCTCATCTCTCCT
TGCCAAATAGTTTGTGCCTTGTCTTGAAGGGGGTTGCTCCCCTTGCCAACCTCACACTGCTATGATTGCCAACTC
CAGCGGTCCCATGTCAGCCTTCTGATGATCCCACTCCACCCCACCTCAACTTATTTAACTTCCTAATTAAATCAG
ACTGTTTGAGCCTGTTGTCTAGAATATTTTCCTGACCAAGACTGAGGGATGGGCTGGAGGTTTTCAACTTTGCTA
CCCAAATAAATTGCTGTAAGTAAGTACTAAAAAAAAAAA

FIGURE 358

MFFTCGPNEAMVVSGFCRSPPVMVAGGRVFVLPCIQQIQRISLNTLTLNVKSEKVYTRHGVPISVTGIAQVKIQG
QNKEMLAAACQMFLGKTEAEIAHIALETLEGHQRAIMAHMTVEEIYKDRQKFSEQVFKVASSDLVNMGISVVSYT
LKDIHDDQDYLHSLGKARTAQVQKDARIGEAEAKRDAGIREAKAKQEKVSAQYLSEIEMAKAQRDYELKKAAYDI
EVNTRRAQADLAYQLQVAKTKQQIEEQRVQVQVVERAQQVAVQEQEIARREKELEARVRKPAEAERYKLERLAEA
EKSQLIMQAEAEAASVRMRGEAEAFAIGARARAEAEQMAKKAEAFQLYQEAAQLDMLLEKLPQVAEEISGPLTSA
NKITLVSSGSGTMGAAKVTGEVLDILTRLPESVERLTGVSISQVNHKPLRTA

FIGURE 359

GACAGCCTCCGCCACATCCTCCACCTCTCTTGGTCCAGCGAGCGTTGCCGGGCCAGGGTCAAGCGGAGGGCTCCG
ACGGCGCGGACGGAGCGAAGCGCCGAGCC**ATG**GCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAAT
TCTTTGCCAAGGCACGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGTG
CCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTGCTGGACGCCCAGCAGC
CCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGCTTCGAATGGCTCTTCCTCGCCTGGTCGCCTG
ATAACTCCCCCGTGCGGCTGAAGATGCTGTACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCC
ACATCAAGGATGAGCTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCGTCCT
GTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAACGAGGTGAAGACAGAGA
TCAGTGTGGAAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTCCCCCTGCAGCCTGAGGCCCAGCGGGCACTCC
AGCAGCTCAAGCAGAAAATGGTCAACTACATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGC
ACACAGAGCCCACGGATGTGGCCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTCT
ACAAGCACACCCATGAGGGCGACCCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCGGGGTACAAGTGCAGCA
TCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTCGACTCCGTGGAGCAGGACTTCCATCTGGAGA
TCGCCAAGAAAATTGAGATTGGCGATGGGGCAGAGCTGACGGCAGAGTTCCTCTACGACGAGGTGCACCCCAAGC
AACACGCCTTCAAGCAGGCCTTCGCCAAGCCCAAGGGCCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGCG
GCCCGGGTGAAAATGGGGATGACAGC**TAG**GAGGCTGGAGCAGGGCCGGCCACGTGTGGACTGTGGGGCTGCCCAC
CTTCCGCTCCCTGCCACCATCCTCCTTCCTGGGCTCCAGGAAAGTGTTTCTGGGAGGTCAGGAGGGCTGGCAGCT
GAACGCACTTGCAGCGTCCGAGGGCCACCGGGCTGGCATTTTGTGACCCTTCCCTGTTGCTGTCCCTGCATCTCG
TCTGTGTGCCCAGGGTGTCCGGGGACCCTGCCTGGCTGGCTTAAGGGGGCTGGGTCAGGGGCCTGGCATGAACCT
GGCCTCCCGGGGAGCTGAGACTAGGGTCCCAGCACAGCCCAGAAACCTTTGGCCACAAGAAGTGGGGTCAGTCAG
GGCTGGGGCAGGGGTCACTGCAGTTTGGGATGGTTGAATGCTGTATTTCTAAAGAATAAAATATTTTTAAATC

FIGURE 360

MAHQTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPLLDAQQPCYLLYRLDS
QNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDELFGTVKDDLSFAGYQKHLSSCAAPAPLTSA
ERELQQIRINEVKTEISVESKHQTLQGLAFPLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQL
PSRVPRDAARYHFFLYKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFKQAFAKPKGPGGKRGHKRLIRGPGENGDDS

FIGURE 361

GGAATTTGGAAGCCCTCAAATCCCATTCCTAATCTGATGAGTCTATGGACCAATTTGTGGAGGACAGTATATTAA
ATAGATCTGATTTTTGCCATCAATGTAAGGAGGATAAAAACTTGCATACCAATTGTACACCCTTGCAAAATCTTT
CTCTGATGTTGGAGAAAATGGGCCAGTGAGATCATGGATATAGAAGTACAGTCAATGTTCAGCTGTACCCTCCCA
CAATCCCACTTCCTTCCTCAACACAATTCAAACAAATAGACTCAGACTGTTTCAGGCTCCAGGACAGGAAGTGCA
GTGTAGGCAAAATTGCAAAAATTGAGGGCACAGGGGTGGAGATGGGGGGGTTGAATAACAAGCTGTGCTAAATAA
TTACGTGTAAATATATTTTTTCATTTTTAAAAATTGATTTCTTTTGCACATTCCATGACAATATATGTCACATTT
TTAAAATAAATGCAAAGAAGCATACATCCAAGCCACTGAGCTCATTTGTCTTCTGTTTTGATAAAGTGGTAAAGA
AGGAACTAACATGGGAATGCATTGCTACAATTTAAATAAGCATACCAAGATAAATTCATTTATGGTGCTTTGAGT
AT**ATG**AGACCCTCTTCTACCAGACAGATGATCAGTGTTAGATTTATAGAGAAGGGATTATCAAATTCCCATGGCC
AAGAAGGTCAGAGA

FIGURE 362

MRPSSTRQMISVRFIEKGLSNSHGQEGQ

FIGURE 363

GGGGGAATACTTCCAAGTTGTAGTGTTGTTGTTTTCAGCCTGCTGCTGCTGCTGCTGTTGCGGCTAGGGGAACCG
TCGTGGGGAAGG**ATG**GTGTGCGAAAAATGTGAAAAGAAACTTGGTACTGTTATCACTCCAGATACATGGAAAGAT
GGTGCTAGGAATACCACAGAAAGTGGTGGAAGAAAGCTGAATGAAAATAAAGCTTTGACTTCAAAAAAAGCAAGA
TTTGATCCATATGGAAAGAATAAGTTCTCCACTTGTAGAATTTGTAAAAGTTCTGTGCACCAACCAGGTTCTCAT
TACTGCCAGGGCTGTGCCTACAAAAAAGGCATCTGTGCGATGTGTGGAAAAAAGGTTTTGGATACCAAAAACTAC
AAGCAAACATCTGTC**TAG**ATGTATTGATGGAATTTCTGGCTTTCTAAATGATTTTACTTTCTGCCTTGAATTTTC
AAGGCATAGATGTCAACTTACAGAATAACATGTTTTAAGATAATTAAGTTTAAACCAGAGATTGATGTTACTCAT
TTGCTCTCATGTTCTAACAGCACAGTGTACTAGTCTTTGTGGTAAATGGTTATTTTCCTTATAAGAATTTTAAGA
ACTAAGTGGCAAATTCCATGAAAATATTTCTCAGTTCTGTATGCACTTTTATTTAACATTATTCATATAATTCTC
CCCCCACCACTTTATTTATAGATACTGCCCAAGTGAGAAGGAGATAATAGATACTTTGCTCTGAATTTGGCATCC
AGAGTAACATTTCTCCCCTCACTCCCTTGCTGGTGTCATAGTTATTAGAATCAGCAGCCTCTTAACTAATTGCGG
TTTCATGGATATATAAATGTTTCAAGCCATTATTGCTGAATGGTTCTTTAGTTATTAACCTAGACCCAATTCAAA
GACCAGTTGGATTTATGATATTTTTTATTTGTTCTTGCAGCCAAAGTGCCAGTTTCTTTAATATGTGACCAAGAA
CACAAGGAGCATCCATATGGCCAAATAAATACATGAATTTTAGAAAAAACATATTACTTTGAATTCAAATTGTCA
TGAAAACCAGAACAGTGTTTGTCCTTGTTGCATGTAATGAAAATAAATCCATGCTATGAGAAAAGCTCTTTGAAG
CTAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 364

MVCEKCEKKLGTVITPDTWKDGARNTTESGGRKLNENKALTSKKARFDPYGKNKFSTCRICKSSVHQPGSHYCQG
CAYKKGICAMCGKKVLDTKNYKQTSV

FIGURE 365

AGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTCGGGAGCCACTGGGGCCAAAGTGAGAGTCCAGC
GGTCTTCCAGCGCTTGGGCCACGGCGGCGGCCCTGGGAGCAGAGGTGGAGCGACCCCATTACGCTAAAG**ATG**AAA
GGCTGGGGTTGGCTGGCCCTGCTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCAC
TGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCATTCAG
ATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCAC
CTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACCCATCGC
AAGAACTACGTACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCA
GATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTT
TCCCGAGAGGCTGACAATGTTAAAGACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATA
TCGCATGATGAGCTA**TGA**ACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTG
GCAATGCCTTTTATATATTATGTTTTTACTGAAATTAACTGAAAAAATATGAAACCAAAAGTAC

FIGURE 366

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGSQSVVEVPYARSE
AHLTELLEEICDRMKEYGEQIDPSTHRKNYVRVVGRNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIE
FFSREADNVKDKLCSKRTDLCDHALHISHDEL

FIGURE 367

TCCGGTCTTGTCCACGCTAGGGGGTGCACGTACTCCCAACTGTGGTCGCGCTCTCACCCCTTCTGCTGCTCTCGT
GGCCCCCTCGCG**ATG**GCGGGCATCCTGTTTGAGGATATTTTCGATGTGAAGGATATTGACCCGGAGGGCAAGAAG
TTTGACCGAGTGTCTCGACTGCATTGTGAGAGTGAATCTTTCAAGATGGATCTAATCTTAGATGTAAACATTCAA
ATTTACCCTGTAGACTTGGGTGACAAGTTCCGGTTGGTCATAGCTAGTACCTTGTATGAAGATGGTACCCTGGAT
GATGGTGAATACAACCCCACTGATGATAGGCCTTCCAGGGCTGACCAGTTTGAGTATGTAATGTATGGAAAAGTG
TACAGGATTGAGGGAGATGAAACTTCTACTGAAGCAGCAACACGCCTCTCTGCGTACGTGTCCTATGGGGGCCTG
CTCATGAGGCTGCAGGGGGATGCCAACAACCTGCATGGATTCGAGGTGGACTCCAGAGTTTATCTCCTGATGAAG
AAGCTAGCCTTC**TGA**ACCTCGCCTGAAGCCAGCCTCTCTGCCAAGTCACTCAGGTCATGGGCATTGTTCAAGCCT
GAGTGGCAGCCGCTCTTGCTCACCTGTTGAGGAAGGGCTGGCTCACTGTCCACCGTGGCGGCATCTTTAACTGGC
CTCCACTCAATGGGAAACTGACTCGCCTGTGAAAGACACAGTGGGAGAGCTGAAAATGAATCAGAAGCTTTATGT
ATATGATTTTTAAATTAAACTTTACTTTTTCAGACTGCCCCTCCCCTTTTTGTAAAAAGTCCATTTACTGT

FIGURE 368

MAGILFEDIFDVKDIDPEGKKFDRVSRLHCESESFKMDLILDVNIQIYPVDLGDKFRLVIASTLYEDGTLDDGEY
NPTDDRPSRADQFEYVMYGKVYRIEGDETSTEAATRLSAYVSYGGLLMRLQGDANNLHGFEVDSRVYLLMKKLAF

FIGURE 369

GAGGCAGTTCTGTTGCCACTCTCTCTCCTGTCA**ATG**ATGGATCTCAGAAATACCCCAGCCAAATCTCTGGACAAG
TTCATTGAAGACTATCTCTTGCCAGACACGTGTTTCCGCATGCAAATCGACCATGCCATTGACATCATCTGTGGG
TTCCTGAAGGAAAGGTGCTTCCGAGGTAGCTCCTACCCTGTGTGTGTGTCCAAGGTGGTAAAGGGTGGCTCCTCA
GGCAAGGGCACCACCCTCAGAGGCCGATCTGACGCTGACCTGGTTGTCTTCCTCAGTCCTCTCACCACTTTTCAG
GATCAGTTAAATCGCCGGGGAGAGTTCATCCAGGAAATTAGGAGACAGCTGGAAGCCTGTCAAAGAGAGAGAGCA
CTTTCCGTGAAGTTTGAGGTCCAGGCTCCACGCTGGGGCAACCCCCGTGCGCTCAGCTTCGTACTGAGTTCGCTC
CAGCTCGGGGAGGGGGTGGAGTTCGATGTGCTGCCTGCCTTTGATGCCCTGGGTCAGTTGACTGGCAGCTATAAA
CCTAACCCCCAAATCTATGTCAAGCTCATCGAGGAGTGCACCGACCTGCAGAAAGAGGGCGAGTTCTCCACCTGC
TTCACAGAACTACAGAGAGACTTCCTGAAGCAGCGCCCCACCAAGCTCAAGAGCCTCATCCGCCTAGTCAAGCAC
TGGTACCAAAATTGTAAGAAGAAGCTTGGGAAGCTGCCACCTCAGTATGCCCTGGAGCTCCTGACGGTCTATGCT
TGGGAGCGAGGGAGCATGAAAACACATTTCAACACAGCCCAAGGATTTCGGACGGTCTTGGAATTAGTCATAAAC
TACCAGCAACTCTGCATCTACTGGACAAAGTATTATGACTTTAAAAACCCCATTATTGAAAAGTACCTGAGAAGG
CAGCTCACGAAACCCAGGCCTGTGATCCTGGACCCGGCGGACCCTACAGGAAACTTGGGTGGTGGAGACCCAAAG
GGTTGGAGGCAGCTGGCACAAGAGGCTGAGGCCTGGCTGAATTACCCATGCTTTAAGAATTGGGATGGGTCCCCA
GTGAGCTCCTGGATTCTGCTGGCTGAAAGCAACAGTACAGACGATGAGACCGACGATCCCAGGACGTATCAGAAA
TATGGTTACATTGGAACACATGAGTACCCTCATTTCTCTCATAGACCCAGCACGCTCCAGGCAGCATCCACCCCA
CAGGCAGAAGAGGACTGGACCTGCACCATCCTC**TGA**ATGCCAGTGCATCTTGGGGGAAAGGGCTCCAGTGTTATC
TGGACCAGTTCCTTCATTTTCAGGTGGGACTCTTGATCCAGAGAAGACAAAGCTCCTCAGTGAGCTGGTGTATAA
TCCAAGACAGAACCCAAGTCTCCTGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATTCTCCACA
GCCTCACTTCATTCCACCTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGAGAATGAAA
TTCCAGCCTTGACTTTCTTCTGTGCACCTGATGGGAGGGTAATGTCTAATGTATTATCAATAACAATAAAAATAA
AGCAAATACCAAAAA

FIGURE 370

MMDLRNTPAKSLDKFIEDYLLPDTCFRMQIDHAIDIICGFLKERCFRGSSYPVCVSKVVKGGSSGKGTTLRGRSD
ADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEACQRERALSVKFEVQAPRWGNPRALSFVLSSLQLGEGVEFDVL
PAFDALGQLTGSYKPNPQIYVKLIEECTDLQKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGK
LPPQYALELLTVYAWERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYYDFKNPIIEKYLRRQLTKPRPVILD
PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCFKNWDGSPVSSWILLAESNSTDDETDDPRTYQKYGYIGTHEYPH
FSHRPSTLQAASTPQAEEDWTCTIL

FIGURE 371

ATGGGGGACGCTCCCAGCCCTGAAGAGAAACTGCACCTTATCACCCGGAACCTGCAGGAGGTTCTGGGGGAAGAG
AAGCTGAAGGAGATACTGAAGGAGCGGGAACTTAAAATTTACTGGGGAACGGCAACCACGGGCAAACCACATGTG
GCTTACTTTGTGCCCATGTCAAAGATTGCAGACTTCTTAAAGGCAGGGTGTGAGGTAACAATTCTGTTTGCGGAC
CTCCACGCATACCTGGATAACATGAAAGCCCCATGGGAACTTCTAGAACTCCGAGTCAGTTACTATGAGAATGTG
ATCAAAGCAATGCTGGAGAGCATTGGTGTGCCCTTGGAGAAGCTCAAGTTCATCAAAGGCACTGATTACCAGCTC
AGCAAAGAGTACACACTAGATGTGTACAGACTCTCCTCCGTGGTCACACAGCACGATTCCAAGAAGGCTGGAGCT
GAGGTGGTAAAGCAGGTGGAGCACCCTTTGCTGAGTGGCCTCTTATACCCCGGACTGCAGGCTTTGGATGAAGAG
TATTTAAAAGTAGATGCCCAATTTGGAGGCATTGATCAGAGAAAGATTTTCACCTTTGCAGAGAAGTACCTCCCT
GCACTTGGCTATTCAAAACGGGTCCATCTGATGAATCCTATGGTTCCAGGATTAACAGGCAGCAAAATGAGCTCT
TCAGAAGAGGAGTCCAAGATTGATCTCCTTGATCGGAAGGAGGATGTGAAGAAAAAACTGAAGAAGGCCTTCTGT
GAGCCAGGAAATGTGGAGAACAATGGGGTTCTGTCCTTCATCAAGCATGTCCTTTTTCCCCTTAAGTCCGAGTTT
GTGATCCTACGAGATGAGAAATGGGGTGGAAACAAAACCTACACAGCTTACGTGGACCTGGAAAAGGACTTTGCT
GCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG
GAAAAGTTTAATACCCCTGCCCTGAAAAAACTGGCCAGCGCTGCCTACCCAGATCCCTCAAAGCAGAAGCCAATG
GCCAAAGGCCCTGCCAAGAATTCAGAACCAGAGGAGGTCATCCCATCCCGGCTGGATATCCGTGTGGGGAAAATC
ATCACTGTGGAGAAGCACCCAGATGCAGACAGCCTGTATGTAGAGAAGATTGACGTGGGGGAAGCTGAACCACGG
ACTGTGGTGAGCGGCCTGGTACAGTTCGTGCCCAAGGAGGAACTGCAGGACAGGCTGGTAGTGGTGCTGTGCAAC
CTGAAACCCCAGAAGATGAGAGGAGTCGAGTCCCAAGGCATGCTTCTGTGTGCTTCTATAGAAGGGATAAACCGC
CAGGTTGAACCTCTGGACCCTCCGGCAGGCTCTGCTCCTGGTGAGCACGTGTTTGTGAAGGGCTATGAAAAGGGC
CAACCAGATGAGGAGCTCAAGCCCAAGAAGAAAGTCTTCGAGAAGTTGCAGGCTGACTTCAAAATTTCTGAGGAG
TGCATCGCACAGTGGAAGCAAACCAACTTCATGACCAAGCTGGGCTCCATTTCCTGTAAATCGCTGAAAGGGGGG
AACATTAGC**TAG**CCAGCCCAGCATCTTCCCCCCTTCTTCCACCACTGAGTCATCTGCTGTCTCTTCAGTCTGCTC
CATCCATCACCCATTTACCCATCTCTCAGGACA

FIGURE 372

MGDAPSPEEKLHLITRNLQEVLGEEKLKEILKERELKIYWGTATTGKPHVAYFVPMSKIADFLKAGCEVTILFAD
LHAYLDNMKAPWELLELRVSYYENVIKAMLESIGVPLEKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGA
EVVKQVEHPLLSGLLYPGLQALDEEYLKVDAQFGGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTGSKMSS
SEEESKIDLLDRKEDVKKKLKKAFCEPGNVENNGVLSFIKHVLFPLKSEFVILRDEKWGGNKTYTAYVDLEKDFA
AEVVHPGDLKNSVEVALNKLLDPIREKFNTPALKKLASAAYPDPSKQKPMAKGPAKNSEPEEVIPSRLDIRVGKI
ITVEKHPDADSLYVEKIDVGEAEPRTVVSGLVQFVPKEELQDRLVVVLCNLKPQKMRGVESQGMLLCASIEGINR
QVEPLDPPAGSAPGEHVFVKGYEKGQPDEELKPKKKVFEKLQADFKISEECIAQWKQTNFMTKLGSISCKSLKGG
NIS

FIGURE 373

GAGAGGCGCCCAGGCGGCGGCGGCGGCGGCCCAGCTTCTTCTTTCCTCGCACAGCCAGGCGGCCCCTGCTCGAGT
CCCGCGTCGCC**ATG**GCCGCGGTTCCCGAGTTGCTGCAGCAGCAGGAGGAGGACCGCAGCAAGCTGAGATCTGTAT
CTGTGGACCTGAATGTTGATCCCTCGCTTCAGATTGACATACCTGATGCGCTCAGTGAGAGAGACAAAGTCAAAT
TTACAGTGCACACAAAGACCACACTGCCCACGTTTCAGAGCCCAGAGTTTTCTGTTACAAGGCAACATGAAGACT
TTGTGTGGCTACATGACACTCTTATTGAAACAACAGACTATGCTGGGCTTATTATTCCACCTGCTCCTACGAAGC
CCGACTTTGATGGTCCTCGAGAGAAGATGCAGAAACTGGGAGAAGGTGAAGGGTCTATGACCAAAGAAGAATTTG
CCAAGATGAAACAAGAACTGGAAGCTGAGTATCTCGCTGTGTTTAAGAAGACTGTGTCCTCCCATGAAGTCTTTC
TTCAGCGGCTTTCTTCTCACCCTGTTCTCAGTAAAGATCGCAACTTTCATGTTTTCCTGGAATATGATCAGGATC
TAAGTGTTAGGCGGAAAAATACTAAAGAGATGTTTGGTGGCTTCTTCAAAAGTGTGGTGAAAAGTGCTGATGAAG
TCCTTTTTACTGGAGTTAAGGAGGTAGATGACTTCTTTGAGCAAGAGAAGAACTTCCTTATTAACTATTACAATA
GGATCAAAGATTCTTGTGTGAAAGCTGACAAAATGACCAGATCTCATAAAAATGTTGCCGATGACTATATCCACA
CCGCAGCCTGCTTACATAGCCTGGCTTTAGAAGAGCCCACAGTCATCAAAAAGTACCTATTGAAGGTTGCTGAGC
TATTTGAAAAACTAAGGAAAGTAGAGGGTCGAGTTTCATCAGATGAAGATTTGAAGCTAACAGAGCTCCTCCGAT
ACTACATGCTCAACATTGAAGCTGCTAAGGATCTCTTATACAGACGCACCAAAGCCCTCATTGACTATGAGAACT
CAAACAAAGCTCTGGATAAGGCCCGGTTAAAGAGCAAAGACGTCAAGTTGGCTGAGGCACACCAGCAGGAGTGCT
GCCAGAAATTTGAACAACTTTCCGAATCTGCAAAAGAAGAACTGATAAATTTCAAACGGAAGAGAGTGGCAGCAT
TTAGAAAGAATCTAATTGAAATGTCTGAACTGGAAATAAAACATGCCAGGAACAATGTCTCCCTTTTGCAGAGCT
GTATTGACTTGTTCAAGAATAAC**TGA**TATGCCTTCACTCAGAAGAAAAGAAATGAATGTGAAAGAAAGCCAAGCA
TCACTTGCACTTAAATCATTACCACGGAAGATATATTAGCTTCAACTTTAGTTTAAAATTATGTGAATAAATATT
TTGATTTCTACAAATCTTAACATTTAACCATGTTGGTTTAAAAATATTATTGCTTGCTACTTGGACATAACTAAT
TTTTCCTTGTGCATTTAATACCTCTGGGCAGAATCCAAATACTGGGTTCTCCCGTAGTTCGTCTTTAGTTACTAA
GAAAGGGTGTAGGACACATTAGCCTTCTGGAAACAAGTAGAAGCCATCACCTGGCCCATGTCCCTACAAACCCAT
GATTGTCAGGGAGGTGCCAGTTACAGCAGGTGATTCAGCTACTTGAGGTCGGTAACAGACCTTCCATTCCTCACT
GAAGGTGGGGTTTGTGTTTTTGTTTTGCCCTGTTACTCCACTGGTAGTCATCTGGTGTTTGTACTATAACAACAG
CAAGAAAATCTCATTTATCTTTATATACTCTTTGCACCTCCTTTTTTTAGTCGAGATATAAATATTTGAGGGGAG
AGAAATATCTACAGGTATATATGGAAACAAATAATGTGGTCTGCTTTATAAGATGGCCAGATCTACATTAGGAAA
AGTATAAGCCCCCTCCCTAATGGCCGCTGGGGGGTGAGGGCGGTGTGTTGTATGTCTTTGGGTGTTTGTTTTTTT
ATAAAGCATATAATAAAATAATCGTGCTACT

FIGURE 374

MAAVPELLQQQEEDRSKLRSVSVDLNVDPSLQIDIPDALSERDKVKFTVHTKTTLPTFQSPEFSVTRQHEDFVWL
HDTLIETTDYAGLIIPPAPTKPDFDGPREKMQKLGEGEGSMTKEEFAKMKQELEAEYLAVFKKTVSSHEVFLQRL
SSHPVLSKDRNFHVFLEYDQDLSVRRKNTKEMFGGFFKSVVKSADEVLFTGVKEVDDFFEQEKNFLINYYNRIKD
SCVKADKMTRSHKNVADDYIHTAACLHSLALEEPTVIKKYLLKVAELFEKLRKVEGRVSSDEDLKLTELLRYYML
NIEAAKDLLYRRTKALIDYENSNKALDKARLKSKDVKLAEAHQQECCQKFEQLSESAKEELINFKRKRVAAFRKN
LIEMSELEIKHARNNVSLLQSCIDLFKNN

FIGURE 375

CCGGACTGCGGAAGG**ATG**GAGCTGGCCGCCGGAAGCTTCTCGGAGGAGCAGTTCTGGGAGGCCTGCGCCGAGCTC
CAGCAGCCCGCTCTGGCCGGGGCCGACTGGCAGCTCCTAGTGGAGACCTCGGGCATCAGCATCTACCGGCTGCTG
GACAAGAAGACTGGACTTCATGAGTATAAAGTCTTTGGTGTTCTGGAGGACTGCTCACCAACTCTACTGGCAGAC
ATCTATATGGACTCAGATTACAGAAAACAATGGGACCAGTATGTTAAAGAACTCTATGAACAAGAATGCAACGGA
GAGACTGTGGTCTACTGGGAAGTGAAGTACCCTTTTCCCATGTCCAACAGAGACTATGTCTACCTTCGGCAGCGG
CGAGACCTGGACATGGAAGGGAGGAAGATCCATGTGATCCTGGCCCGGAGCACCTCCATGCCTCAGCTTGGCGAG
AGGTCTGGGGTGATCCGGGTGAAGCAATACAAGCAGAGCCTGGCGATTGAGAGTGACGGCAAGAAGGGGAGCAAA
GTTTTCATGTATTACTTCGATAACCCGGGTGGCCAAATTCCGTCCTGGCTCATTAACTGGGCCGCCAAGAATGGA
GTTCCTAACTTCTTGAAAGACATGGCAAGAGCCTGTCAGAACTACCTCAAGAAAACC**TAA**GAAAGAGAACTGGGA
ACATTGCATCCATGGGTTGATGTCTCTGGAAGTGCAACCACCCAATGTCTCTGGAAGTGCCACCTGGAAGTGCCA
CCTGGAAGTGTCTCTGGAAGAGCACCCACCACTGTTCAGCCTTCCCCTGCTGTTTCTGTCTTCAGAGGCCTACAC
ACTACCACATCCTTTCTAAGCATGTTTGCCTGACATCCAGCTCACTCGTCTGCTTCCTTTCTCGCTCCCCCCATC
CTGGGCTGGGCTGCCTTCTTCTACAGTTCAATATGGGGCAGACTAGGGAAACCTTTGCTTGCTTACTATTAGGAG
GGGAAGTCTTCAGTAGGGAACACGATCATTCCATTGTGCAATTTTACGGGGATGGGTGGGCGGAGGGACACAACA
AAATTTAAGAATGACTATTTGGGCGGGCTGGCTCTTTTGCAGCTTGTGATTTCTTCCAGCTTGGGAGGGGCTGCT
GGAAGTGGCATTTCGTTCAGAGCTGACTTTCAGTGCACCCAAACTGGATGACGTGCCAATGTCCATTTGCCTTAT
GCTTTGTGGAGCTGATTAGGCTGGGATTTGAGGTGATAATCCAGTAAGTCTTTCCTCGTTCCTACTTGTGGAGGA
TCAGTAGCTGTTATGATGCCAGACCATTTGGAGAAGTATCAGAGGCCTGACCGGACACATAATACGACAACCACA
TTTTTCCTCATCATCCATGAGGAAATGGATGATTTCTCTTTTCCATATGTCACTGGGGGAAAGGCTGCCTGTACC
TCTCAAGCTTTGCATTTTACTGGAAACTGAGGCGTCAAGATGGCTGTGGCAGCTAGCAAAAGCAAAGATGCTTTG
TGCATAGCCTTGTGAAAAAGTATCTTTCTATGCAATAAGATGAATTTTCCTCCCAGAATATTTAGAAATGTAGAA
GGGATAACAGTTCACAGCCAGGTAAAATTTAACTGGTGGCTTAATGACTCTGCACCTTTTTCTCAGGAATTCTGC
CTAAGTTGTCTGCCTTTTCTACCACCAAAAAGACTTTTAGTTTTCTATGCTTTCTCCTGAATTTTGGTAGGGTAA
GTATTTCTATGTCAAAGGCACAGCCTTGATGATCTCAGGGAAAAATTTTAATCACTGTGTATAATGATACTGAAC
CTTGATTAATAACAGAAATTCAGGATGTAAAGCCACAGAATGGGATTTATTAATGTGGGATACCTCAGACTGTTT
GTTTTCTTTCTGGGAAGAAAAGTGTGTTCTATAATGAATAAATATAGAGTGGTTTTT

FIGURE 376

MELAAGSFSEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLHEYKVFGVLEDCSPTLLADIYMDS
DYRKQWDQYVKELYEQECNGETVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSMPQLGERSGVI
RVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIPSWLINWAAKNGVPNFLKDMARACQNYLKKT

FIGURE 377

GCTGGTGGTGGCGCGCGGCGCGGCGCGGCG**ATG**GCGGCGGGTGGCAGCGATCCGCGGGCTGGCGACGTAGAGGAG
GACGCCTCACAGCTCATCTTTCCTAAAGAGTTTGAAACAGCTGAGACACTTCTAAATTCAGAAGTTCATATGCTT
CTGGAACATCGAAAGCAGCAGAATGAGAGTGCAGAGGACGAACAGGAGCTCTCAGAAGTCTTCATGAAAACATTA
AACTACACAGCCCGTTTCAGTCGTTTCAAAAACAGAGAGACCATTGCCAGTGTTCGTAGCTTGCTACTCCAGAAA
AAGCTTCATAAGTTTGAGTTGGCCTGTTTGGCCAACCTTTGCCCAGAGACTGCTGAGGAGTCCAAGGCTCTAATC
CCAAGCTTGGAGGGACGGTTTGAAGATGAGGAGCTGCAGCAGATTCTTGATGATATCCAGACAAAGCGCAGCTTT
CAGTAT**TAA**TCTCCAAACATCACTGCTGCTCGGAGAAACCACATCCCCAGGCATAACACCACCTTCCCACTGTCT
GGGGCTGACTTGCACAGAAATTCTGTTGAAGACAGTTGAGAATTCCTTTGGAGAAAACAGCCCAGCTTGGCGTGG
GGTTAGGTTGCTGTTTCAAATAACTCACAGGCCCAGGTGACATGGAATCTTGGAGCAGCCTTGTGCAGTGGCAGC
CAGTGGCTTCCTGAACGTGCCTCTGCGAAGTGTGAGATGAGGGGTCACATAACCACACTGTTGACTACCTCATTC
CTGGTTTTTGGCCTCCACATCATCTTTTTTCTTAATATTTCATGTTTTAATTTCAGGGTGTTTATACTTTTTGAA
ACTAGACCAGAAGATAGTAGACTTTATAGAGAAAGACCAGTTTTACCTAGATACTAAAGGAAGAATTAAACCGCT
GTTAGTTTGAAATGCTTTTTTTTTTTTTTTTTAAATGGAGATAGGGTCTTAACTCTTGTCCAGGCTGGAGGAGTG
CAGTCGTACAGTCATGGCTCACTGAAGTCTTGACCCCGCTGCCTCAGCCTCCCAAATAACTGGGGCCACAGGTGT
GCACCACAACTCTCAGCTAATTTTTAAAATTTTTATAGAGGTGGGGTTTTACTATGCTGTCCAGACTGGTCTTA
AACTCCTGGGCTCAAGTGATCCCCCTGCCTTGGCCTCCCAAACTGGTGAGATTACAGGCATGAGCCACCACAACT
GGCCTGAAATTCTTAAAGGATGGGAGTGTCGATGACAGCACCTTGGCATCGTTGTGCCTAACCTGGGAGACGGAA
GAAGCACGCCATGGGAAGTGTTTACACTTGGGGGACAAGTGCTAAGTATTGTGGAGCCCATAGCCCCTTGAGATA
GATGGCTACTTTGCCTTTCTTCTTGAACTGTCTTGCAGAATGTGGATTTGGGGTAAGTGGTCTTGAAGGATTCAT
TTAGTCACCCTCAAATTAAGATTTTTACTTCATCTTTCTTGGGCCTGCACCTCCAAGATAACAAAGAAGAAGCAA
TGGTCGTGCCAAAGAGGTCCACAACCAGGTGTGCACTGTTCACTGCAGCCCATTTGCTGTATGAACTGTGGTTGT
TGTGTGCCCAATGACAAGGCTACTAAGAAATTCATCATTTGAAACGTAGAGGCCGCAGCAGTCAGCGATGTTTCT
GAAATGAGCATCCTTGACGCCTGTGTACTTCCCAGGCTGGATGTGAAGCTACATTACCATGTGAGTTGTGCCATT
CACAGCACAGTGGTGAGGAATTGAGCTCATGAAGCAGGCAAGGACCGAACACCTCCACCCCAACGTAGACCTGCA
GGTGCTGCCCCATGACCTCCACCAAAGCCCATATAAGGAGCGGAGTTGTTAAGGACTGAAGAAAAACTTCTCTGG
AGAAAAATAAAATTGCAATTCTACTTAAAAAAAA

FIGURE 378

MAAGGSDPRAGDVEEDASQLIFPKEFETAETLLNSEVHMLLEHRKQQNESAEDEQELSEVFMKTLNYTARFSRFK
NRETIASVRSLLLQKKLHKFELACLANLCPETAEESKALIPSLEGRFEDEELQQILDDIQTKRSFQY

FIGURE 379

GTCCTGAGCAGCCAACACACCAGCCCAGACAGCTGCAAGTCACC**ATG**GACGCTGAAGGCCTGGCGCTGCTGCTGC
CGCCCGTCACCCTGGCAGCCCTGGTGGACAGCTGGCTCCGAGAGGACTGCCCAGGGCTCAACTACGCAGCCTTGG
TCAGCGGGGCAGGCCCCTCGCAGGCGGCGCTGTGGGCCAAATCCCCTGGGGTACTGGCAGGGCAGCCTTTCTTCG
ATGCCATATTTACCCAACTCAACTGCCAAGTCTCCTGGTTCCTCCCCGAGGGATCGAAGCTGGTGCCGGTGGCCA
GAGTGGCCGAGGTCCGGGGCCCTGCCCACTGCCTGCTGCTGGGGGAACGGGTGGCCCTCAACACGCTGGCCCGCT
GCAGTGGCATTGCCAGTGCTGCCGCCGCTGCAGTGGAGGCCGCCAGGGGGGCCGGCTGGACTGGGCACGTGGCAG
GCACGAGGAAGACCACGCCAGGCTTCCGGCTGGTGGAGAAGTATGGGCTCCTGGTGGGCGGGGCCGCCTCGCACC
GCTACGACCTGGGAGGGCTGGTGATGTTGAAGGATAACCATGTGGTGCCCCCCGGTGGCGTGGAGAAGGCGGTGC
GGGCGGCCAGACAGGCGGCTGACTTCGCTCTGAAGGTGGAAGTGGAATGCAGCAGCCTGCAGGAGGTCGTCCAGG
CAGCTGAGGCTGGCGCCGACCTTGTCCTGCTGGACAACTTCAAGCCAGAGGAGCTGCACCCCACGGCCACCGCGC
TGAAGGCCCAGTTCCCGAGTGTGGCTGTGGAAGCCAGTGGGGGCATCACCCTGGACAACCTCCCCCAGTTCTGCG
GGCCGCACATAGACGTCATCTCCATGGGGATGCTGACCCAGGCGGTCCCAGCCCTTGATTTCTCCCTCAAGCTGT
TTGCCAAAGAGGTGGCTCCAGTGCCCAAAATCCAC**TAG**TCCTAAACCGGAAGAGGATGACACCGGCCATGGGTTA
ACGTGGCTCCTCAGGACCCTCTGGGTCACACATCTTTAGGGTCAGTGAACAATGGGGCACATTTGGCACTAGCTT
GAGCCCAACTCTGGCTCTGCCACCTGCTGCTCCTGTGACCTGTCAGGGCTGACTTCACCTCTGCTCATCTCAGTT
TCCTAATCTGTAAAATGGGTCTAATAAAGGATCAACCAAAAAAAAAAAAAAAAAAA

FIGURE 380

MDAEGLALLLPPVTLAALVDSWLREDCPGLNYAALVSGAGPSQAALWAKSPGVLAGQPFFDAIFTQLNCQVSWFL
PEGSKLVPVARVAEVRGPAHCLLLGERVALNTLARCSGIASAAAAAVEAARGAGWTGHVAGTRKTTPGFRLVEKY
GLLVGGAASHRYDLGGLVMLKDNHVVPPGGVEKAVRAARQAADFALKVEVECSSLQEVVQAAEAGADLVLLDNFK
PEELHPTATALKAQFPSVAVEASGGITLDNLPQFCGPHIDVISMGMLTQAVPALDFSLKLFAKEVAPVPKIH

FIGURE 381

TAACGGTCTAAGGTAGCGAGATGATGCGAGGGGAAAACCCGAGCAGTGTGCCAAGAGGAGGAAATAGGCCAATGT
GGTCTGGGACGGTTGGATATACTTAAACATCTTAATAATCAGAGTAATTTTCATTTACAAAGAGAGGTCGGTACT
TAAAATAACCCTGAAAAATAACACTGGAATTCCTTTTCTAGCATTATATTTATTCCTGATTTGCCTTTGCCATAT
AATCTAATGCTTGTTTATATAGTGTCTGGTATTGTTTAACAGTTCTGTCTTTTCTATTTAAATGCCACTAAATTT
TAAATTCATACCTTTCCATGATTCAAAATTCAAAAGATCCCATGGGAGATGGTTGGAAAATCTCCACTTCATCCT
CCAAGCCATTCAAGTTTCCTTTCCAGAAGCAACTGCTACTGCCTTTCATTCATATGTTCTTCTAAAGATAGTCTA
CATTTGGAAATGTATGTTAAAAGCACGTATTTTTAAAATTTTTTTCCTAAATAGTAACACATTGTATGTCTGCTG
TGTACTTTGCTATTTTTATTTATTTTAGTGTTTCTTATATAGCAGATGGAATGAATTTGAAGTTCCCAGGGCTGA
GGATCCATGCCTTCTTTGTTTCTAAGTTATCTTTCCCATAGCTTTTCATTATCTTTCATATGATCCAGTATATGT
TAAATATGTCCTACATATACATTTAGACAACCACCATTTGTTAAGTATTTGCTCTAGGACAGAGTTTGGATTTGT
TTATGTTTGCTCAAAAGGAGACCCATGGGCTCTCCAGGGTGCACTGAGTCAATCTAGTCCTAAAAAGCAATCTTA
TTATTAACTCTGTATGACAGAATCATGTCTGGAACTTTTGTTTTCTGCTTTCTGTCAAGTATAAACTTCACTTTG
ATGCTGTACTTGCAAAATCACATTTTCTTTCTGGAAATTCCGGCAGTGTACCTTGACTGCTAGCTACCCTGTGCC
AGAAAAGCCTCATTCGTTGTGCTTGAACCCTTGAATGCCACCAGCTGTCATCACTACACAGCCCTCCTAAGAGGC
TTCCTGGAGGTTTCGAGATTCAGATGCCCTGGGAGATCCCAGAGTTTCCTTTCCCTCTTGGCCATATTCTGGTGT
CAATGACAAGGAGTACCTTGGCTTTGCCACATGTCAAGGCTGAAGAAACAGTGTCTCCAACAGAGCTCCTTGTGT
TATCTGTTTGTACATGTGCATTTGTACAGTAATTGGTGTGACAGTGTTCTTTGTGTGAATTACAGGCAAGAATTG
TGGCTGAGCAAGGCACATAGTCTACTCAGTCTATTCCTAAGTCCTAACTCCTCCTTGTGGTGTTGGATTTGTAAG
GCACTTTATCCCTTTTGTCTCATGTTTCATCGTAAATGGCATAGGCAGAGATGATACCTAATTCTGCATTTGATT
GTCACTTTTTGTACCTGCATTAATTTAATAAAATATTCTTATTTATTTTGTTACTTGGTACACCAGCATGTCCAT
TTTCTTGTTTATTTTGTGTTTAATAAA**ATG**TTCAGTTTAACATCCCAGTGGAGAAAGTTAAAAAA

FIGURE 382

MFSLTSQWRKL

FIGURE 383

CCCAAATATATATTTAATCTTGTGGTTCAAATAAGCTTTTGGCTCACATCTAAGCACATCATAAAGAACGCTGTA
GAAGAGGTGACATG**ATG**AGGCGGGAAGACGAGGAAGAGGAGGGAACAATGATGAAGGCAAAAGGGGACTTAGAGA
TGAAGGAGGAGGAAGAGATTAGTGAGACAGGAGAACTGGTTGGCCCTTTTGTGAGTGCTATGCCCACTCCAATGC
CCCACAACAAGGGCACCCGGTTCTCTGAGGCATGGGAATATTTCCACCTAGCTCCTGCTCGTGCTGGGCACCATC
CCAACCAGTATGCCACCTGCCGCCTGTGTGGCAGGCAGGTGAGCCGTGGCCCTGGGGTCAACGTGGGCACCACTG
CACTGTGGAAGCATCTGAAAAGCATGCACAGAGAGGAGCTGGAGAAGAGTGGCCATGGTCAGGCTGGGCAGCGCC
AGGATCCAAGGCCCCACGGGCCCCAGCTCCCCACAGGCATTGAGGGTAACTGGGGTAGGCTCCTGGAGCAGGTGG
GCACCATGGCTTTGTGGGCCAGCCAAAGGGAAAAGGAGGTGCTTAGGAGGGAAAGGGCAGTGGAATGGCGGGAGA
GGGCTGTGGAAAAAAGGGAGCGAGCCCTGGAGGAGGTGGAAAGGGCCATCCTGGAGATGAAGTGGAAGGTGAGGG
CTGAGAAGGAGGCATGCCAGCGGGAGAAAGAGCTGCCTGCAGCAGTACATCCCTTCCATTTTGTT**TAA**ATTGGGC
TTGGAGAATCTATTCTGAAAACATTGACTCTAGACTTGTAGAAAAGAGCCATTTTAGTTTCAACTCAAATGTAAA
GCAAAGTAGTTTGGTGACATTTTGCTTTTATGTGAAATAGTGCACAGTATGAGTTAATCTGAGCAGGTCTGAATT
GACCAAATGCTTATCTACGAGGTTCCTAGAGCTCTGCTGACCCTTGGCCGAAACTCTAAAATGTACCTATTAAAG
ATAAATGCTTCTACCAAAGTAAAACTCTGTGAGTTGTTTCAGGGCAGAATGTACCAGCCAGTCAGCGTTGTTTAA
CAAAATAATCAGATTTTTGCCTAGCACTCGGTTTTGGTGGAGCTGACGATTTTGAGGGCTGAGGCTGGTTAGGTA
GCTGGAATGTGCCTATGTGACCAGCTCACTTGCAGACACCCTGCCGGAAGCAGAGCTTAATCTTCCTAGGACTGA
GGTCTTAGCACATGTACTGGTGGAGTTTCCAGACCACCAGTATGAATAAAAGCTTGTTCTGTGTGACCCAGCAAG
TGGAAGGACAAAGAACTGTGAGCCTCAGATCTTTGGACCTTTCCAATGCGTCTCTTTCTCCTGTTATTGCTGCAA
TGTATTTTCTTGCTTATATTAAAGTTGTTTCATCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 384

MRREDEEEEGTMMKAKGDLEMKEEEEISETGELVGPFVSAMPTPMPHNKGTRFSEAWEYFHLAPARAGHHPNQYA
TCRLCGRQVSRGPGVNVGTTALWKHLKSMHREELEKSGHGQAGQRQDPRPHGPQLPTGIEGNWGRLLEQVGTMAL
WASQREKEVLRRERAVEWRERAVEKRERALEEVERAILEMKWKVRAEKEACQREKELPAAVHPFHFV

FIGURE 385

GGCCGGAGGGAGCCCGCGCTCGGGGCGGCGGCTGGAGGCAGCGCACCGAGTTCCCGCGAGGATCCATGACCTGAC
GGGGCCCCGGAGCCGCGCTGCCTCTCGGGTGTCCTGGGTCGGTGGGGAGCCCAGTGCTCGCAGGCCGGCGGGCGG
GCCGGAGGGCTGCAGTCTCCCTCGCGGTGAGAGGAAGGCGGAGGAGCGGGAACCGCGGCGGCGCTCGCGCGGCGC
CTGCGGGGGGAAGGGCAGTTCCGGGCCGGGCCGCGCCTCAGCAGGGCGGCGGCTCCCAGCGCAGTCTCAGGGCCC
GGGTGGCGGCGGCGACTGGAGAAATCAAGTTGTGCGGTCGGTGATGCCCGAGTGAGCGGGGGGCCTGGGCCTCTG
CCCTTAGGAGGCAACTCCCACGCAGGCCGCAAAGGGCTCTCGCGGCCGAGAGGCTTCGTTTCGGTTTCGCGGCGG
CGGCGGCGTTGTTGGCTGAGGGGACCCGGGACACCTGAATGCCCCCGGCCCCGGCTCCTCCGACGCG**ATG**GGGAA
GGTGCTATCCAAAATCTTCGGGAACAAGGAAATGCGGATCCTCATGTTGGGCCTGGACGCGGCCGGCAAGACAAC
AATCCTGTACAAGTTGAAGCTGGGCCAGTCGGTGACCACCATTCCCACTGTGGGTTTCAACGTGGAGACGGTGAC
TTACAAAAATGTCAAGTTCAACGTATGGGATGTGGGCGGCCAGGACAAGATCCGGCCGCTCTGGCGGCATTACTA
CACTGGGACCCAAGGTCTCATCTTCGTAGTGGACTGCGCCGACCGCGACCGCATCGATGAGGCTCGCCAGGAGCT
GCACCGCATTATCAATGACCGGGAGATGAGGGACGCCATAATCCTCATCTTCGCCAACAAGCAGGACCTGCCCGA
TGCCATGAAACCCCACGAGATCCAGGAGAAACTGGGCCTGACCCGGATTCGGGACAGGAACTGGTATGTGCAGCC
CTCCTGTGCCACCTCAGGGGACGGACTCTATGAGGGGCTCACATGGTTAACCTCTAACTACAAATCT**TAA**TGAGC
ATTCTCCACCCATCCCCTGGAAGGAGAGAAATCAAAAACCCATTCATAGGATTATCGCCACCATCACCTCTTTCA
ATTGCCACTTTCTCTTCTTTTGAATTTGAACTCTGGAGTTACTGTTCTACAGTTTGGCGGGGACGGGGCTTGGGG
GTTTTCTCTTTTGTTTGTTTCCCTTTCTTTTTCCTTTTTTTTTTTTTTTTTTTGTTGGCTTTGCGTTAGGATGGC
TCTGATCTGACATTTGACATGAACACAAAGTTGCCAAGATGCTCCTTGTTGACTTCCAGCAGAATGGGAATGGGG
GAAACACAGCAGTTCTTGGGTAAAAGTCCCTTTGTAATAATAGGTTTGGGATTTTTTTATTTCGAGAGAATCTTT
CATTTTCCTATGTATGCTTTTTTCCTTTTTTGCCCAGTTTCCTTATCACTTGCTGTAGATGGCTTATTTTGCATT
CATGCAGACTATGTTGCAAGTCTGTTTCATCTAGTAAACTGAAAATTATTGCTTAATCAAACTGCCGTTTGTCTT
TTATATTTAAGGCCTTCCCCCCCCTTCCTTATGAGTTCTAACTTAGTAATTTCAAATGTGACCTTTTATATCTAA
GACCAGTATAGTAAACTTAGCCCACAGTGGCAAATAATGAGTAATATTGTAATATGTTCCAGTTGCACCTCAGTA
TGTTAAACAGGTAATGTAAGAAGTTCTCTGAAATGTCAGCAAGTAAGTTCTGAAACACATCATGCATGAGTAGGA
ATAAAC

FIGURE 386

MGKVLSKIFGNKEMRILMLGLDAAGKTTILYKLKLGQSVTTIPTVGFNVETVTYKNVKFNVWDVGGQDKIRPLWR
HYYTGTQGLIFVVDCADRDRIDEARQELHRIINDREMRDAIILIFANKQDLPDAMKPHEIQEKLGLTRIRDRNWY
VQPSCATSGDGLYEGLTWLTSNYKS

FIGURE 387

CGGCAGTGCGCCTGCGCAAGTTACGCGAAAGCTAACAGAATCTGCGGTGCTCTGCTGGCGACTGGCAGGACGCGG
TGCAGAGAGCGGACTTCCGCGACGCGGGTCCTACAGTGTAGGGGAAGCAATGGAAGAACTTCTACCTGATGGACA
AATATGGGCTAATATGGATCCAGAAGAACGAATGTTGGCAGCTGCTACAGCTTTTACCCACATCTGTGCAGGGCA
GGGTGAAGGAGATGTCAGGAGAGAAGCCCAATCTATCCAATATGATCCCTACAGTAAAGCTTCAGTAGCCCCAGG
GAAGCGACCTGCTCTTCCTGTGCAACTACAGTACCCACATGTAGAAAGTAATGTCCCTTCAGAAACAGTCTCTGA
GGCCTCCCAAAGACTCCGAAAGCCAGTGATGAAGAGAAAGGTGCTGCGCAGAAAGCCAGATGGGGAAGTATTAGT
AACAGATGAGTCGATTATCAGTGAATCAGAATCTGGTACAGAAAATGATCAGGATCTCTGGGACTTAAGACAAAG
GCTGATGAATGTACAGTTCCAGGAAGACAAGGAATCTTCATTTGATGTTTCACAAAAATTTAACCTACCACATGA
ATACCAAGGAATTTCTCAAGATCAGCTCATTTGCTCTCTACAAAGAGAAGGAATGGGCTCTCCAGCTTACGAACA
AGACCTGATTGTTGCCAGCAGACCCAAGTCCTTTATTCTCCCAAAGCTGGACCAGTTAAGCCGAAACCGGGGCAA
GACAGACCGGGTAGCCCGGTATTTTGAGTACAAACGGGACTGGGACTCAATACGTTTACCTGGTGAAGATCATAG
AAAGGAATTACGCTGGGGTGTCCGAGAGCAGATGCTTTGTCGAGCAGAACCCCAATCCAAACCTCAGCATATATA
TGTCCCAAACAATTATCTAGTACCAACAGAGAAGAAAAGGTCTGCACTCCGTTGGGGTGTTCGTTGTGACCTTGC
AAATGGTGTCATACCCAGGAAGCTTCCCTTCCCTCTTTCTCCTTCT**TAA**ATCTTTTTAAACTTCTTTCACAGGAT
TGTTTGAGATAACCTAGCTCTTTATATCTTCCCTTTTAAATAGAAACAACTGTCTTGAGAAGCTCTTCGAAACAT
TTTATGGTAAGGACTTCACCTATCATTGGTCTTTCCTAGCTATATATCACATTGGTATCAGATGATACTTCCAAA
TTGCCACTCAAATCCAGCAATTGCAAGATAAATCATATCAGAGAAAGAACAACAGACCTGGTCTTTCTATTTTGT
CAAATTAGTAAGGGCCCTTTGTGTCCTGTAACTTTTTTTACCTATCAATATGAGTTGCTGTGCTTCAGTGTGTGT
TTTTTAAGTTGCTGGGCATTACACTTACCAATTAAAGAATTTTGGAAATTCAAAAAAA

FIGURE 388

GSAPAQVTRKLTESAVLCWRLAGRGAESGLPRRGSYSVGEAMEELLPDGQIWANMDPEERMLAAATAFTHICAGQ
GEGDVRREAQSIQYDPYSKASVAPGKRPALPVQLQYPHVESNVPSETVSEASQRLRKPVMKRKVLRRKPDGEVLV
TDESIISESESGTENDQDLWDLRQRLMNVQFQEDKESSFDVSQKFNLPHEYQGISQDQLICSLQREGMGSPAYEQ
DLIVASRPKSFILPKLDQLSRNRGKTDRVARYFEYKRDWDSIRLPGEDHRKELRWGVREQMLCRAEPQSKPQHIY
VPNNYLVPTEKKRSALRWGVRCDLANGVIPRKLPFPLSPS

FIGURE 389

TGGAAGACTTCGAGACCCATTTAGGATCACGGCGCTACGGATGACCTGAGAATTAATTTATGGCACTTAGAAATC
ACAGATAGAAGCTTTAACATCGTGGACATCAAGCCTGCTAAC**ATG**GAGGAGCTGACCGAAGTCATCACTGCAGCC
GAGTTCCACCCGCACCAGTGCAACGTGTTCGTCTACAGCAGTAGCAAAGGGACCATCCGCCTGTGTGACATGCGC
TCCTCGGCCCTGTGCGACAGACACTCCAAGTTTTTTGAAGAGCCTGAAGATCCCAGCAGTAGGTCCTTCTTCTCA
GAAATAATTTCATCCATATCCGATGTAAAATTCAGTCATAGTGGGCGGTACATGATGACCAGAGACTTACCTGTC
GGTGAAGGTGTGGGACCTCAACATGGGAGAGCAGGCCGGTGGAGACCCACCAGGTCCACGAGTACCTGCGCAGCA
AGCTCTGCTCTCTCTATGAGAACGACTGCATCTTTGACAAGTTTGAGTGTTGCTGGAACGGTTCGGATAGCGCCA
TCA**TGA**CCGGGTCCTATAACAACTTCTTCAGGATGTTTGATAGAGACACGCGGAGGGATGTGACCCTGGAGGCCT
CGAGAGAGAGCAGCAAACCGCGCGCCAGCCTCAAACCCCGGAAGGTGTGTACGGGGGGTAAGCGGAGGAAAGACG
AGATCAGTGTGGACAGTCTGGACTTCAACAAGAAGATCCTGCACACAGCCTGGCACCCCGTGGACAATGTCATTG
CCGTGGCTGCCACCAATAACTTGTACATATTCCAGGACAAAATCAACTAGAGACGCGAACGTGAGGACCAAGTCT
TGTCTTGCATAGTTAAGCCGGACATTTTTCTGTCAGAGAAAAGGCATCATTGTCCGCTCCATTAAGAACAGTGAC
GCACCTGCTACTTCCCTTCACAGACACAGGAGAAAGCCGCCTCCGCTGGAGGCCCGGTGTGGTTCCGCCTCGGCG
AGGCGCGAGACAGGCGCTGCTGCTCACGTGGAGACGCTCTCGAAGCAGAGTTGACGGACACTGCTCCCAAAAGGT
CATTACTCAGAATAAATGTATTTATTTCAAAAAA

FIGURE 390

MEELTEVITAAEFHPHQCNVFVYSSSKGTIRLCDMRSSALCDRHSKFFEEPEDPSSRSFFSEIISSISDVKFSHS
GRYMMTRDLPVGEGVGPQHGRAGRWRPTRSTSTCAASSALSMRTTASLTSLSVAGTVRIAPS

FIGURE 391

GCGCCGAGCGCCGCCGCCGCCGCCGCCGCCGCCGCTCCGCTGCCCGCGCCGCCCGCGGCTCCCG**ATG**GAGACTGA
CGCGCCCCAGCCCGGCCTCGCCTCCCCGGACTCGCCGCACGACCCCTGCAAGATGTTCATCGGGGGACTCAGTTG
GCAGACTACGCAGGAAGGGCTGCGCGAATACTTCGGCCAGTTCGGGGAGGTGAAGGAGTGTCTGGTGATGCGGGA
CCCCCTGACCAAGAGATCCAGGGGTTTCGGCTTCGTCACTTTCATGGACCAGGCGGGGGTGGATAAAGTGCTGGC
GCAATCGCGGCACGAGCTCGACTCCAAAACAATTGACCCTAAGGTGGCCTTCCCTCGGCGAGCACAGCCCAAGAT
GGTGACTCGAACGAAGAAGATCTTTGTGGGGGGGCTGTCGGTGAACACCACGGTGGAGGACGTGAAGCAATATTT
TGAGCAGTTTGGGAAGGTGGACGACGCCATGCTGATGTTTGACAAAACCACCAACCGGCACCGAGGGTTCGGGTT
TGTCACGTTTGAGAGTGAGGACATCGTGGAGAAAGTGTGTGAAATTCATTTTCATGAAATCAACAACAAAATGGT
GGAATGTAAGAAAGCTCAGCCAAAGGAGGTGATGTCGCCAACGGGCTCAGCCCGGGGGAGGTCTCGAGTCATGCC
CTACGGAATGGACGCCTTCATGCTGGGCATCGGCATGCTGGGTTACCCAGGTTTCCAAGCCACAACCTACGCCAG
CCGGAGTTATACAGGCCTCGCCCCTGGCTACACCTACCAGTTCCCCGAATTCCGTGTAGAGCGGACCCCTCTCCC
GAGCGCCCCAGTCCTCCCCGAGCTTACAGCCATTCCTCTCACTGCCTACGGACCAATGGCGGCGGCAGCGGCGGC
AGCGGCTGTGGTTCGAGGGACAGGCTCTCACCCCTGGACGATGGCTCCCCCTCCAGGTTCGACTCCCAGCCGCAC
AGGGGGCTTCCTGGGGACCACCAGCCCCGGCCCCATGGCCGAGCTCTACGGGGCGGCCAACCAGGACTCGGGGGT
CAGCAGTTACATCAGCGCCGCCAGCCCTGCCCCCAGCACCGGCTTCGGCCACAGTCTTGGGGGCCCTTTGATTGC
CACAGCCTTCACCAATGGGTACCAC**TGA**AGCAGGGGACGGTGGCAGGAGCGCCCCAGCCTGCAGCTGACTGAGGA
CCACGAGTGAGCCAGCGAGGGGGCGGGAGACCTCAGCCGCAGCCGCCGCCCCCTCCCCTGCAGCGACTCGGACCC
GCTACTGCCTGCCCCCAACTCCCCGGGCCCGGCCCCTGCCCTGCTGCCCCCAACAGCGTCTGGCTCCCCTACTAA
CGTCCCCCTCTTCGCCCTTGCCCCCATCCCCACCCGCCCCTCTCCCGGCCCTGCTTTTATTTATTTTGGATTAGC
CGGTTGCCCACCCCAGCCCTCTGGTCCATCCCTCCCTCCGTGCCGCGCCCCCCTAGGACCGCCCCCTCCCCAAAA
GGCTTTTGGATTTGTGCATAGCTGGAGTGAAGGCGGAGGGAGCCTGCTACAGGCCGCAGCCCAACCCCTGTTTTT
TATTCAGATTTCCCCTCCTTTACCCTTTCCCTTTTTTTTTTTTTTTTTTTTTTGTTTAAAGAAACCTTTTTTAAA
CTATTTCTAGGTTTGTGAATGTGAAGCCCCAGGCCGCAGGGGGCAAGGGGCCAGGTGCCCCCCACCAGCTGAGAA
CAAAGTGTCTATCTGGGTGTGGGCCCCTGGCCGCCTCCCTCCAGCCCTGGAGAGGAGGGCAGGGCTGCGGGGAGG
CCAGGCCGAGCCCCTGGAACCATCCCGTCCTGTATCATATGTAAATACTGTGAGGTGATGTGCCCACCCCTCTCT
AAGACCCCTCGGGGGTGAGGGGCTCCCCCCTCCCCTGTTTCTGTCCCCTCAGACACCGTTACTGT

FIGURE 392

METDAPQPGLASPDSPHDPCKMFIGGLSWQTTQEGLREYFGQFGEVKECLVMRDPLTKRSRGFGFVTFMDQAGVD
KVLAQSRHELDSKTIDPKVAFPRRAQPKMVTRTKKIFVGGLSVNTTVEDVKQYFEQFGKVDDAMLMFDKTTNRHR
GFGFVTFESEDIVEKVCEIHFHEINNKMVECKKAQPKEVMSPTGSARGRSRVMPYGMDAFMLGIGMLGYPGFQAT
TYASRSYTGLAPGYTYQFPEFRVERTPLPSAPVLPELTAIPLTAYGPMAAAAAAAAVVRGTGSHPWTMAPPPGST
PSRTGGFLGTTSPGPMAELYGAANQDSGVSSYISAASPAPSTGFGHSLGGPLIATAFTNGYH

FIGURE 393

CGCGTGAACTGCTTCCTGCAGGCTGGCC**ATG**GCGCTTCACGTTCCCAAGGCTCCGGGCTTTGCCCAGATGCTCAA
GGAGGGAGCGAAACACTTTTCAGGATTAGAAGAGGCTGTGTATAGAAACATACAAGCTTGCAAGGAGCTTGCCCA
AACCACTCGTACAGCATATGGACCAAAAGGAATGAACAAAATGGTTATCAACCACTTGGAGAAGTTGTTTGTGAC
AAACGATGCAGCAACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAAAATGATTGTAATGGCTTCTCA
TATGCAAGAGCAAGAAGTTGGAGATGGCACAAACTTTGTTCTGGTATTTGCTGGAGCTCTCCTGGAATTAGCTGA
AGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAATAGCCTGCAGAAAAGCTCATGA
GATTCTTCCTAATTTGGTATGTTGTTCTGCAAAAAACCTTCGAGATATTGATGAAGTCTCATCTCTACTTCGTAC
CTCCATAATGAGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGCTCAGGCATGCGTATCTATTTT
TCCTGATTCCGGCCATTTCAATGTTGATAACATCAGAGTTTGTAAAATTCTGGGCTCTGGTATCAGTTCCTCTTC
AGTATTGCATGGCATGGTTTTTAAGAAGGAAACCGAAGGTGATGTAACATCTGTCAAAGATGCAAAAATAGCAGT
GTACTCTTGTCCTTTTGATGGCATGATAACAGAAACTAAGGGAACAGTGTTGATAAAGACTGCTGAAGAATTGAT
GAATTTTAGTAAGGGAGAAGAAAACCTCATGGATGCACAAGTCAAAGCTATTGCTGATACTGGTGCAAATGTCGT
AGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAAATAAATATAATATCATGTTAGTGAGGCTAAA
CTCAAAATGGGATCTCCGAAGACTTTGTAAAACTGTTGGTGCTACAGCTCTTCCTAGATTGACACCTCCTGTCCT
TGAAGAAATGGGACACTGTGACAGTGTTTACCTCTCAGAAGTTGGAGATACTCAGGTGGTGGTTTTTAAGCATGA
AAAGGAAGATGGCGCCATTTCTACCATAGTACTTCGAGGCTCTACAGACAATCTGATGGATGACATAGAAAGGGT
AGTAGACGATGGTGTTAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTACCCGGAGGTGGAGCAACAGA
AATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCCTGGACTTGAACAGTATGCTATTAAGAAGTT
TGCTGAGGCATTTGAAGCTATTCCCCGCGCACTGGCAGAAAACTCTGGAGTTAAGGCCAATGAAGTAATCTCTAA
ACTTTATGCAGTACATCAAGAAGGAAATAAAAACGTTGGATTAGATATTGAGGCTGAAGTCCCTGCTGTAAAGGA
CATGCTGGAAGCTGGTATTCTAGATACTTACCTGGGAAAATATTGGGCTATCAAACTCGCTACTAATGCTGCAGT
CACTGTACTTAGAGTGGATCAGATCATCATGGCAAAACCAGCTGGTGGGCCCAAGCCTCCAAGTGGGAAGAAAGA
CTGGGATGATGACCAAAATGAT**TGA**AATTGGCTTAATTTTTACTGTAGGTGAAGGCTGTATTTGTAGTAGTACTC
AAGAATCACCTGATGTTTTCTTATTCTCCTTAAATTAAGAGTTATTTTGTGTTTGTATTCTTGGCTGGATGTTAT
AATAAACATATTGTTACTGTC

FIGURE 394

MALHVPKAPGFAQMLKEGAKHFSGLEEAVYRNIQACKELAQTTRTAYGPKGMNKMVINHLEKLFVTNDAATILRE
LEVQHPAAKMIVMASHMQEQEVGDGTNFVLVFAGALLELAEELLRIGLSVSEVIEGYEIACRKAHEILPNLVCCS
AKNLRDIDEVSSLLRTSIMSKQYGNEVFLAKLIAQACVSIFPDSGHFNVDNIRVCKILGSGISSSSVLHGMVFKK
ETEGDVTSVKDAKIAVYSCPFDGMITETKGTVLIKTAEELMNFSKGEENLMDAQVKAIADTGANVVVTGGKVADM
ALHYANKYNIMLVRLNSKWDLRRLCKTVGATALPRLTPPVLEEMGHCDSVYLSEVGDTQVVVFKHEKEDGAISTI
VLRGSTDNLMDDIERVVDDGVNTFKVLTRDKRLVPGGGATEIELAKQITSYGETCPGLEQYAIKKFAEAFEAIPR
ALAENSGVKANEVISKLYAVHQEGNKNVGLDIEAEVPAVKDMLEAGILDTYLGKYWAIKLATNAAVTVLRVDQII
MAKPAGGPKPPSGKKDWDDDQND

FIGURE 395

AGTCCTGCGATTTCGGTGTAGAGGAGCAGGGGCTGCGGGACCTGGTGTGGGTGGAGTGGGACAAGCGGTGGAGAA
GGGTACGCCAGGGTCGCTGAGAGACTCTGTTCTCCCTGGAGGGACTGGTTGCCATGAGAGCAGCCGTCTGAGGGG
ACGCAGCCTGCACTACGCGCCCCAAGAGGCTGTGCGTGGCGAGCAGGTCACGTGACGGGAGCGCGGGCTTTGGAA
GGCGGCTGAACGTCAGGCCACCCGCCGCTAAGCTGAGAAGGGAGAGCGAGCTTAGGACCGCCTGCCCGGGGCAAC
CCCGAACCAAGCTTTAGCCGCCGAGGCCGCGTGTCCCAAAGGCCAGTCATCCCTCCTCTGTGTTGCC**ATG**GGAAT
TCAAGGCCTGGCCAAACTAATTGCTGATGTGGCCCCCAGTGCCATCCGGGAGAATGACATCAAGAGCTACTTTGG
CCGTAAGGTGGCCATTGATGCCTCTATGAGCATTTATCAGTTCCTGATTGCTGTTCGCCAGGGTGGGGATGTGCT
GCAGAATGAGGAGGGTGAGACCACCAGCCACCTGATGGGCATGTTCTACCGCACCATTCGCATGATGGAGAACGG
CATCAAGCCCGTGTATGTCTTTGATGGCAAGCCGCCACAGCTCAAGTCAGGCGAGCTGGCCAAACGCAGTGAGCG
GCGGGCTGAGGCAGAGAAGCAGCTGCAGCAGGCTCAGGCTGCTGGGGCCGAGCAGGAGGTGGAAAAATTCACTAA
GCGGCTGGTGAAGGTCACTAAGCAGCACAATGATGAGTGCAAACATCTGCTGAGCCTCATGGGCATCCCTTATCT
TGATGCACCCAGTGAGGCAGAGGCCAGCTGTGCTGCCCTGGTGAAGGCTGGCAAAGTCTATGCTGCGGCTACCGA
GGACATGGACTGCCTCACCTTCGGCAGCCCTGTGCTAATGCGACACCTGACTGCCAGTGAAGCCAAAAAGCTGCC
AATCCAGGAATTCCACCTGAGCCGGATTCTGCAGGAGCTGGGCCTGAACCAGGAACAGTTTGTGGATCTGTGCAT
CCTGCTAGGCAGTGACTACTGTGAGAGTATCCGGGGTATTGGGCCCAAGCGGGCTGTGGACCTCATCCAGAAGCA
CAAGAGCATCGAGGAGATCGTGCGGCGACTTGACCCCAACAAGTACCCTGTGCCAGAAAATTGGCTCCACAAGGA
GGCTCACCAGCTCTTCTTGGAACCTGAGGTGCTGGACCCAGAGTCTGTGGAGCTGAAGTGGAGCGAGCCAAATGA
AGAAGAGCTGATCAAGTTCATGTGTGGTGAAAAGCAGTTCTCTGAGGAGCGAATCCGCAGTGGGGTCAAGAGGCT
GAGTAAGAGCCGCCAAGGCAGCACCCAGGGCCGCCTGGATGATTTCTTCAAGGTGACCGGCTCACTCTCTTCAGC
TAAGCGCAAGGAGCCAGAACCCAAGGGATCCACTAAGAAGAAGGCAAAGACTGGGGCAGCAGGGAAGTTTAAAAG
GGGAAAA**TAA**ATGTGTTTCCCCATTATACCTCCTTCACCCCAGAATATTTGCCGTCTTGTACCCTTAAGAGCTAC
AGCTAGAGAAACCTTCACGGGGTGGAGAGAGGATTCTAAGGCTTTTCTAGCGTGACCCTTTTCAGTAGTGCTAGT
CCCTTTTTTACTTGATCTTAATGGCAAGAAGGCCACAGAGGTACTTTTCCTTTTTTTAGCTCAGGAAAATATGTC
AGGCTCAAACCACTTCTCAGGCAGTTTAATGG

FIGURE 396

MGIQGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVRQGGDVLQNEEGETTSHLMGMFYRTIRMM
ENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEKQLQQAQAAGAEQEVEKFTKRLVKVTKQHNDECKHLLSLMGI
PYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQEFHLSRILQELGLNQEQFVD
LCILLGSDYCESIRGIGPKRAVDLIQKHKSIEEIVRRLDPNKYPVPENWLHKEAHQLFLEPEVLDPESVELKWSE
PNEEELIKFMCGEKQFSEERIRSGVKRLSKSRQGSTQGRLDDFFKVTGSLSSAKRKEPEPKGSTKKKAKTGAAGK
FKRGK

FIGURE 397

CCTAAG**ATG**AGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTTCTTCCAAAGGTGCAGTC
TCCAAAGAGATTACGAATGCCTTGGAAACCTGGGGTGCCTTGGGTCAGGACATCAACTTGGACATTCCTAGTTTT
CAAATGAGTGATGATATTGACGATATAAAATGGGAAAAAACTTCAGACAAGAAAAAGATTGCACAATTCAGAAAA
GAGAAAGAGACTTTCAAGGAAAAAGATACATATAAGCTATTTAAAAATGGAACTCTGAAAATTAAGCATCTGAAG
ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAAATGTGTTGGAAAAAATATTTGAT
TTGAAGATTCAAGAGAGGGTCTCAAAACCAAAGATCTCCTGGACTTGTATCAACACAACCCTGACCTGTGAGGTA
ATGAATGGAACTGACCCCGAATTAAACCTGTATCAAGATGGGAAACATCTAAAACTTTCTCAGAGGGTCATCACA
CACAAGTGGACCACCAGCCTGAGTGCAAAATTCAAGTGCACAGCAGGGAACAAAGTCAGCAAGGAATCCAGTGTC
GAGCCTGTCAGCTGTCCAGAGAAAGGTCTGGACATCTATCTCATCATTGGCATATGTGGAGGAGGCAGCCTCTTG
ATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACCAAAAGGAAAAAACAGAGGAGTCGGAGAAATGATGAGGAG
CTGGAGACAAGAGCCCACAGAGTAGCTACTGAAGAAAGGGGCCGGAAGCCCCAACAAATTCCAGCTTCAACCCCT
CAGAATCCAGCAACTTCCCAACATCCTCCTCCACCACCTGGTCATCGTTCCCAGGCACCTAGTCATCGTCCCCCG
CCTCCTGGACACCGTGTTCAGCACCAGCCTCAGAAGAGGCCTCCTGCTCCGTCGGGCACACAAGTTCACCAGCAG
AAAGGCCCGCCCCTCCCCAGACCTCGAGTTCAGCCAAAACCTCCCCATGGGGCAGCAGAAAACTCATTGTCCCCT
TCCTCTAAT**TAA**AAAAGATAGAAACTGTCTTTTTCAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCAT
ATCCGTACTTCCATGAGGTGTTTTCTGTGTGCAGAACATTGTCACCTCCTGAGGCTGTGGGCCACAGCCACCTCT
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTGGTCTCCTCAGAGAGCTCCATCACACCAGTAAG
GAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGCACAGAAATCTTAGAGATTTCTTGTCCCCTC
TCAGGTCATGTGTAGATGCGATAAATCAAGTGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAA
GAGACTCTGGAGTTTCTTATGTGCCCTGGTGGACACTTGCCCACCATCCTGTGAGTAAAAGTGAAATAAAAGCTT
TGAC

FIGURE 398

MSFPCKFVASFLLIFNVSSKGAVSKEITNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEK
ETFKEKDTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQERVSKPKISWTCINTTLTCEVMN
GTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGSLLMV
FVALLVFYITKRKKQRSRRNDEELETRAHRVATEERGRKPQQIPASTPQNPATSQHPPPPPGHRSQAPSHRPPPP
GHRVQHQPQKRPPAPSGTQVHQQKGPPLPRPRVQPKPPHGAAENSLSPSSN

FIGURE 399

CTGGTGTGAGCCACCACGCCCAGCTCAAAAACAATTTTTTAGGGGCACTTCTACAAATCATGAAAGGGGGATAA
AAGCACTGACTTTAAAAAGCCATGTT**TAA**GATGCTATAAATGTTCTCCCCTTTTCATTGATTGGAGAGTTGTAGA
GGACCTTAGAGATCATTTTGTCTAACTCCCTCATCCCAAAGATAAACTGAGGCCTAGAGATCGTTCAGGGTGTTG
TAACTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTTGTAACTGGGAACATCTGAATGCTGAGG
CCTAGAGATCGTTCAGGGTGTTGTAACTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTTGTAA
CTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTTGTAACTGGGAACATCTGAATGCTGAGGCCT
AGAGATCGTTCAGGGTGTTGTAACTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTTGTAACTG
GGAACATCTGAATGCTGAGGCTTAGTCCAGTGTTCTCTCTCCCTTACCACTCCTCTTCCCCTTCCCTCTATAATG
GCAGTACCCAGGGCCCGGTCCATAGACTACTATCGAGTGCTCCTATGTGCATCTTAGTACGTATCATTTTCCCTT
GCCTTTTTCCTTCTATCCTTTCAGTGGTAGCAACTGCCCTTGCTAATCACCGTAACCTCGGCTGAGAAAGAAGAG
GAAGCGAAATCCAAGATGCAGCTCAGTTCATCAAAGCCTAGCAGGTCCCCTCAGCTGCCTTTTCATGCCTGCCAC
AGACTACAGTAGGACAAAACCTGACCTGGTCTTTGAAGTTAAGAGCTAAGAAAGCTTCCTATAGTAGTATCTCCC
ATGGCACTTACCACATTCTATCTGGTATTACAATTATTTGTATGCAATTAATCACTCTTAGATTGTATGTTCCTG
GAGGGCAGAATATGCCCATTCATATTTGTATCTTCTTCCTTCTGCTCTTGGCACCTAACACAGTGCCTTGCACAC
AAACAATAAATGATTGTTGAGTGAATAAGTAAACCTGATTGTGGTGTTCTATTGCTTTTTCAGCAAGAAGTCAAA
CTGATGGCCTTTAAGTCAGAGAAGCAGCAATGGAGCAAC

FIGURE 400

GVSHHAQLKNNFFRGTSTNHERGIKALTLKSHV

FIGURE 401

GGCGGCGACGGATCGAGCTCACCGCGCCGAGCGCGCCGGCACCGCCTGCACCGCCCTTCCGCCCGCCCTCCGGAC
GGCCGCAGCCTGCGGTCTCCGTCCAGACCCACCCCCGCCCCACCCCGCGCGCCTCTGCCGCCTCTTCCAGAGACC
CAGCTTGCCGAGCGGCCGCCGCTGCCGTGTCGCCGCCGCCGCCGCCACCGCGCCAGGTTCCGGCCGCGGCCACCC
TCCGCCGTCCAGGGCCTCTCCGTCTCGGCCCCGGGACCCCGCCTCCCCGCCAGCCCCGGCCCCGGCCCCGGCACC
ATGTCGGAGAAAAGCGTGGAGGCAGCGGCCGAGTTGAGCGCCAAGGACCTGAAGGAGAAGAAGGAGAAGGTGGAG
GAGAAGGCAAGCCGGAAAGAGCGAAAGAAAGAAGTGGTGGAGGAGGAGGAGAACGGGGCTGAGGAGGAAGAAGAA
GAAACTGCCGAGGATGGAGAGGAGGAAGATGAAGGGGAAGAAGAAGATGAGGAAGAAGAAGAAGAGGATGATGAA
GGGCCCGCGCTGAAGAGAGCTGCCGAAGAGGAGGATGAAGCGGATCCCAAACGGCAGAAGACAGAAAATGGGGCA
TCGGCG**TGA**CGCCTGCCAACAGGCTGGGTTGGGAGGCCTCTCTGGGCTGGAGGTGGGGGTGGGGGCAGCCAAGTC
CAGCCACTCTTCACCTGGCTCCCTGCTCTGGGCCCTGCACCGAGAGCTGCCACCCTCTTCTTTCTCCCCAGCCTT
CTCATTTCCGCCTCTCCAGACACTGCGCCCTCCACCCTCACTCTGCCATTGTTCCACCTCCTGACCTGCTCCATC
TGAGCTCTCCAGCTGGCCCCCAATTGCTCCTCTCTCTCTTTGCTCTCTTTCTCCCTCCCCTACCAGCCTCATTCT
TCTCCGGTAGCCTCTCCCACCTAACCTCTGCATCCCCCAGCGTCATGTCCTGCCCCATCCCTATCCTGCCTGATC
CCTGGATCTCCCTCAGATCCCCTCTTCTCAGACAGCGCCAGGCCGGGGTGGGGCCGGGGTTGCCGAGCCCCACAG
CTGCCCCCCTCCCCTCCCTTTTTGTATAATTTAATAAAGAAATGGTCGCGCTTCTGTTT

FIGURE 402

MSEKSVEAAAELSAKDLKEKKEKVEEKASRKERKKEVVEEEENGAEEEEEETAEDGEEEDEGEEEDEEEEEEDDE
GPALKRAAEEEDEADPKRQKTENGASA

FIGURE 403

GGCACGAGGGGGAAGGCAAGATGGCGGCGCCCATGGAGGTGGCCGTGTGTACGGACTCGGCGGCCCCGATGTGGA
GCTGCATCGTGTGGGAACTTCACTCGGGCGCCAACCTGCTCACCTACCGCGGCGGCCAGGCGGGACCCCGCGGCC
TGGCGCTGCTCAATGGCGAGTATCTGCTGGCGGCGCAGCTGGGCAAGAACTACATCAGCGCCTGGGAGCTGCAGC
GGAAGGACCAGCTCCAGCAGAAGATCATGTGCCCCGGGCCTGTCACCTGTCTGACTGCATCACCCAATGGTCTCT
ACGTCCTGGCAGGAGTTGCAGAAAGCATCCACCTGTGGGAGGTCTCCACCGGGAACCTTCTGGTCATCCTGAGTC
GACACTACCAGGACGTCTCCTGCCTTCAGTTCACAGGGGACAGCAGCCACTTCATCTCAGGGGGCAAGGACTGCC
TGGTGCTGGTTTGGAGCCTCTGCAGCGTGCTGCAGGCCGACCCCTCCAGGATTCCGGCGCCCAGGCACGTCTGGT
CTCACCACACGCTCCCCATCACGGACCTGCACTGCGGCTTTGGGGGCCCCCTGGCCCGGGTGGCCACCTCCTCAC
TGGACCAGACGGTGAAGCTATGGGAGGTCTCCTCGGGGGAGCTGCTGCTCTCCGTCCTCTTTGACGTGTCCATCA
TGGCAGTGACCATGGACCTGGCTGAGCACCATATGTTCTGCGGGGGCAGTGAGGGCTCCATCTTCCAGGTCGACC
TCTTCACCTGGCCCGGACAGAGGGAGAGGAGCTTCCACCCAGAGCAGGACGCCGGGAAGGTCTTCAAAGGGCACA
GGAACCAGGTGACTTGCCTGTCAGTGTCCACTGACGGCAGCGTGCTGCTCTCAGGCTCCCACGACGAGACCGTGC
GCCTCTGGGACGTGCAGAGCAAGCAGTGCATCCGGACGGTGGCCCTCAAAGGCCCAGTCACCAATGCCGCCATCC
TGCTGGCGCCCGTCAGCATGCTGAGCTCAGACTTCAGGCCCAGCCTGCCGCTGCCCCACTTCAACAAGCACCTGC
TGGGCGCCGAGCACGGGGACGAGCCGCGCCACGGGGGCCTCACTCTGCGCCTGGGCCTCCACCAGCAGGGCTCGG
AGCCCAGCTACCTGGACCGCACGGAGCAGCTGCAGGCCGTCCTGTGCAGCACCATGGAGAAGAGCGTGCTCGGCG
GCCAGGACCAGCTGCGCGTCCGTGTGACGGAGCTGGAGGACGAGGTGCGCAACCTGCGCAAGATCAATCGGGACC
TGTTCGACTTCTCCACGCGCTTCATCACGCGGCCGGCCAAG**TGA**GGCCCGGAGACCCCGGCCCGAGGCGCCCAGG
CCTGAGCCCCATGCCTCCCAGCAACCAGGGCCCGCGGGTGTGGCCCCCACCAGCCCAGGCCTGGACTCTCCTCAG
TTCTGTGTCGTGTTCGGGTTTTTCCTCTGTGACTGGGCCGTCTTGGTGTCTCGTGGCACGCGTCACAGTGGTGCT
AGTCTGTTTTTAACAAAAGAGGATGAAAAGCCAAAAAAAAAAAAAAAAA

FIGURE 404

HEGEGKMAAPMEVAVCTDSAAPMWSCIVWELHSGANLLTYRGGQAGPRGLALLNGEYLLAAQLGKNYISAWELQR
KDQLQQKIMCPGPVTCLTASPNGLYVLAGVAESIHLWEVSTGNLLVILSRHYQDVSCLQFTGDSSHFISGGKDCL
VLVWSLCSVLQADPSRIPAPRHVWSHHTLPITDLHCGFGGPLARVATSSLDQTVKLWEVSSGELLLSVLFDVSIM
AVTMDLAEHHMFCGGSEGSIFQVDLFTWPGQRERSFHPEQDAGKVFKGHRNQVTCLSVSTDGSVLLSGSHDETVR
LWDVQSKQCIRTVALKGPVTNAAILLAPVSMLSSDFRPSLPLPHFNKHLLGAEHGDEPRHGGLTLRLGLHQQGSE
PSYLDRTEQLQAVLCSTMEKSVLGGQDQLRVRVTELEDEVRNLRKINRDLFDFSTRFITRPAK

FIGURE 405A

ATGCTGGGGAAGAGCCATGGTAGGACCACTCATGGCCCTCTTCCTTTGGCGGACCTTGGAATCCACCTTCCCTGC
GTTAAAGTGCTCCACCAGGTGACGCCGGAAGAGAAGCCAGCAGGCGGCGGCGGCGTCAGCATCAGCGGCCTCCTG
CCCGTATCTATCGTGGCGGCGACGGGACCCGCCTCCCTGGGCGCCGGAGTCATGTGACCCACACAATGGCTGAGT
GGCTACTCTCGGCTTCCTGGCAACGCCGAGCGAAAGCT**ATG**ACTGCGGCCGCGGGTTCGGCGGGCCGCGCCGCGG
TGCCCTTGCTGCTGTGTGCGCTGCTGGCGCCCGGCGGCGCGTACGTGCTCGACGACTCCGACGGGCTGGGCCGGG
AGTTCGACGGCATCGGCGCGGTCAGCGGCGGCGGGGCAACCTCCCGACTTCTAGTAAATTACCCAGAGCCCTATC
GTTCTCAGATATTGGATTATCTCTTTAAGCCGAATTTTGGTGCCTCTTTGCATATTTTAAAAGTGGAAATAGGTG
GTGATGGGCAGACAACAGACGGCACTGAGCCCTCCCACATGCATTATGCACTAGATGAGAATTATTTCCGAGGAT
ACGAGTGGTGGTTGATGAAAGAAGCTAAGAAGAGGAATCCCAATATTACACTCATTGGGTTGCCATGGTCATTCC
CTGGATGGCTGGGAAAAGGTTTCGACTGGCCTTATGTCAATCTTCAGCTGACTGCCTATTATGTCGTGACCTGGA
TTGTGGGCGCCAAGCGTTACCATGATTTGGACATTGATTATATTGGAATTTGGAATGAGAGGTCATATAATGCCA
ATTATATTAAGATATTAAGAAAAATGCTGAATTATCAAGGTCTCCAGCGAGTGAAAATCATAGCAAGTGATAATC
TCTGGGAGTCCATCTCTGCATCCATGCTCCTTGATGCCGAACTCTTCAAGGTGGTTGATGTTATAGGGGCTCATT
ATCCTGGAACCCATTCAGCAAAAGATGCAAAGTTGACTGGGAAGAAGCTTTGGTCTTCTGAAGACTTTAGCACTT
TAAATAGTGACATGGGTGCAGGCTGCTGGGGTCGCATTTTAAATCAGAATTATATCAATGGCTATATGACTTCCA
CAATCGCATGGAATTTAGTGGCTAGTTACTATGAACAGTTGCCTTATGGGAGATGCGGGTTGATGACGGCCCAAG
AGCCATGGAGTGGGCACTACGTGGTAGAATCTCCTGTCTGGGTATCAGCTCATACCACTCAGTTTACTCAACCTG
GCTGGTATTACCTGAAGACAGTTGGCCATTTAGAGAAAGGAGGAAGCTACGTAGCTCTGACTGATGGCTTAGGGA
ACCTCACCATCATCATTGAAACCATGAGTCATAAACATTCTAAGTGCATACGGCCATTTCTTCCTTATTTCAATG
TGTCACAACAATTTGCCACCTTTGTTCTTAAGGGATCTTTTAGTGAAATACCAGAGCTACAGGTATGGTATACCA
AACTTGGAAAAACATCCGAAAGATTTCTTTTTAAGCAGCTGGATTCTCTATGGCTCCTTGACAGCGATGGCAGTT
TCACACTGAGCCTGCATGAAGATGAGCTGTTCACACTCACCACTCTCACCACTGGTCGCAAAGGCAGCTACCCGC
TTCCTCCAAAATCCCAGCCCTTCCCAAGTACCTATAAGGATGATTTCAATGTTGATTACCCATTTTTTAGTGAAG
CTCCAAACTTTGCTGATCAAACTGGTGTATTTGAATATTTTACAAATATTGAAGACCCTGGCGAGCATCACTTCA
CGCTACGCCAAGTTCTCAACCAGAGACCCATTACGTGGGCTGCCGATGCATCCAACACAATCAGTATTATAGGAG
ACTACAACTGGACCAATCTGACTATAAAGTGTGATGTTTACATAGAGACCCCTGACACAGGAGGTGTGTTCATTG
CAGGAAGAGTAAATAAAGGTGGTATTTTGATTAGAAGTGCCAGAGGAATTTTCTTCTGGATTTTTGCAAATGGAT
CTTACAGGGTTACAGGTGATTTAGCTGGATGGATTATATATGCTTTAGGACGTGTTGAAGTTACAGCAAAAAAAT
GGTATACACTCACGTTAACTATTAAGGGTCATTTCGCCTCTGGCATGCTGAATGACAAGTCTCTGTGGACAGACA
TCCCTGTGAATTTTCCAAAGAATGGCTGGGCTGCAATTGGAACTCACTCCTTTGAATTTGCACAGTTTGACAACT
TTCTTGTGGAAGCCACACGC**TAA**TACTTAACAGGGCATCATAGAATACTCTGGATTTTCTTCCCTTCTTTTTGGT
TTTGGTTCAGAGCCAATTCTTGTTTCATTGGAACAGTATATGAGGCTTTTGAGACTAAAAATAATGAAGAGTAAA
AGGGGAGAGAAATTTATTTTTAATTTACCCTGTGGAAGATTTTATTAGAATTAATTCCAAGGGGAAAACTGGTGA
ATCTTTAACATTACCTGGTGTGTTCCCTAACATTCAAACTGTGCATTGGCCATACCCTTAGGAGTGGTTTGAGTA
GTACAGACCTCGAAGCCTTGCTGCTAACACTGAGGTAGCTCTCTTCATCTTATTTGCAAGCGGTCCTGTAGATGG
CAGTAACTTGATCATCACTGAGATGTATTTATGCATGCTGACCGTGTGTCCAAGTGAGCCAGTGTCTTCATCACA
AGATGATGCTGCCATAATAGAAAGCTGAAGAACACTAGAAGTAGCTTTTTGAAAACCACTTCAACCTGTTATGCT
TTATGCTCTAAAAAGTATTTTTTTATTTTCCTTTTTAAGATGATACTTTTGAAATGCAGGATATGATGAGTGGGA
TGATTTTAAAAACGCCTCTTTAATAAACTACCTCTAACACTATTTCTGCGGTAATAGATATTAGCAGATTAATTG
GGTTATTTGCATTATTTAATTTTTTTGATTCCAAGTTTTGGTCTTGTAACCACTATAACTCTCTGTGAACGTTTT
TCCAGGTGGCTGGAAGAAGGAAGAAAACCTGATATAGCCAATGCTGTTGTAGTCGTTTCCTCAGCCTCATCTCAC
TGTGCTGTGGTCTGTCCTCACATGTGCACTGGTAACAGACTCACACAGCTGATGAATGCTTTTCTCTCCTTATGT
GTGGAAGGAGGGGAGCACTTAGACATTTGCTAACTCCCAGAATTGGATCATCTCCTAAGATGTACTTACTTTTTA
AAGTCCAAATATGTTTATATTTAAATATACGTGAGCATGTTCATCATGTTGTATGATTTATACTAAGCATTAATG
TGGCTCTATGTAGCAAATCAGTTATTCATGTAGGTAAAGTAAATCTAGAATTATTTATAAGAATTACTCATTGAA
CTAATTCTACTATTTAGGAATTTATAAGAGTCTAACATAGGCTTAGCTACAGTGAAGTTTTGCATTGCTTTTGAA
GACAAGAAAAGTGCTAGAATAAATAAGATTACAGAGAAAATTTTTTGTTAAAACCAAGTGATTTCCAGCTGATGT
ATCTAATATTTTTTAAAACAAACATTATAGAGGTGTAATTTATTTACAATAAAATGTTCCTACTTTAAATATACA

FIGURE 405B

ATTCAGTGAGTTTTGATAAATTGATATACCCATGTAACCAACACTCCAGTCAAGCTTCAGAATATTTCCATCACC
CCAGAAGGTTCTCTTGTATACCTGCTCAGTCAGTTCCTTTCACTCCCAATTGTTGGCAGCCATTGATAGGAATTC
TATCACTATAGGTTAGTTTTCTTTGTTCCAGAACATCATGAAAGCGGCGTCATGTACTGTGTATTCTTATGAATG
GTTTCTTTCCATCAGCATAATGATTTGAGATTGGTCCATGTTGTGTGATTCAGTGGTTTGTTCCTTCTTATTTCT
GAAGAGTTTTCCATTGTATGAATATACCACAATTTGTTTCCTCCCCACCAGTTTCTGATACTACAATTAAAACTG
TCTACATTTAC

FIGURE 406

MTAAAGSAGRAAVPLLLCALLAPGGAYVLDDSDGLGREFDGIGAVSGGGATSRLLVNYPEPYRSQILDYLFKPNF
GASLHILKVEIGGDGQTTDGTEPSHMHYALDENYFRGYEWWLMKEAKKRNPNITLIGLPWSFPGWLGKGFDWPYV
NLQLTAYYVVTWIVGAKRYHDLDIDYIGIWNERSYNANYIKILRKMLNYQGLQRVKIIASDNLWESISASMLLDA
ELFKVVDVIGAHYPGTHSAKDAKLTGKKLWSSEDFSTLNSDMGAGCWGRILNQNYINGYMTSTIAWNLVASYYEQ
LPYGRCGLMTAQEPWSGHYVVESPVWVSAHTTQFTQPGWYYLKTVGHLEKGGSYVALTDGLGNLTIIIETMSHKH
SKCIRPFLPYFNVSQQFATFVLKGSFSEIPELQVWYTKLGKTSERFLFKQLDSLWLLDSDGSFTLSLHEDELFTL
TTLTTGRKGSYPLPPKSQPFPSTYKDDFNVDYPFFSEAPNFADQTGVFEYFTNIEDPGEHHFTLRQVLNQRPITW
AADASNTISIIGDYNWTNLTIKCDVYIETPDTGGVFIAGRVNKGGILIRSARGIFFWIFANGSYRVTGDLAGWII
YALGRVEVTAKKWYTLTLTIKGHFASGMLNDKSLWTDIPVNFPKNGWAAIGTHSFEFAQFDNFLVEATR

FIGURE 407

ACGAACAGGCCAATAAGGAGGGAGCAGTGCGGGGTTTAAATCTGAGGCTAGGCTGGCTCTTCTCGGCGTGCTGCG
GCGGAACGGCTGTTGGTTTCTGCTGGTTGTAGGTCCTTGGCTGGTCGGGCCTCCGGTGTTCTGCTTCTCCCCGCT
GAGCTGCTGCCTGGTGAAGAGGAAGCC**ATG**GCGCTCCGAGTCACCAGGAACTCGAAAATTAATGCTGAAAATAAG
GCGAAGATCAACATGGCAGGCGCAAAGCGCGTTCCTACGGCCCCTGCTGCAACCTCCAAGCCCGGACTGAGGCCA
AGAACAGCTCTTGGGGACATTGGTAACAAAGTCAGTGAACAACTGCAGGCCAAAATGCCTATGAAGAAGGAAGCA
AAACCTTCAGCTACTGGAAAAGTCATTGATAAAAAACTACCAAAACCTCTTGAAAAGGTACCTATGCTGGTGCCA
GTGCCAGTGTCTGAGCCAGTGCCAGAGCCAGAACCTGAGCCAGAACCTGAGCCTGTTAAAGAAGAAAAACTTTCG
CCTGAGCCTATTTTGGTTGATACTGCCTCTCCAAGCCCAATGGAAACATCTGGATGTGCCCCTGCAGAAGAAGAC
CTGTGTCAGGCTTTCTCTGATGTAATTCTTGCAGTAAATGATGTGGATGCAGAAGATGGAGCTGATCCAAACCTT
TGTAGTGAATATGTGAAAGATATTTATGCTTATCTGAGACAACTTGAGGAAGAGCAAGCAGTCAGACCAAAATAC
CTACTGGGTCGGGAAGTCACTGGAAACATGAGAGCCATCCTAATTGACTGGCTAGTACAGGTTCAAATGAAATTC
AGGTTGTTGCAGGAGACCATGTACATGACTGTCTCCATTATTGATCGGTTCATGCAGAATAATTGTGTGCCCAAG
AAGATGCTGCAGCTGGTTGGTGTCACTGCCATGTTTATTGCAAGCAAATATGAAGAAATGTACCCTCCAGAAATT
GGTGACTTTGCTTTTGTGACTGACAACACTTATACTAAGCACCAAATCAGACAGATGGAAATGAAGATTCTAAGA
GCTTTAAACTTTGGTCTGGGTCGGCCTCTACCTTTGCACTTCCTTCGGAGAGCATCTAAGATTGGAGAGGTTGAT
GTCGAGCAACATACTTTGGCCAAATACCTGATGGAACTAACTATGTTGGACTATGACATGGTGCACTTTCCTCCT
TCTCAAATTGCAGCAGGAGCTTTTTGCTTAGCACTGAAAATTCTGGATAATGGTGAATGGACACCAACTCTACAA
CATTACCTGTCATATACTGAAGAATCTCTTCTTCCAGTTATGCAGCACCTGGCTAAGAATGTAGTCATGGTAAAT
CAAGGACTTACAAAGCACATGACTGTCAAGAACAAGTATGCCACATCGAAGCATGCTAAGATCAGCACTCTACCA
CAGCTGAATTCTGCACTAGTTCAAGATTTAGCCAAGGCTGTGGCAAAGGTG**TAA**CTTGTAAACTTGAGTTGGAGT
ACTATATTTACAAATAAAATTGGCACCATGTGCCATCTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 408

MALRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALGDIGNKVSEQLQAKMPMKKEAKPSATGKVI
DKKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSGCAPAEEDLCQAFSDVI
LAVNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQETMYM
TVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRP
LPLHFLRRASKIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALKILDNGEWTPTLQHYLSYTEES
LLPVMQHLAKNVVMVNQGLTKHMTVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV

FIGURE 409

AGAGAGCTGTTTACTAGGCACGACTGCGAAGGCAAGGGGGCACCAGCTCAGGACTGCATCTGCCTGCCATTTCCC
TTCCACTCCTCCTTTCTGGAGTCTGACATTAGAAAGCCAGCGAGAAGGAAGATTCAAACAACCAACCCTGATTTC
CTGCTTCTCCTTTTCATGAGTGTTCCTGTGGTCTCTGCACCTCCTTTCTGTCCCCCGGCAGAGGGCAGTAGAG**AT**
GGCCGGCCCAAGGCCTCGGTGGCGCGACCAGCTGCTGTTCATGAGCATCATAGTCCTCGTGATTGTGGTCATCTG
CCTGATGTTATACGCTCTTCTCTGGGAGGCTGGCAACCTCACTGACCTGCCCAACCTGAGAATCGGCTTCTATAA
CTTCTGCCTGTGGAATGAGGACACCAGCACCCTACAGTGTCACCAGTTCCCTGAGCTGGAAGCCCTGGGGGTGCC
TCGGGTTGGCCTGGGCCTGGCCAGGCTTGGCGTGTACGGGTCCCTGGTCCTCACCCTCTTTGCCCCCCAGCCTCT
CCTCCTAGCCCAGTGCAACAGTGATGAGAGAGCGTGGCGGCTGGCAGTGGGCTTCCTGGCTGTGTCCTCTGTGCT
GCTGGCAGGCGGCCTGGGCCTCTTCCTCTCCTATGTGTGGAAGTGGGTCAGGCTCTCCCTCCCGGGGCCTGGGTT
TCTAGCTCTGGGCAGCGCCCAGGCCTTACTCATCCTCTTGCTTATAGCCATGGCTGTGTTCCCTCTGAGGGCTGA
GAGGGCTGAGAGCAAGCTTGAGAGCTGC**TAA**AGGCTTACGTGATTGCAAGGGTTCAGTTCCAACCATAGTCAGAG
GTGGCACATCTGCTCAGCCATCTCATTTTACAGCTAACGCTGATCTCCAGCTCCAGCGATGGAACCCACTACAGA
GGAGGTGGGGCCCCTGTGTCAAAGAGGCCGAGGGGCAGCAAGGGCAGCCAGGGCACCTGTGACTTCTTAGTACAA
GATTGTCTGTCCTTCAGGACTTCCAAGGCTCCCAAAGACTCCCTAAACCATGCAGCTCATTGTCACACCAATTCC
TGCTTTAATTAATGGATCTGAGCAAATCTTCCTCTAGCTTCAGGAGGGTGGGGAGGGAGTGATTGCCGTCATGGG
GCCAGACTTCCAGGCTGATTTGCCAAATGCCAAAATGAAACCTAGCAAAGAACTTACGGCAACAAACGAGGACAT
TAAAAGAGCGAGCACCTCAGTGTCTCTGGGGACATGGTTAAGGAGCTTCCACTCAGCCCACCATAGTGAGTGGGC
CGCCATAAGCCATCACTGGAACTCCAACCCCAGAGGTCCAGGAGTGATCTCTGAGTGACTCAACAAAGACAGGAC
ACATGGGGTACAAAGACAAGGCTTGACTGCTTCAAAGCTTCCCTGGACCTGAAGCCAGACAGGGCAGAGGCGTCC
GCTGACAAATCACTCCCATGATGAGACCCTGGAGGACTCCAAATCCTCGCTGTGAACAGGACTGGACGGTTGCGC
ACAAACAAACGCTGCCACCCTCCACTTCCCAACCCAGAACTTGGAAAGACATTAGCACAACTTACGCATTGGGGA
ATTGTGTGTATTTTCTAGCACTTGTGTATTGGAAAACCTGTATGGCAGTGATTTATTCATATATTCCTGTCCAAA
GCCACACTGAAAACAGAGGCAGAGACATGT

FIGURE 410

MAGPRPRWRDQLLFMSIIVLVIVVICLMLYALLWEAGNLTDLPNLRIGFYNFCLWNEDTSTLQCHQFPELEALGV
PRVGLGLARLGVYGSLVLTLFAPQPLLLAQCNSDERAWRLAVGFLAVSSVLLAGGLGLFLSYVWKWVRLSLPGPG
FLALGSAQALLILLLIAMAVFPLRAERAESKLESC

FIGURE 411

CTGGTCCCGAGCACGAGCTGTGAGGGGATTCACTTGTGTGCGGAACTCCTCGGAACC**ATG**GCGTCCCTTTCCCTT
GCACCTGTTAACATCTTTAAGGCAGGAGCTGATGAAGAGAGAGCAGAGACAGCTCGTCTGACTTCTTTTATTGGT
GCCATCGCCATTGGAGACTTGGTAAAGAGCACCTTGGGACCCAAAGGCATGGACAAAATTCTTCTAAGCAGTGGA
CGAGATGCCTCTCTTATGGTAACCAATGATGGTGCCACTATTCTAAAAAACATTGGTGTTGACAATCCAGCAGCT
AAAGTTTTAGTTGATATGTCAAGGGTTCAAGATGATGAAGTTGGTGATGGCACTACCTCTGTTACCGTTTTAGCA
GCAGAATTATTAAGGGAAGCAGAATCTTTAATTGCAAAAAAGATTCATCCACAGACCATCATAGCGGGTTGGAGA
GAAGCCACGAAGGCTGCAAGAGAGGCGCTGTTGAGTTCTGCAGTTGATCATGGTTCCGATGAAGTTAAATTCCGT
CAAGATTTAATGAATATTGCGGGCACAACATTATCCTCAAAACTTCTTACTCATCACAAAGACCACTTTACAAAG
TTAGCTGTAGAAGCAGTTCTCAGACTGAAAGGCTCTGGCAACCTGGAGGCAATTCATATTATCAAGAAGCTAGGA
GGAAGTTTGGCAGATTCCTATTTAGATGAAGGCTTCCTGTTGGATAAAAAAATTGGAGTAAATCAACCAAAACGA
ATTGAAAATGCTAAAATTCTTATTGCAAATACTGGTATGGATACAGACAAAATAAAGATATTTGGTTCCCGGGTA
AGAGTTGACTCTACAGCAAAGGTTGCAGAAATAGAACATGCGGAAAAGGAAAAAATGAAGGAGAAAGTTGAACGT
ATTCTTAAGCATGGAATAAATTGCTTTATTAACAGGCAATTAATTTATAATTATCCTGAACAGCTCTTTGGTGCT
GCTGGTGTCATGGCTATTGAGCATGCAGATTTTGCAGGTGTGGAACGCCTAGCTCTTGTCACAGGTGGTGAAATT
GCCTCTACCTTTGATCACCCAGAACTGGTGAAGCTTGGAAGTTGCAAACTTATCGAGGAAGTCATGATTGGAGAA
GACAAACTCATTCACTTTTCTGGGGTTGCCCTTGGTGAGGCTTGTACCATTGTTTTGCGTGGTGCCACTCAACAA
ATTTTAGATGAAGCAGAAAGATCATTGCATGATGCTCTTTGTGTTCTTGCGCAAACTGTAAAGGACTCTAGAACA
GTTTATGGAGGAGGCTGTTCTGAGATGTTGATGGCTCATGCTGTGACACAGCTTGCCAATAGAACACCAGGCAAA
GAAGCTGTTGCAATGGAGTCTTATGCTAAAGCACTGAGAATGTTGCCAACCATCATAGCTGACAATGCAGGCTAT
GACAGTGCAGACCTGGTGGCACAGCTCAGGGCTGCTCACAGTGAAGGCAATACCACTGCTGGATTGGATATGAGG
GAAGGCACCATTGGAGATATGGCTATCCTGGGTATAACAGAAAGTTTTCAAGTGAAGCGACAGGTTCTTCTGAGT
GCAGCTGAAGCAGCAGAGGTGATTCTGCGTGTGGACAACATCATCAAAGCGGCACCCAGGAAACGTGTCCCTGAT
CACCACCCCTGT**TAA**GCATTCCCACGTGCTGTCGATCTTTGGACCAGTTTCTAGCAAAGTTGTGTTTGAAAGATA
CTCTATTAAAGAAGACTGTGGAATCTGTTTATCGGTGCCCATTATATCCTTAAGTTTGGATATTTAGCTGACCTT
CGCTTTAACATAGGTCTAATTTATTTGCCGTGTCATTTTCCATACAAATCAGTTGATTTAAAGGAGTTCATTTCG
CATACTGGGCATTAAAATAAAAATTTGAACAATGAAAGGAAAAAAAGGAGAAAAAAAAAA

FIGURE 412

MASLSLAPVNIFKAGADEERAETARLTSFIGAIAIGDLVKSTLGPKGMDKILLSSGRDASLMVTNDGATILKNIG
VDNPAAKVLVDMSRVQDDEVGDGTTSVTVLAAELLREAESLIAKKIHPQTIIAGWREATKAAREALLSSAVDHGS
DEVKFRQDLMNIAGTTLSSKLLTHHKDHFTKLAVEAVLRLKGSGNLEAIHIIKKLGGSLADSYLDEGFLLDKKIG
VNQPKRIENAKILIANTGMDTDKIKIFGSRVRVDSTAKVAEIEHAEKEKMKEKVERILKHGINCFINRQLIYNYP
EQLFGAAGVMAIEHADFAGVERLALVTGGEIASTFDHPELVKLGSCKLIEEVMIGEDKLIHFSGVALGEACTIVL
RGATQQILDEAERSLHDALCVLAQTVKDSRTVYGGGCSEMLMAHAVTQLANRTPGKEAVAMESYAKALRMLPTII
ADNAGYDSADLVAQLRAAHSEGNTTAGLDMREGTIGDMAILGITESFQVKRQVLLSAAEAAEVILRVDNIIKAAP
RKRVPDHHPC

FIGURE 413

CGGCTTCCTCCCGCTTTTTCTTCTCTCTCCTTGCGGTCTGAAGATGCCCTCGGCCACCAGCCACAGCGGGAGCGC
AGCAAGTCGTCCGGACCGCCACCGCCGTCGGGTTCCTCCGGGAGTGAGGCGGCCGCGGGAGCCGGGGCCGCCGCG
CCGGCTTCTCAGCACCCCGCAACCGGCACCGGCGCTGTCCAGACCGAGGCC**ATG**AAGCAGATTCTCGGGGTGATC
GACAAGAAACTTCGGAACCTGGAGAAGAAAAAGGGTAAGCTTGATGATTACCAGGAACGAATGAACAAAGGGGAA
AGGCTTAATCAAGATCAGCTGGATGCCGTTTCTAAGTACCAGGAAGTCACAAATAATTTGGAGTTTGCAAAAGAA
TTACAGAGGAGTTTCATGGCACTAAGTCAAGATATTCAGAAAACAATAAAGAAGACAGCACGTCGGGAGCAGCTT
ATGAGAGAAGAAGCTGAACAGAAACGTTTAAAAACTGTACTTGAGCTACAGTATGTTTTGGACAAATTGGGAGAT
GATGAAGTGCGGACTGACCTGAAACAAGGTTTGAATGGAGTGCCAATATTGTCCGAAGAGGAGTTGTCATTGTTG
GATGAATTCTATAAGCTAGTAGACCCTGAACGGGACATGAGCTTGAGGTTGAATGAACAGTATGAACATGCCTCC
ATTCACCTGTGGGACCTGCTGGAAGGGAAGGAAAAACCTGTATGTGGAACCACCTATAAAGTTCTAAAGGAAATT
GTTGAGCGTGTTTTTCAGTCAAACTACTTTGACAGCACCCACAACCACCAGAATGGGCTGTGTGAGGAAGAAGAG
GCAGACTCAGCACCTGCAGTTGAAGACCAGGTACCTGAAGCTGAACCTGAGCCAGCAGAAGAGTACACTGAGCAA
AGTGAAGTTGAATCAACAGAGTATGTAAATAGACAGTTCATGGCAGAAACACAGTTCACCAGTGGTGAAAAGGAG
CAGGTAGATGAGTGGACAGTTGAAACGGTTGAGGTGGTAAATTCACTCCAGCAGCAACCTCAGGCTGCATCCCCT
TCAGTACCAGAGCCCCACTCTTTGACTCCAGTGGCTCAGGCAGATCCCCTTGTGAGAAGACAGCGAGTACAAGAC
CTTATGGCACAAATGCAGGGTCCCGATAATTTCATACAGGATTCAATGCTGGATTTTGAAAATCAGACACTTGAT
CCTGCCATTGTATCTGCACAGCCTATGAATCCAACACAAAACATGGACATGCCCCAGCTGGTTTGCCCTCCAGTT
CATTCTGAATCTAGACTTGCTCAGCCTAATCAAGTTCCTGTACAACCAGAAGCGACACAGGTTCCTTTGGTATCA
TCCACAAGTGAGGGGTACACAGCATCTCAACCCTTGTACCAGCCTTCTCATGCTACAGAGCAACGACCACAGAAG
GAACCAATTGATCAGATTCAGGCAACAATCTCTTTAAATACAGACCAGACTACAGCATCATCATCCCTTCCTGCT
GCGTCTCAGCCTCAAGTATTTCAGGCTGGGACAAGCAAACCTTTACATAGCAGTGGAATCAATGTAAATGCAGCT
CCATTCCAATCCATGCAAACGGTGTTCAATATGAATGCCCCAGTTCCTCCTGTTAATGAACCAGAAACTTTAAAA
CAGCAAAATCAGTACCAGGCCAGTTATAACCAGAGCTTTTCTAGTCAGCCTCACCAAGTAGAACAAACAGAGCTT
CAGCAAGAACAGCTTCAAACAGTGGTTGGCACTTACCATGGTTCCCCAGACCAGTCCCATCAAGTGACTGGTAAC
CACCAGCAGCCTCCTCAGCAGAACACTGGATTTCCACGTAGCAATCAGCCCTATTACAATAGTCGTGGTGTGTCT
CGTGGAGGCTCCCGTGGTGCTAGAGGCTTGATGAATGGATACCGGGGCCCTGCAATGGATTCAGAGGAGGATATG
ATGGTTACCGCCCTTCATTCTCTAACACTCCAAACAGTGGTTATACACAGTCTCAGTTCAGTGCTCCCCGGGATT
ACTCTGGCTATCAACGGGATGGATATCAGCAGAATTTCAAGCGAGGCTCTGGGCAGAGTGGACCACGGGGAGCCC
CACGAGGTCGTGGAGGGCCCCCAAGACCCAACAGAGGGATGCCGCAAA**TGA**ACACTCAGCAAGTGAATTAATCTG
ATTCACAGGATTATGTTTAATCGCCAAAAACACACTGGCCAGTGTACCATAATATGTTACCAGAAGAGTTATTAT
CTATTTGTTCTCCCTTTCAGGAAACTTATTGTAAAGGGACTGTTTTCATCCCATAAAGACAGGACTACAATTGTC
AGCTTTCTATTACCTGGATATGGAAGGAAACTATTTTTACTCTGCATGTTCTGTCCTAAGCGTCATCTTGAGCCT
TGCACATGATACTCAGATTCCTCACCCTTGCTTAGGAGTAAAACAATATACTTTACAGGGTGATAATAATCTCCA
TAGTTATTTGAAGTGGCTTGAAAAAGGCAAGATTGACTTTTATGACATTGGATAAAATCTACAAATCAGCCCTCG
AGTTATTCAATGATAACTGACAAACTAAATTATTTCCCTAGAAAGGAAGATGAAAGGAGTGGAGTGTGGTTTGGC
CAGAACAACTGCATTTCACAGCTTTTCCAGTTAAATTGGAGCACTGAACGTTCAGATGCATACCAAATTATGCAT
GGGTCCTAATCACACATATAAGGCTGGCTACCAGCTTTGACACAGCACTGTTCATCTGGCCAAACAACTGTGGTT
AAAAACACATGTAAAATGGCTTTTTAACAGCTGATACTGTATAAGACAAAGCCAAGATGCAAAATTAGGCTTTGA
TTGGCACTTTTTGAAAAATATGCAACAAATATGGGATGTAATCCGGATGGCCGCTTCTGTACTTAATGTGAAATA
TTTAGATACCTTTTTGAACACTTAACAGTTTCTTTGAGACAATGACTTTGTAAGGATTGGTACTATCTATCATTC
CTTATGACATGTACATTGTCTGTCACTAATCCTTGGATTTTGCTGTATTGTCACCGGGATTGGTACAGGTACTGA
TGAAAATCTCTAGTGGATAATCATAACACTCTCGGTCACATGTTTTTCCTTCAGCTTGAAAGCTTTTTTTAAAAG
GAAAAGATACCAAATGCCTGCTGCTACCACCCTTTTCAATTGCTATGTTTTGAAAGGCACCAGTATGTGTTTTAG
ATTGATTTCCCTGTTTCAGGGAAATCACGGACAGTAGTTTCCG

FIGURE 414

MKQILGVIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIK
KTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSLLDEFYKLVDPERDMSLRL
NEQYEHASIHLWDLLEGKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEADSAPAVEDQVPEAEPE
PAEEYTEQSEVESTEYVNRQFMAETQFTSGEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQADPL
VRRQRVQDLMAQMQGPDNFIQDSMLDFENQTLDPAIVSAQPMNPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPE
ATQVPLVSSTSEGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHS
SGINVNAAPFQSMQTVFNMNAPVPPVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVGTYHGSPD
QSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGSRGARGLMNGYRGPAMDSEEDMMVTALHSLTLQTVVIHS
LSSVLPGITLAINGMDISRISSEALGRVDHGEPHEVVEGPQDPTEGCRK

FIGURE 415

ATGGAAGGAGACTTCTCGGTGTGCAGGAACTGTAAAAGACATGTAGTCTCTGCCAACTTCACCCTCCATGAGGCT
TACTGCCTGCGGTTCCTGGTCCTGTGTCCGGAGTGTGAGGAGCCTGTCCCCAAGGAAACCATGGAGGAGCACTGC
AAGCTTGAGCACCAGCAGGTTGGGTGTACGATGTGTCAGCAGAGCATGCAGAAGTCCTCGCTGGAGTTTCATAAG
GCCAATGAGTGCCAGGAGCGCCCTGTTGAGTGTAAGTTCTGCAAACTGGACATGCAGCTCAGCAAGCTGGAGCTC
CACGAGTCCTACTGTGGCAGCCGGACAGAGCTCTGCCAAGGCTGTGGCCAGTTCATCATGCACCGCATGCTCGCC
CAGCACAGAGATGTCTGTCGGAGTGAACAGGCCCAGCTCGGGAAAGGGGAAAGAATTTCAGCTCCTGAAAGGGAA
ATCTACTGTCATTATTGCAACCAAATGATTCCAGAAAATAAGTATTTCCACCATATGGGTAAATGTTGTCCAGAC
TCAGAGTTTAAGAAACACTTTCCTGTTGGAAATCCAGAAATTCTTCCTTCATCTCTTCCAAGTCAAGCTGCTGAA
AATCAAACTTCCACGATGGAGAAAGATGTTCGTCCAAAGACAAGAAGTATAAACAGATTTCCTCTTCATTCTGAA
AGTTCATCAAAGAAAGCACCAAGAAGCAAAAACAAAACCTTGGATCCACTTTTGATGTCAGAGCCCAAGCCCAGG
ACCAGCTCCCCTAGAGGAGATAAAGCAGCCTATGACATTCTGAGGAGATGTTCTCAGTGTGGCATCCTGCTTCCC
CTGCCGATCCTAAATCAACATCAGGAGAAATGCCGGTGGTTAGCTTCATCAAAAAGGAAAACAAGTGAGAAATTT
CAGCTAGATTTGGAAAAGGAAAGGTACTACAAATTCAAAAGATTTCACTTT**TAA**CACTGGCATTCCTGCCTACTT
GCTGTGGTGGTCTTGTGAAAGGTGATGGGTTTTATTCGTTGGGCTTTAAAAGAAAAGGTTTGGCAGAACTAAAAA
CAAAACTCACGTATCATCTCAATAGATACAGAAAAGGCTTTTGATAAAATTCAACTTGACTTCATGTTAAAAACC
CTCAACAAACCAGGCGTCGAAGGAACATACCTCAAAATAATAAGAGCCATCTATGACAAAACCACAGCCAACATC
ATACTGAATGAGCAAAAGCTGGAGCATTACTCTTGAGAAGTAGAACAAGGCACTTCAGTCCTATTCAACATAGTA
CTGGAAGTCTCGCCACAGCAATCAGGCAAGAGAAAGAAGTAAAAGGCACCC

FIGURE 416

MEGDFSVCRNCKRHVVSANFTLHEAYCLRFLVLCPECEEPVPKETMEEHCKLEHQQVGCTMCQQSMQKSSLEFHK
ANECQERPVECKFCKLDMQLSKLELHESYCGSRTELCQGCGQFIMHRMLAQHRDVCRSEQAQLGKGERISAPERE
IYCHYCNQMIPENKYFHHMGKCCPDSEFKKHFPVGNPEILPSSLPSQAAENQTSTMEKDVRPKTRSINRFPLHSE
SSSKKAPRSKNKTLDPLLMSEPKPRTSSPRGDKAAYDILRRCSQCGILLPLPILNQHQEKCRWLASSKRKTSEKF
QLDLEKERYYKFKRFHF

FIGURE 417

AAACTGGGAGAGGGAGGAAGGGAGAAAGTGAGAAGGAAATCGGAAAGAGAAAAGGGAGGAAACGGCAGAGCCAG
AGAGAAAGAGGAAGAGACTGAGTGTGAAGGAGAGAGGACACAGGGGATGACTGAGAGACAGAGAGAGAGAGAGAG
AGAGAATGAGACAGAGACTTAAGGAAGAGACCCTGTGAGTCTGACAATAAAAGATTTGGACAGAAACAGAAAGAT
TGGAGAGAGAGAGAGAGGGAGAGAATGAGTGAGAGAGAGACTGGAAGAGACAGAGATCAGAGGGAGACACAGAAA
GTGAGAGTGGGGAGAGAGGTAGTGTAAAAGGAAGAGAGAGAGAGAGAGACCGTAAGAGACAGGAGACAAAGAGAC
AAAAAGTGTGAGTGAGCAGGTGAGGAGAGAGATTGAGAACTATGAGAGACAGCAGCTAAGAGACAAAGGAGGCGG
GAGACTGCCTAGGTGCCGCAGCACCCACACCGTCCTCTTGCCCCCCCGTCACTGGGACCCCAGAGCTGGCCCTTG
ATGGAGGGGAGCCGACCTCGCAGCAGCCTGAGCCTGGCCAGCAGCGCCTCCACCATCTCCTCGCTCAGCAGCCTG
AGCCCCAAGAAGCCCACCCGGGCAGTAAACAAGATCCACGCCTTTGGGAAGAGAGGCAATGCGCTCAGGAGGGAT
CCCAACCTTCCCGTGCACATCCGAGGCTGGCTTCATAAGCAGGACAGCTCGGGGCTCCGTCTCTGGAAACGCCGC
TGGTTCGTCCTCTCCGGCCATTGCCTCTTTTATTACAAGGACAGCCGCGAGGAGAGTGTCCTAGGCAGCGTCCTG
CTCCCCAGCTACAATATTAGACCAGATGGGCCGGGAGCCCCCCGAGGGCGGCGCTTCACCTTCACCGCAGAGCAC
CCGGGCATGAGGACCTACGTTTTGGCCGCTGACACCTTAGAAGACCTGCGGGGCTGGCTACGGGCGCTGGGCCGG
GCCTCCCGTGCGGAGGGGGACGACTATGGGCAACCCAGGTCACCTGCACGACCCCAGCCCGGGGAGGGCCCCGGC
GGCCCCGGTGGTCCCCCGGAGGTGAGCAGAGGGGAAGAGGGGCGCATCTCAGAATCACCGGAAGTGACTCGACTC
TCCAGAGGTCGTGGTAGACCCAGGCTGCTCACTCCCAGCCCCACAACCGACCTCCACTCTGGACTCCAGATGCGG
AGGGCGAGGAGCCCCGACCTGTTCACCCCCCTCTCTCGCCCTCCCTCGCCTCTGAGCCTCCCCCGTCCCCGTTCT
GCCCCTGCGCGGCGACCCCCTGCCCCCTCAGGAGACACAGCACCCCCTGCCCGACCTCACACCCCGTTGAGTCGC
ATTGATGTCCGACCTCCTCTGGATTGGGGCCCCCAACGCCAGACCCTCTCCCGACCCCCTACTCCCCGCCGAGGA
CCTCCCTCTGAGGCTGGGGGAGGAAAGCCCCCCAGGAGTCCCCAGCACTGGAGTCAGGAGCCCAGAACACAGGCA
CACTCTGGCTCCCCCACTTATCTCCAGCTCCCCCCGCGGCCCCCTGGGACCCGGGCCTCCATGGTTTTATTGCCG
GGTCCTCCCCTGGAGTCAACTTTCCACCAAAGCTTGGAGACAGATACGCTGCTGACCAAGTTGTGCGGGCAGGAC
CGGCTTCTGCGGAGGCTGCAGGAGGAGATAGACCAGAAGCAGGAGGAGAAGGAGCAACTAGAAGCAGCTCTGGAG
TTGACCCGGCAACAGCTGGGCCAAGCCACCAGGGAGGCTGGGGCTCCCGGGAGGGCCTGGGGTCGCCAGCGCCTC
TTGCAGGACCGGCTGGTCAGTGTGAGGGCCACCCTCTGTCACTTGACTCAGGAGCGAGAGAGGGTTTGGGACACG
TACAGTGGCCTGGAGCAGGAGCTGGGCACCTTAAGAGAGACGCTGGAGTACCTGCTGCACCTTGGTTCTCCCCAG
GACAGAGTGTCTGCTCAGCAGCAGCTGTGGATGGTGGAAGACACGCTGGCAGGTCTGGGTGGCCCCCAGAAACCG
CCCCCACACACTGAGCCTGACTCCCCATCTCCCGTGCTCCAGGGCGAGGAGTCCTCAGAGAGGGAGAGCCTGCCA
GAGTCCTTGGAACTGAGCTCCCCTAGGTCCCCCGAGACTGACTGGGGGCGGCCTCCTGGAGGCGACAAAGACCTC
GCCAGCCCTCACTTAGGTCTTGGGTCTCCGAGGGTCTCCCGGGCTTCCAGCCCTGAGGGTCGCCACCTCCCTTCC
CCACAGCTAGGAACCAAGGCCCCGGTGGCCCGGCCCCGGATGAATGCCCAGGAGCAGCTGGAGCGGATGCGCAGA
AACCAGGAATGTGGACGGCCCTTCCCTCGCCCGACCTCCCCCCGGCTTCTCACCCTGGGAAGGACACTGTCCCCA
GCCAGACGCCAGCCTGACGTGGAGCAAAGGCCTGTCGTAGGACACTCGGGAGCCCAGAAATGGCTCAGAAGCTCT
GGGTCCTGGAGTAGTCCAAGGAACACCACCCCTTACTTGCCGACTTCCGAAGGTCACCGGGAGCGGGTTCTCAGC
CTCTCCCAAGCCCTGGCTACTGAGGCGTCGCAGTGGCACAGAATGATGACAGGTGGAAATTTGGACTCCCAGGGA
GACCCTCTTCCCGGTGTGCCGCTGCCTCCTTCGGACCCCACGCGCCAGGAGACCCCTCCCCCCAGATCTCCCCCG
GTGGCTAATTCGGGTTCCACGGGGTTCTCTCGCCGAGGGAGTGGGCGTGGAGGAGGTCCCACCCCCTGGGGGCCC
GCGTGGGATGCCGGGATCGCCCCTCCGGTCCTGCCACAAGACGAGGGGGCATGGCCTCTGCGAGTCACTCTGCTA
CAATCCAGCTTG**TAA**TCCGCCCAAAAGCGGCAGCCAATCGGAGCGCGAGGACGTGGTCTGGAGGTACCGCCGAAG
ATCTGGGACCACTCAGGGCATCAGGGGGCGTGGTCTGGTCCCCATTGCGGGCCCGGGAGGGGAATGGTTTCTATG
GCCAAAGTTTGGTTTTCTCAACACTGTCTAAATTTGGATTAAAACTTTGAACTTTT

FIGURE 418

MEGSRPRSSLSLASSASTISSLSSLSPKKPTRAVNKIHAFGKRGNALRRDPNLPVHIRGWLHKQDSSGLRLWKRR
WFVLSGHCLFYYKDSREESVLGSVLLPSYNIRPDGPGAPRGRRFTFTAEHPGMRTYVLAADTLEDLRGWLRALGR
ASRAEGDDYGQPRSPARPQPGEGPGGPGGPPEVSRGEEGRISESPEVTRLSRGRGRPRLLTPSPTTDLHSGLQMR
RARSPDLFTPLSRPPSPLSLPRPRSAPARRPPAPSGDTAPPARPHTPLSRIDVRPPLDWGPQRQTLSRPPTPRRG
PPSEAGGGKPPRSPQHWSQEPRTQAHSGSPTYLQLPPRPPGTRASMVLLPGPPLESTFHQSLETDTLLTKLCGQD
RLLRRLQEEIDQKQEEKEQLEAALELTRQQLGQATREAGAPGRAWGRQRLLQDRLVSVRATLCHLTQERERVWDT
YSGLEQELGTLRETLEYLLHLGSPQDRVSAQQQLWMVEDTLAGLGGPQKPPPHTEPDSPSPVLQGEESSERESLP
ESLELSSPRSPETDWGRPPGGDKDLASPHLGLGSPRVSRASSPEGRHLPSPQLGTKAPVARPRMNAQEQLERMRR
NQECGRPFPRPTSPRLLTLGRTLSPARRQPDVEQRPVVGHSGAQKWLRSSGSWSSPRNTTPYLPTSEGHRERVLS
LSQALATEASQWHRMMTGGNLDSQGDPLPGVPLPPSDPTRQETPPPRSPPVANSGSTGFSRRGSGRGGGPTPWGP
AWDAGIAPPVLPQDEGAWPLRVTLLQSSL

FIGURE 419

GGCACGAGGGGGACCCAACCGCGGCGACCGGACGTGCACTCCTCCAGTAGCGGCTGCACGTCGTGCCA**ATG**GCCC
GCTATGAGGAGGTGAGCGTGTCCGGCTTCGAGGAGTTCCACCGGGCCGTGGAACAGCACAATGGCAAGACCATTT
TCGCCTACTTTACGGGTTCTAAGGACGCCGGGGGAAAAGCTGGTGCCCCGACTGCGTGCAGGCTGAACCAGTCG
TACGAGAGGGGCTGAAGCACATTAGTGAAGGATGTGTGTTCATCTACTGCCAAGTAGGAGAAAAGCCTTATTGGA
AAGATCCAAATAATGACTTCAGAAAAAACTTGAAAGTAACAGCAGTGCCTACACTACTTAAGTATGGAACACCTC
AAAAACTGGTAGAATCTGAGTGTCTTCAGGCCAACCTGGTGGAAATGTTGTTCTCTGAAGAT**TAA**GATTTTAGGA
TGGCAATCATGTCTTGATGTCCTGATTTGTTCTAGTATCAATAAACTGTATACTTGCTTTGAATTCATGTTAGCA
ATAAATGATGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 420

MARYEEVSVSGFEEFHRAVEQHNGKTIFAYFTGSKDAGGKSWCPDCVQAEPVVREGLKHISEGCVFIYCQVGEKP
YWKDPNNDFRKNLKVTAVPTLLKYGTPQKLVESECLQANLVEMLFSED

FIGURE 421

GAAAAATGTTTATATAAGCGTAAAGCTGGTAGGACAGGAAAGGAAGCCGAAACAAAAAGTAAAGAAAAATCCACA
AGGACAACTTTTGGAGCTAGTGCCTGAGATTTTGGATTTC**<u>TGA</u>**GTCCCAGGAGGTGCTGATATCATTTATCTGCG
GACTCGTATTATGAAGCGCAAGGTCCTAGAGCGTGTGATTTTACAGGCATAAGGAATATAAGATGAAGGCTGAGA
CAAAATAGGATGGGTGGCCTAATTTTCTTCCCCCACCCTCTCGTCCCTCCCATACACATACAACCTGACAACTAA
AAGGGCCGCACTCCATGGAAGAACTCCTGCAGAGTTGGACTCCCCACCGGCAAACAGGAGGAGGCTATGAAGAAA
CTTGCCTGTCTCCGATTTTCTTGGGAATTGAAAAAATAAAATTTTTAAGCCTTTCATGAAAA

FIGURE 422

KNVYISVKLVGQERKPKQKVKKNPQGQLLELVPEILDF

FIGURE 423

CTCAGCTTGCGCCGCCGCCGCCGCCGCCGCCGCGCACGCC**ATG**GGAGCCGTGACTGACGACGAAGTTATACG
GAAGCGTCTCCTCATTGATGGAGATGGTGCTGGAGGTGATCGGAGAATTAATCTGCTAGTGAAGAGTTTCATTAA
ATGGTGCAACTCTGGGTCCCAGGAGGAGGGATATAGCCAGTACCAACGTATGCTGAGCACGCTGTCTCAATGTGA
ATTTTCAATGGGCAAAACTTTACTAGTATATGATATGAATCTCAGAGAAATGGAAAATTATGAAAAAATTTACAA
GGAAATAGAATGTAGCATAGCTGGAGCACATGAAAAAATTGCTGAGTGCAAAAAGCAAATTCTTCAAGCAAAACG
AATACGAAAAAATCGCCAAGAATATGATGCTTTGGCAAAAGTGATTCAGCACCATCCAGACAGGCATGAGACATT
AAAGGAACTAGAGGCTCTGGGAAAAGAATTAGAGCATCTTTCACACATTAAAGAAAGTGTTGAAGATAAGCTGGA
ATTGAGACGGAAACAGTTTCATGTTCTTCTTAGTACCATCCATGAACTTCAGCAAACATTGGAAAATGATGAAAA
ACTCTCAGAGGTAGAAGAAGCTCAGGAAGCAAGCATGGAATCAGATCCTAAGCCA**TAG**ACAGGCTAATTGCCCAC
CACTCCCAGGAATATTGAAATAGCTACATGACCATAATGTGTTTAAAATGTGGTATGCTCTTGAGATATTTAAAG
TTTTGGCAGTAAAATACTCTGTTTTTAAGTATGAATGTATTTCATTCATATTTCCTCTCACAAAGGAAAATGACT
TCAGTATAGATTTGTTTTTATTAAAATGCATTTTTTATTCTTAAGTGGTAGGAAGCAACATCCAAAAATGCTTAA
TAAAATGCTTTTAAGCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 424

MGAVTDDEVIRKRLLIDGDGAGGDRRINLLVKSFIKWCNSGSQEEGYSQYQRMLSTLSQCEFSMGKTLLVYDMNL
REMENYEKIYKEIECSIAGAHEKIAECKKQILQAKRIRKNRQEYDALAKVIQHHPDRHETLKELEALGKELEHLS
HIKESVEDKLELRRKQFHVLLSTIHELQQTLENDEKLSEVEEAQEASMESDPKP

FIGURE 425

CCGAGCGCCAGCGCGGGGAACCGGGAAAAGGAAACCGTGTTGTGTACGTAAGATTCAGGAAACGAAACCAGGAGC
CGCGGGTGTTGGCGCAAAGGTTACTCCCAGACCCTTTTCCGGCTGACTTCTGAGAAGGTTGCGCACAGCTGTGCC
CGGCAGTCTAGAGGCGCAGAAGAGGAAGCCATCGCCTGGCCCCGGCTCTCTGGACCTTGTCTCGCTCGGGAGCGG
AAACAGCGGCAGCCAGAGAACTGTTTTAATC**ATG**GACAAACAAAACTCACAGATGAATGCTTCTCACCCGGAAAC
AAACTTGCCAGTTGGGTATCCTCCTCAGTATCCACCGACAGCATTCCAAGGACCTCCAGGATATAGTGGCTACCC
TGGGCCCCAGGTCAGCTACCCACCCCCACCAGCCGGCCATTCAGGTCCTGGCCCAGCTGGCTTTCCTGTCCCAAA
TCAGCCAGTGTATAATCAGCCAGTATATAATCAGCCAGTTGGAGCTGCAGGGGTACCATGGATGCCAGCGCCACA
GCCTCCATTAAACTGTCCACCTGGATTAGAATATTTAAGTCAGATAGATCAGATACTGATTCATCAGCAAATTGA
ACTTCTGGAAGTTTTAACAGGTTTTGAAACTAATAACAAATATGAAATTAAGAACAGCTTTGGACAGAGGGTTTA
CTTTGCAGCGGAAGATACTGATTGCTGTACCCGAAATTGCTGTGGGCCATCTAGACCTTTTACCTTGAGGATTAT
TGATAATATGGGTCAAGAAGTCATAACTCTGGAGAGACCACTAAGATGTAGCAGCTGTTGTTGTCCCTGCTGCCT
TCAGGAGATAGAAATCCAAGCTCCTCCTGGTGTACCAATAGGTTATGTTATTCAGACTTGGCACCCATGTCTACC
AAAGTTTACAATTCAAAATGAGAAAAGAGAGGATGTACTAAAAATAAGTGGTCCATGTGTTGTGTGCAGCTGTTG
TGGAGATGTTGATTTTGAGATTAAATCTCTTGATGAACAGTGTGTGGTTGGCAAAATTTCCAAGCACTGGACTGG
AATTTTGAGAGAGGCATTTACAGACGCTGATAACTTTGGAATCCAGTTCCCTTTAGACCTTGATGTTAAAATGAA
AGCTGTAATGATTGGTGCCTGTTTCCTCATTGACTTCATGTTTTTTGAAAGCACTGGCAGCCAGGAACAAAAATC
AGGAGTGTGG**TAG**TGGATTAGTGAAAGTCTCCTCAGGAAATCTGAAGTCTGTATATTGATTGAGACTATCTAAAC
TCATACCTGTATGAATTAAGCTGTAAGGCCTGTAGCTCTGGTTGTATACTTTTGCTTTTCAAATTATAGTTTATC
TTCTGTATAACTGATTTATAAAGGTTTTTGTACATTTTTTAATACTCATTGTCAATTTGAGAAAAAGGACATATG
AGTTTTTGCATTTATTAATGAAACTTCCTTTGAAAAACTGCTTTGAATTATGATCTCTGATTCATTGTCCATTTT
ACTACCAAATATTAACTAAGGCCTTATTAATTTTTATATAAATTATATCTTGTCCTATTAAATCTAGTTACAATT
TATTTCATGCATAAGAGCTAATGTTATTTTGCAAATGCCATATATTCAAAAAAGCTCAAAGATAATTTTCTTTAC
TATTATGTTCAAATAATATTCAATATGCATATTATCTTTAAAAAGTTAAATGTTTTTTTAATCTTCAAGAAATCA
TGCTACACTTAACTTCTCCTAGAAGCTAATCTATACCATAATATTTTCATATTCACAAGATATTAAATTACCAAT
TTTCAAATTATTGTTAGTAAAGAACAAAATGATTCTCTCCCAAAGAAAGACACATTTTAAATACTCCTTCACTCT
AAAACTCTGGTATTATAACTTTTGAAAGTTAATATTTCTACATGAAATGTTTAGCTCTTACACTCTATCCTTCCT
AGAAAATGGTAATTGAGATTACTCAGATATTAATTAAATACAATATCATATATATATTCACAGAGTATAAACCTA
AATAATGATCTATTAGATTCAAATATTTGAAATAAAAACTTGATTTTTTTGT

FIGURE 426

MDKQNSQMNASHPETNLPVGYPPQYPPTAFQGPPGYSGYPGPQVSYPPPPAGHSGPGPAGFPVPNQPVYNQPVYN
QPVGAAGVPWMPAPQPPLNCPPGLEYLSQIDQILIHQQIELLEVLTGFETNNKYEIKNSFGQRVYFAAEDTDCCT
RNCCGPSRPFTLRIIDNMGQEVITLERPLRCSSCCCPCCLQEIEIQAPPGVPIGYVIQTWHPCLPKFTIQNEKRE
DVLKISGPCVVCSCCGDVDFEIKSLDEQCVVGKISKHWTGILREAFTDADNFGIQFPLDLDVKMKAVMIGACFLI
DFMFFESTGSQEQKSGVW

FIGURE 427

GTTTTCTTCGAAGATTTGGGGCTCCGCGATACAGTTAGG**ATG**GCTGTAGTACCTCTGCTGTTGTTGGGGGGTTTG
TGGAGCGCTGTGGGAGCGTCCAGCCTGGGTGTCGTTACTTGCGGCTCCGTGGTGAAGCTACTCAATACGCGCCAC
AACGTCCGACTGCACTCACACGACGTGCGCTATGGGTCAAGTAGTGGGCAGCAGTCAGTGACAGGTGTAACCTCT
GTGGATGACAGCAACAGTTACTGGAGGATACGGCGGAAGAGTGCCACAGTGTGTGAGAGGGGAACCCCCATCAAG
TGTGGCCAGCCCATCCGGCTGACACATGTCAACACTGGCCGAAACCTCCATAGTCACCACTTCACTTCACCTCTT
TCTGGAAACCAGGAAGTGACTGCTTTTGGTGAAGAAGGTGAAGGTGATTATCTGGATGACTGGACAGTGCTCTGT
AATGGACCCTACTGGGTGAGAGATGGTGAGGTGCGGTTCAAACACTCTTCCACTGAGGTACTGCTGTCTGTCACA
GGAGAACAATATGGTCGACCTATCAGTGGGCAAAAAGAGGTGCATGGCATGGCCCAGCCAAGTCAGAACAACTAC
TGGAAAGCCATGGAAGGCATCTTCATGAAGCCCAGTGAGTTGTTGAAGGCAGAAGCCCACCATGCAGAGCTG**TGA**

ATCTTGAGGCTCTGAGGCACTGTTAACGCACAATGTTCACAGACATCTGTTGCTGCCTCACCTTGGGATCCCTGC
CACAAGTTCCTTGGGCAGTGGCCATGTCACCATTGAGATGAAGATATACAACAGAGAAATAGTGGCTGTGTTTGG
GAAGCTTCAGCCCTGCACATTTTGAACTAGTCACTCTCCCAGACTTGGCGGTGGGTCAGTTCTTTCCTGAGTAGA
GGACTTGCTGGTAAAAGGGGCAGATGCTTTTTATTAGTACTGATTAAACCACACTGAGGGAAACATCCCTCTTAG
CTGGGAAACTGTTTACTCTTCAGGAGCTTGGCATCATGGACTGTTAATGTATGTGATTTTCCCCCTATTTTCTCT
CCCCCACAATGATAAAAACAATAATTTTATTATGA

FIGURE 428

MAVVPLLLLGGLWSAVGASSLGVVTCGSVVKLLNTRHNVRLHSHDVRYGSSSGQQSVTGVTSVDDSNSYWRIRRK
SATVCERGTPIKCGQPIRLTHVNTGRNLHSHHFTSPLSGNQEVTAFGEEGEGDYLDDWTVLCNGPYWVRDGEVRF
KHSSTEVLLSVTGEQYGRPISGQKEVHGMAQPSQNNYWKAMEGIFMKPSELLKAEAHHAEL

FIGURE 429

TGCGAACGGCGAGCAGCGGCGGCGGCGCGGAGAGACGCAGCGGAGGTTTTCCTGGTTTCGGACCCCAGCGGCCGG
ATGGTGAAATCCTCCCTGCAGCGGATCCTCAATAGCCACTGCTTCGCCAGAGAGAAGGAAGGGGATAAACCCAGC
GCCACCATCCACGCCAGCCGCACCATGCCGCTCCTTAGCCTGCACAGCCGCGGCGGCAGCAGCAGTGAGAGTTCC
AGGGTCTCCCTCCACTGCTGTAGTAACCCGGGTCCGGGGCCTCGGTGGTGCTCCTGATGCCCCTCACCCACCCCT
GAAGATCCCAGGTGGGCGAGGGAATAGTCAGAGGGATCACAATCTTTCAGCTAACTTATTCTACTCCGATGATCG
GCTGAATGTAACAGAGGAACTAACGTCCAACGACAAGACGAGGATTCTCAACGTCCAGTCCAGGCTCACAGACGC
CAAACGCATTAACTGGCGAACAGTGCTGAGTGGCGGCAGCCTCTACATCGAGATCCCGGGCGGCGCGCTGCCCGA
GGGGAGCAAGGACAGCTTTGCAGTTCTCCTGGAGTTCGCTGAGGAGCAGCTGCGAGCCGACCATGTCTTCATTTG
CTTCCACAAGAACCGCGAGGACAGAGCCGCCTTGCTCCGAACCTTCAGCTTTTTGGGCTTTGAGATTGTGAGACC
GGGGCATCCCCTTGTCCCCAAGAGACCCGACGCTTGCTTCATGGCCTACACGTTCGAGAGAGAGTCTTCGGGAGA
GGAGGAGGAG**TAG**GGCCGCCTCGGGGCTGGGCATCCGGCCCCTGGGGCCACCCCTTGTCAGCCGGGTGGGTAGGA
ACCGTAGACTCGCTCATCTCGCCTGGGTTTGTCCGCATGTTGTAATCGTGCAAATAAACGCTCACTCCGAATTAG
CGGTGTATTTCTTGAAGTTTAATATTGTGTTTGTGATACTGAAGTATTTGCTTTAATTCTAAATAAAAATTTATA
TTTTACTTTTT

FIGURE 430

MVKSSLQRILNSHCFAREKEGDKPSATIHASRTMPLLSLHSRGGSSSESSRVSLHCCSNPGPGPRWCSDAPHPPL
KIPGGRGNSQRDHNLSANLFYSDDRLNVTEELTSNDKTRILNVQSRLTDAKRINWRTVLSGGSLYIEIPGGALPE
GSKDSFAVLLEFAEEQLRADHVFICFHKNREDRAALLRTFSFLGFEIVRPGHPLVPKRPDACFMAYTFERESSGE
EEE

FIGURE 431

GATTGGAAGCAGAGGAAGCTGAAGAAAAGTAATGTAGTTTCCTTAAAGGCATACAAAGGACTGGCAGAAGTCGCT
GTGAAGAGCTTGTGTGAGCTGTTGGTGGCACTACCTCATTTTAACTTTCACAACAACATCATCGTATTGATTGTC
CCTCTC**ATG**AATGACATGTCAAAATTGATATCTGAAATGTGTTGTGAAGCTGTGAAGAAACTCTTTAAGCAAGAT
AAATTAGGCCAAGCTTCTCTTGGTGTAATTAAAGTGATTTCTGGTTTTGTGAAGGGCAGAAATTACGAAGTTAGG
CCAGAGATGTTAAAAACATTTTTATGCCTAAGAATCAAGGAAGTAGAAGTGAAAAAAGATACAGAAGACATTAAT
AAACCAAAAAAATTTATGACTTTCAAAGAAAAGAGAAAATCTCTATCAAGAATGCAGAGAAAGTGGAAGAAAGCA
GAAGAGAAACTAGCGCGAGAGCTTCGAGAGGCAGAAGCTTCAGAGAGTACTGAGAAAAAACTTAAACTGCACACA
GAGACTCTGAATATTGTGTTTGTAACCTACTTCAGAATATTGAAGAAGGCCCAGAGGTCACCTCTCCTGCCAGCA
GTTCTAGAAGGTCTTGCCAAGTTTGCTCACCTTATAAATGTGGAATTTTTTGATGATCTGTTAGTAGTTCTTCAT
ACTCTCATTGAGTCTGGTGACCTAAGCTATCAAGAAAGTCTTCACTGTGTCCAGACTGCTTTTCATATTCTTTCT
GGACAAGGTGATGTTCTGAATATTGATCCATTGAAATTCTACACACATCTCTACAAAACACTGTTCAAATTACAT
GCAGGTGCTACCAATGAAGGTGTTGAGATTGTACTCCAGTGCCTTGATGTCATGCTAACTAAGCGCAGAAAGCAA
GTTTCTCAGCAGCGAGCTCTTGCCTTCATCAAACGCCTTTGTACCCTTGCTCTTCATGTTCTTCCAAATTCAAGT
ATTGGCATTTTAGCAACTACCAGAATATTAATGCATACTTTCCCCAAAACAGATCTACTGCTTGACAGTGAATCT
CAGGGAAGTGGAGTTTTCCTTCCTGAACTGGATGAGCCTGAGTACTGCAATGCTCAGAACACTGCTCTGTGGGAA
CTGCATGCTCTGCGGAGGCATTATCATCCCATAGTGCAGAGATTTGCAGCCCACCTGATCGCTGGAGCACCTTCT
GAAGGCTCTGGAGCACTCAAACCAGAGTTGAGTCGAAGATCTGCTACTGAACTTTTTGAGGCATATAGCATGGCA
GAAATGACATTCAATCCTCCTGTTGAATCTTCAAACCCCAAAATAAAGGGTAAATTTTTACAAGGGGATTCATTT
TTGAATGAAGATTTAAATCAGCTAATCAAAAGATACTCCAGTGAAGTTGCTACTGAATCGCCTCTGGATTTCACG
AAATATTTGAAAACATCACTACAC**TAG**TAGAGGAATGAAGTCAGTGGACTTTCTTGTATATTTGTGTGTGCAGAT
GTACATAAAGATGAGTTGTTAACTTAGGATCTTTTCTTTTTATACAAGGAAAGCTTCCTAAGAATGTCTAGGAAG
AAGAGGAAGAATGACCCTTTGCATGGCACAGGGTTCTGCCCCTATTCTGAATATGTCATTCCATCAAGGAGATCA
AAAGCCTTTTTTTCTCCCCAGTATTTGGAAATTACTTTCTTGATGATGCTGCCTTTTAAAAGCTTCACGTACATT
ATAGTTTTTTAAAAAAATCTTTGGACTGGATCTTACTGAAGTGCAGTTGCTATATTAAAATTAGGGCATAGAGCA
CAGAAAAATCAAGACCATGAGAAGACATTTTACCATTTAGCTACTTTTTATAACTAAATACTCTTTAAATATTTT
TATTTCAATACTGTGGATGGAAATGAGAAGCATTCTAAATTTGAGTTAATATATTTTTATGAAGATATTTGAGAA
AAGAAAAAAATAGCTTGTATTCAGGTTCATTGGCTTTTGCTGGATGATCCACCTAAAGAAGTTACCTAATTTGGC
CTTTTAAAAAAGGTGTTAGTGTTTATTATAGCTACTTTCAAGGAAAGTTTGAATATGATTCTAGTCTCTAAAGTT
CTTCACGTTTTCTGACATTCCCTGGAGGGTGACTGGGGAAGAATTGCTCCAGGGTAGAAGAACCAGGCCCAAGAC
TTTACCATTCTGATCTAGAGACAAAGGATACTCAATGAGGAGCTTTTTTCCCCTCTTGGAACAGGTAAAATGCTT
TTTCTTATTAATATAATTATAAAACAGTATTTTATGTAACAGCTATTCCCATATTCTAGGAGTGGCCTAAGAAAT
GCGTGTTTCAGTGACTAGATTATAAATATTCTCTATTGTGAATAGTTGAATAAAACAGCTGTTTTTTTCTGCTTC
T

FIGURE 432

MNDMSKLISEMCCEAVKKLFKQDKLGQASLGVIKVISGFVKGRNYEVRPEMLKTFLCLRIKEVEVKKDTEDINKP
KKFMTFKEKRKSLSRMQRKWKKAEEKLARELREAEASESTEKKLKLHTETLNIVFVTYFRILKKAQRSPLLPAVL
EGLAKFAHLINVEFFDDLLVVLHTLIESGDLSYQESLHCVQTAFHILSGQGDVLNIDPLKFYTHLYKTLFKLHAG
ATNEGVEIVLQCLDVMLTKRRKQVSQQRALAFIKRLCTLALHVLPNSSIGILATTRILMHTFPKTDLLLDSESQG
SGVFLPELDEPEYCNAQNTALWELHALRRHYHPIVQRFAAHLIAGAPSEGSGALKPELSRRSATELFEAYSMAEM
TFNPPVESSNPKIKGKFLQGDSFLNEDLNQLIKRYSSEVATESPLDFTKYLKTSLH

FIGURE 433

GGTGGCCCTGAGCGCCGGCGACACCTTTCCTGGACTATAAATTGAGCACCTGGGATGGGTAGGGGGCCAACGCAG
TCACCGCCGTCCGCAGTCACAGTCCAGCCACTGACCGCAGCAGCGCCCTTGCGTAGCAGCCGCTTGCAGCGAGAA
CACTGAATTGCCAACGAGCAGGAGAGTCTCAAGGCGCAAGAGGAGGCCAGGGCTCGACCCACAGAGCACCCTCAG
CCATCGCGAGTTTCCGGGCGCCAAAGCCAGGAGAAGCCGCCCATCCCGCAGGGCCGGTCTGCCAGCGAGACGAGA
GTTGGCGAGGGCGGAGGAGTGCCGGGAATCCCGCCACACCGGCTATAGCCAGGCCCCCAGCGCGGGCCTTGGAGA
GCGCGTGAAGGCGGGCATCCCCTTGACCCGGCCGACCATCCCCGTGCCCCTGCGTCCCTGCGCTCCAACGTCCGC
GCGGCCACC**ATG**ATGCAAATCTGCGACACCTACAACCAGAAGCACTCGCTCTTTAACGCCATGAATCGCTTCATT
GGCGCCGTGAACAACATGGACCAGACGGTGATGGTGCCCAGCTTGCTGCGCGACGTGCCCCTGGCTGACCCCGGG
TTAGACAACGATGTTGGCGTGGAGGTAGGCGGCAGTGGCGGCTGCCTGGAGGAGCGCACGCCCCCAGTCCCCGAC
TCGGGAAGCGCCAATGGCAGCTTTTTCGCGCCCTCTCGGGACATGTACAGCCACTACGTGCTTCTCAAGTCCATC
CGCAACGACATCGAGTGGGGGGTCCTGCACCAGCCGCCTCCACCGGCTGGGAGCGAGGAGGGCAGTGCCTGGAAG
TCCAAGGACATCCTGGTGGACCTGGGCCACTTGGAGGGTGCGGACGCCGGCGAAGAAGACCTGGAACAGCAGTTC
CACTACCACCTGCGCGGGCTGCACACTGTGCTCTCGAAACTCACGCGCAAAGCCAACATCCTCACTAACAGATAC
AAGCAGGAGATCGGCTTCGGCAATTGGGGCCAC**TGA**GGCGTGGCGCCCGTGGCTGCCCAGCACCTTCTTCGACCC
ATCTCACCCTCTCTCATTCCTCAAAGCTTTTTTTTTTTTTCCTGGCTGGGGGGCGGGAAGGGCAGACTGCAAACT
GGGGGGCTGCGTACGTGCAGGAGGCGCGGTGGGGCTGCGTGGAGGAGGGGGCCACGTGTGAGAGAGAAGAAAATG
GTGGCCGGAGATGGGAGGGCCCAAGGAACCTCCTGGGAGGGGGCCTGCATTCTATGTTGGTGGGAATGGGACTGG
GCTGACGCCCTGCATTCAGCCTGTGCCTTTCCTGGGGTTTCTTTTCTGTTCTTTTCGGAGGAGAGGGCCCGAGAA
GGGGCCATACCAGGGCGCGGCGCTGGGTTGCCACACTTGGGAAAGCAGCCCGGAGCTGGGTGCTGGGGAAGGCGG
GGCGCGTAGCCTCCCGCCGCCCTGCGGTTGGGCCGGTGGAGGCCCAGGCGTTGCTAGGATTGCATCAGTTTTCCT
GTTTGCACTATTTCTTTTTGTAACATTGGCCCTGTGTGAAGTATTTCGAATCTCCTCCTTGCTCTGAAACTTCAG
CGATTCCATTGTGATAAGCGCACAAACAGCACTGTCTGTCGGTAATCGGTACTACTTTATTAATGATTTTCTGTT
ACACTGTATAGTAGTCCTATGGCACCCCCACCCCATCCCTTTCGTGCCACTCCCGTCCCCACCCCCACCCCAGTG
TGTATAAGCTGGCATTTCGCCAGCTTGTACGTAGCTTGCCACTCAGTGAAAATAATAACATTATTATGAGAAAGT
GGACTTAACCGAAATGGAACCAACTGACATTCTATCGTGTTGTACATAGAATGATGAAGGGTTCCACTGTTGTTG
TATGTCTTAAATTTATTTAAAACTTTTTTAATCCAGATGTAGACTATATTCTAAAAAATAAAAAAGCAAATGTG
TCAACT

FIGURE 434

MMQICDTYNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDNDVGVEVGGSGGCLEERTPPVPDSGS
ANGSFFAPSRDMYSHYVLLKSIRNDIEWGVLHQPPPPAGSEEGSAWKSKDILVDLGHLEGADAGEEDLEQQFHYH
LRGLHTVLSKLTRKANILTNRYKQEIGFGNWGH

FIGURE 435

GGCACGAGGCTCCAGC**ATG**GAGGAGGCCACCGGCTGTGCAGGGTTCAATCTCATCCACTTGGTGGCCACGGGCAT
CTCCTGCTTCTTGGGCTCTGGGCTCCTGACCCTAGCAGTGTACCTGTCTTGCCAGCACTGCCAGCGTCAGTCCCA
GGAGTCCACACTGGTCCATCCTGCCACCCCCAACCATTTGCACTACAAGGGCGGAGGCACCCCGAAGAATGAAAA
GTACACACCCATGGAATTCAAGACCCTGAACAAGAATAACTTGATCCCTGATGACAGAGCCAACTTCTACCCATT
GCAGCAGACCAATGTGTACACGACTACTTACTACCCAAGCCCCCTGAACAAACACAGCTTCCGGCCCGAGGCCTC
ACCTGGACAACGGTGCTTCCCCAACAGC**TGA**TACCGCCGTCCTGGGGACTTGGGCTTCTTGCCTTCATAAGGCAC
AGAGCAGATGGAGATGGGACAGTGGAGCCAGTTTGGTTTTCTCCCTCTGCACTAGGCCAAGAACTTGCTGCCTTG
CCTGTGGGGGGTCCCATCCGGCTTCAGAGAGCTCTGGCTGGCATTGACCATGGGGGAAAGGGCTGGTTTCAGGCT
GACATATGGCCGCAGGTCCAGTTCAGCCCAGGTCTCTCATGGTTATCTTCCAACCCACTGTCACGCTGACACTAT
GCTGCCATGCCTGGGCTGTGGACCTACTGGGCATTTGAGGAATTGGAGAATGGAGATGGCAAGAGGGCAGGCTTT
TAAGTTTGGGTTGGAGACAACTTCCTGTGGCCCCCACAAGCTGAGTCTGGCCTTCTCCAGCTGGCCCCAAAAAAG
GCCTTTGCTACATCCTGATTATCTCTGAAAGTAATCAATCAAGTGGCTCCAGTAGCTCTGGATTTTCTGCCAGGG
CTGGGCCATTGTGGTGCTGCCCCAGTATGACATGGGACCAAGGCCAGCGCAGGTTATCCACCTCTGCCTGGAAGT
CTATACTCTACCCAGGGCATCCCTCTGGTCAGAGGCAGTGAGTACTGGGAACTGGAGGCTGACCTGTGCTTAGAA
GTCCTTTAATCTGGGCTGGTACAGGCCTCAGCCTTGCCCTCAATGCACGAAAGGTGGCCCAGGAGAGAGGATCAA
TGCCATAGGAGGCAGAAGTCTGGCCTCTGTGCCTCTATGGAGACTATCTTCCAGTTGCTGCTCAACAGAGTTGTT
GGCTGAGACCTGCTTGGGAGTCTCTGCTGGCCCTTCATCTGTTCAGGAACACACACACACACACACTCACACACG
CACACACAATCACAATTTGCTACAGCAACAAAAAAGACATTGGGCTGTGGCATTATTAATTAAAGATGATATCCA
GTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 436

MEEATGCAGFNLIHLVATGISCFLGSGLLTLAVYLSCQHCQRQSQESTLVHPATPNHLHYKGGGTPKNEKYTPME
FKTLNKNNLIPDDRANFYPLQQTNVYTTTYYPSPLNKHSFRPEASPGQRCFPNS

FIGURE 437

GAAAAATGAAACGTCTTTGTGGTCCGGGGCTGAGACCCACGAGGAGACTGGGCGGGATTTCTGGCGTTAGGAGGC
GGGGCCTTTCGGCTTTGGGCGCGAGTGGT**TAA**AAGACAGTTGGTGTCGGTTCGGCTTCTCGGGTCGGATTCCGCG
GTCCCAACCCTTCCCCATGGCCGACCCTGAGGAGTTGCAGGTTTCTTCGCCGCCCCCGCCGCCTCCCTCTTCTCC
CTCCTCTTCAGACGCCTCTGCAGCATCTTCCCCGGGCGGCCCAGTGAGTTTGGGCTGGCCAGTTCCGAGCAGGAG
CAGCGGCCCAACGGTGGACCAGCTGGAGGAAGTGGAGCTGCAGATCGGAGACGCAGCCTTTTCATTAACCAAACT
TCTTGAAGCCACATCTGCAGTATCAGCTCAAGTGGAAGAACTTGCCTTCAAATGTACAGAAAATGCACGTTTCCT
TAAAACGTGGCGGGACCTCTTGAAAGAAGGCTATGATTCTTTGAAACCTGATGACTGATTTGGCATACTTCGTTG
TTTAATAATGACTGCAATAATTCATACTTCTTATGTCATATTTTGTACATGTACCACACATATAGGATGACCTCT
GTCCAGCAGTTCTGTATATACTCAGAATGAAATTTTTCTTGGTTTTCTTGGTTTTTGTGAAAGCAGAATACCGAT
GCTATTTTTGTTGCGGACCAGTACTTGTTTGTCCTTAAATACTTTATGCCTCTGAACTTTCATAGAATCCTTTAT
GAAAGTTAACTTCATCAATAGACGGTTAATATTAATAGAGCCACAGTGCTACCAGTAGCAAACTAGGTAGACCAT
TATTTGTTTTGCAACAAGATGCTAAGCATGGCAGACTTTGAAGTTGCGTTTCATCTTAAGGACCAAGGGAGGTAA
CTTTAAGGTTGCCAGTGGTGGATCCAGCTCCGTTAGGCTAAGTTGTCTACAGCTAATGATTGTGTCTTTATTCTA
TATCCCCAGCACCTAAAACAGGGTCACACAACATTCACTAAATGTTTGTTGAATAAAAGAGTTAACAAACATAAT
TGAAAGCTTTTTTTCTTCCTATATTTAGCATGAAGACTGTCATTGTTTCTCTAGGAAATGTATGAATCTGAACTT
TTTTGACTTGAAGAAAAACATTCTTTTTTTACAGAGATTTGGACTTTGATGATAGGTTTTAAAAATATATGATAA
ATATTTTTTGTACTTGTTTGATTTTTTTTTTAAAGACTTTACTTCAGAAAGGGAAAGACTGTTTAGAAAGAATGC
ATATTTTTTCCCTATTTATTTCTGTGGTTACTGCTTTTGCAGTTTAACAGTGTTTGTATTTGATATTTGTATATG
TTTGATTGCTATCTTTAAAGTGCCTTATCAGATTTATGGGCTCTGTGCTATTACTTTTTGAGCTTTGCAAGTTGT
GTACATAATAATTCTAAAGAAGTTACTTTGTTTGCAATGCATCAAATTTAAATGATGTGATTTTTTTTGTATTAT
TTGATCTTAGTGACAGTGTTCTATTTTGCATCCTGTATCTTATGTTGCTTTTGGTGTTTTGTGTTGTGTGTCAAC
GATTAAGCCAACTAATTCTCTACCATATATAACTTCTGGACATTTTTGATACAACATCTTAATTCTTTGTAGATA
TGGAGATAGGTACAGAACTATATTCTAATGCCCCACAATGGGGCTATGAGAGGGGACAGATGGATGGGCAAAGAA
TAGTTTTGTTTAACATATTAGGTCATAGTTCTTGATTAGTTTTTTTAGTTAAAGATAAACACATAGGGTGTGATT
TCTATACCAAAGATATGCTTATTTCAGTATTAGAAAAATATTCTTCTTACATCTCCTGAAAATTGCAATTTTTAA
AATGTGTAAAAATAAATTATTATTAAAAGCACATTTTATTTCCATTTGTTTGGATTCATTACCTTAAAACTTTAT
TGACATATTTCAAAGATATAGGAAAGGTAAATGATTTCAAGAAAATCCGTGTATTTCTACCATGCAGATGTAATA
AATGTTAGCATTTGGCTATATTTTCTTCAGACACACATATGCATGTAATTGCAAATGTTAGATACATTTGAAGTT
TGCTTTGTTACCTGTTTGATCCTGTCCCGTTCCTCCCTCCCCAGAGTCCCCAGAGGTAACCACTAGAGGGGGCAT
AATATAGCATGTGTTTTTATATTTTTAATACAAATATATTTTTTAAAAGCGCTACAAAATATTGTTTTATATATG
TGGTAGCCAGCTTCCAGATGGCCCCAGTGATCCCTGGCCTCCTGGTGTTCATGCCCCAGTATAGCCTTCTCCTGC
ATTTTACAGTGCTGACTTTTGTAACTACCAGGATATTGAGCAAATGCAGTGTGTGATTTCTGAGGCCATANNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAGCACTGGGAGTACAGGC
ATTTTTGCTCATTTTTCTATGTTGTTTTTTTTACTTGTCAGTTTTTAGATATTACATATTTTGAATACTAATGAT
CTGTTATGTATGTTCCAATTATCTTTTTTAGTCTGGTTTGTCTTCATATTTTGGTTATGAAATCTTGAATTTTTA
AAAACGTAATTTTACCAATCTTTCATAATGATTTGCTTTTTCTGGTTTTTGTATAGGAAATGTCATAAAAAATAGT
CCTATTCAGCCTTCCAAAAGTTACAAAATTTTTGGTTTTTAACATTTAGATGTTTAGTCCAACTGGAAATTGGTT
TCCTTTTATGGCATGATTTTGGAATCTTGTTTTAATTATTTTTACATATTTATAGCTGTTCCTCCAAGTATCAAT
TTTTCAAGTGCAACATCTGTCATGCAGTTACTATGTAAGGGCCAGATTCTGACCTTTCTGTTCTTTTTATCTGAA
GGAAATTTGAACATGCCACCCCCAAATATGCCGATTTGGCATACTGATTATTTCGAGCTAAAGGTGCTTGACTAA
CAGTAGTTGCAGAAATGGCTATTTTAACTGTCCTTTCCTACCTGTAGCAAGCCATACAAACTTCTTTGATAAAGA
TGCTTTCCTGATACCAAGATGAGAAGATGGCTCTAATCAGCTGAGACAGCACCAGAGGAATCTACAAACAAGAAA
CTATTAGTTTCTTAACATATATTTACCTTCCACAGTTTCTGCCTCTGGAAGCCTAAAACTGCTTTCCTTCGTCTT
GTCACACTTCTCTGAAATGTATTCTTTGTGGAAGATGCTATATAGTCCAGAGTTGTAAGCCACTACTTGTGTTTA
CCTTTTCATTGAGTTTTCTCCTGTGTGATGTACGTTGCATATATTAATAAAATTACTTGTTTTTCTCTT

FIGURE 438

KMKRLCGPGLRPTRRLGGISGVRRRGLSALGASG

FIGURE 439

ACAGAG**<u>ATG</u>**GCACTGATGCAGGAACTGTATAGCACACCAGCCTCCAGGCTGGACTCCTTCGTGGCTCAGTGGCTG
CAGCCCCACCGGGAGTGGAAGGAAGAGGTGCTAGACGCTGTGCGGACCGTGGAGGAGTTTCTGAGGCAGGAGCAT
TTCCAGGGGAAGCGTGGGCTGGACCAGGATGTGCGGGTGCTGAAGGTAGTCAAGGTGGGCTCCTTCGGGAATGGC
ACGGTTCTCAGGAGCACCAGAGAGGTGGAGCTGGTGGCGTTTCTGAGCTGTTTCCACAGCTTCCAGGAGGCAGCC
AAGCATCACAAAGATGTTCTGAGGCTGATATGGAAACCATGTGGCAAAGCCAGGACCTGCTGGACCTCGGGCTC
GAGGACCTGAGGATGGAGCAGAGAGTCCCCGATGCTCTTGTCTTCACCATCCAGACCAGGGGGACTGCGGAGCCC
ATCACGGTCACCATTGTGCCTGCCTACAGAGCCCTGGGGCCTTCTCTTCCCAACTCCCAGCCACCCCCTGAGGTC
TATGTGAGCCTGATCAAGGCCTGCGGTGGTCCTGGAAATTTCTGCCCATCCTTCAGCGAGCTGCAGAGAAATTTC
GTGAAACATCGGCCAACTAAGCTGAAGAGCCTCCTGCGCCTGGTGAAACACTGGTACCAGCAGTATGTGAAAGCC
AGGTCCCCCAGAGCCAATCTGCCCCCTCTCTATGCTCTTGAACTTCTAACCATCTATGCCTGGGAAATGGGTACT
GAAGAAGACGAGAATTTCATGTTGGACGAAGGCTTCACCACTGTGATGGACCTGCTCCTGGAGTATGAAGTCATC
TGTATCTACTGGACCAAGTACTACACACTCCACAATGCAATCATTGAGGATTGTGTCAGAAAACAGCTCAAAAAA
GAGAGGCCCATCATCCTGGATCCGGCCGACCCCACCCTCAACGTGGCAGAAGGGTACAGATGGGACATCGTTGCT
CAGAGGGCCTCCCAGTGCCTGAAACAGGACTGTTGCTATGACAACAGGGAGAACCCCATCTCCAGCTGGAACGTG
AAGAGGGCACGAGACATCCACTTGACAGTGGAGCAGAGGGGTTACCCAGATTTCAACCTCATCGTGAACCCTTAT
GAGCCCATAAGGAAGGTTAAAGAGAAAATCCGGAGGACCAGGGGCTACTCTGGCCTGCAGCGTCTGTCCTTCCAG
GTTCCTGGCAGTGAGAGGCAGCTTCTCAGCAGCAGGTGCTCCTTAGCCAAATATGGGATCTTCTCCCACACTCAC
ATCTATCTGCTGGAGACCATCCCCTCCGAGATCCAGGTCTTCGTGAAGAATCCTGATGGTGGGAGCTACGCCTAT
GCCATCAACCCCAACAGCTTCATCCTGGGTCTGAAGCAGCAGATTGAAGACCAGCAGGGGCTTCCTAAAAAGCAG
CAGCAGCTGGAATTCCAAGGCCAAGTCCTGCAGGACTGGTTGGGTCTGGGGATCTATGGCATCCAAGACAGTGAC
ACTCTCATCCTCTCGAAGAAGAAAGGAGAGGCTCTGTTTCCAGCCAGT**<u>TAG</u>**TTTTCTCTGGGAGACTTCTCTGTA
CATTTCTGCCATGTACTCCAGAACTCATCCTGTCAATCACTCTGTCCCATTGTCTACTGGGAAGGTCCCAGGTCT
TCACCAGTTTTACAATGAGTTATCCCAGGCCAGACGTGGTAGCTCACACCTGTAATCCCAGAACTTTGGGAGGCC
GAGGTGGGAGGAGCGCTTGAGCCGAGGAGTTCAAGACCAGCCTGGGTATCATAGGGAGACCCCGTCTCTACAAAA
TAAAAAAATAATTCACTGGG

FIGURE 440

MALMQELYSTPASRLDSFVAQWLQPHREWKEEVLDAVRTVEEFLRQEHFQGKRGLDQDVRVLKVVKVGSFGNGTV
LRSTREVELVAFLSCFHSFQEAAKHHKDVLRLIWKTMWQSQDLLDLGLEDLRMEQRVPDALVFTIQTRGTAEPIT
VTIVPAYRALGPSLPNSQPPPEVYVSLIKACGGPGNFCPSFSELQRNFVKHRPTKLKSLLRLVKHWYQQYVKARS
PRANLPPLYALELLTIYAWEMGTEEDENFMLDEGFTTVMDLLLEYEVICIYWTKYYTLHNAIIEDCVRKQLKKER
PIILDPADPTLNVAEGYRWDIVAQRASQCLKQDCCYDNRENPISSWNVKRARDIHLTVEQRGYPDFNLIVNPYEP
IRKVKEKIRRTRGYSGLQRLSFQVPGSERQLLSSRCSLAKYGIFSHTHIYLLETIPSEIQVFVKNPDGGSYAYAI
NPNSFILGLKQQIEDQQGLPKKQQQLEFQGQVLQDWLGLGIYGIQDSDTLILSKKKGEALFPAS

FIGURE 441

CTTTCCGTCCCCTTGCTTCGTCTTCGCTTTTCTTTCTACTTATTCTTATCTGTGTCTTTCGCTTTGTTTGCCTCT
CCGTCTGTTTTCCCTCAGGGCCCCCTTCTTTCCTCGACCTTTTCAAATCGCAAAT**ATG**GCGCCGGAGCGGCTGCG
GAGCCGGGCGCCCTCCGCCTTCAAGTTGCGGGGCTTGCTGCTCCGTGGTGAAGCTATTAAGTACCTCACAGAAGC
TCTTCAGTCTATCAGTGAATTAGAGCTTGAAGATAAACTGGAAAAGATAATTAATGCAGTTGAGAAGCAACCCTT
GTCATCAAACATGATTGAACGATCTGTGGTGGAAGCAGCAGTCCAGGAATGCAGTCAGTCTGTTGATGAAACTAT
AGAGCACGTTTTCAATATCATAGGAGCATTTGATATTCCACGCTTTGTGTACAATTCAGAAAGAAAAAAATTTCT
TCCTCTGTTAATGACCAACCACCCTGCACCAAATTTATTTGGAACACCAAGAGATAAAGCAGAGATGTTTCGTGA
GCGATATACCATTTTGCACCAGAGGACCCACAGGCATGAATTATTTACTCCTCCGGTGATAGGTTCTCACCCTGA
TGAAAGCGGAAGCAAATTCCAGCTTAAAACAATAGAAACCTTATTGGGTAGTACAACCAAAATCGGAGATGCGAT
TGTTCTTGGAATGATAACGCAGTTAAAAGAGGGAAAATTTTTCTGGAAGATCCTACTGGAACAGTCCAACTAGA
CCTTAGTAAAGCTCAGTTCCATAGTGGTTTATACACAGAGGCATGCTTTGTCTTAGCAGAAGGTTGGTTTGAAGA
TCAAGTGTTTCATGTCAATGCCTTTGGATTTCCACCCACTGAGCCCTCTAGTACTACTAGGGCATACTATGGAAA
TATTAATTTTTTTGGAGGTCCTTCTAATACATCTGTGAAGACTTCTGCAAAACTAAAACAGCTAGAAGAGGAGAA
TAAAGATGCTATGTTTGTGTTTTTATCTGATGTTTGGTTGGACCAGGTGGAAGTATTGGAAAAACTTCGCATAAT
GTTTGCTGGTTATTCACCAGCACCTCCAACCTGCTTTATTCTGTGTGGTAATTTTTCATCTGCACCATATGGAAA
AAATCAAGTTCAAGCTTTGAAAGATTCCCTAAAAACTTTGGCAGATATAATATGTGAATACCCAGATATTCACCA
AAGTCGTTTTGTGTTTGTACCTGGTCCAGAGGATCCTGGATTTGGTTCCATCTTACCAAGGCCACCACTTGCTGA
AAGCATCACTAATGAATTCAGACAAAGGGTACCATTTTCAGTTTTTACTACTAATCCTTGCAGAATTCAGTACTG
TACACAGGAAATTACTGTCTTCCGTGAAGACTTAGTAAATAAAATGTGCAGAAACTGCGTCCGTTTTCCTAGCAG
CAATTTGGCTATTCCTAATCACTTTGTAAAGACTATCTTATCCCAAGGACATCTGACTCCCCTACCTCTTTATGT
CTGCCCAGTGTATTGGGCATATGACTATGCTTTGAGAGTGTATCCTGTGCCCGATCTACTTGTCATTGCAGACAA
ATATGATCCTTTCACTACGACAAATACCGAATGCCTCTGCATAAACCCTGGCTCTTTTCCAAGAAGTGGATTTTC
ATTCAAAGTTTTTTATCCTTCTAATAAGACAGTAGAAGATAGCAAACTTCAAGGCTTT**TGA**GATTCTTAAAGATC
ATCTGAAGAAAATTCATCAGTTTTCTGCTTAACTCTATATCTTATGTGATTCTGATATTACAATAAAATTATGGT
AAACTTT

FIGURE 442

MAPERLRSRAPSAFKLRGLLLRGEAIKYLTEALQSISELELEDKLEKIINAVEKQPLSSNMIERSVVEAAVQECS
QSVDETIEHVFNIIGAFDIPRFVYNSERKKFLPLLMTNHPAPNLFGTPRDKAEMFRERYTILHQRTHRHELFTPP
VIGSHPDESGSKFQLKTIETLLGSTTKIGDAIVLGMITQLKEGKFFLEDPTGTVQLDLSKAQFHSGLYTEACFVL
AEGWFEDQVFHVNAFGFPPTEPSSTTRAYYGNINFFGGPSNTSVKTSAKLKQLEEENKDAMFVFLSDVWLDQVEV
LEKLRIMFAGYSPAPPTCFILCGNFSSAPYGKNQVQALKDSLKTLADIICEYPDIHQSRFVFVPGPEDPGFGSIL
PRPPLAESITNEFRQRVPFSVFTTNPCRIQYCTQEITVFREDLVNKMCRNCVRFPSSNLAIPNHFVKTILSQGHL
TPLPLYVCPVYWAYDYALRVYPVPDLLVIADKYDPFTTTNTECLCINPGSFPRSGFSFKVFYPSNKTVEDSKLQG
F

FIGURE 443

GCGGCTCTCTGATCCAGCCCGGGAGAGGACCGAGCTGGAGGAGCTGGGTGTGGGGTGCGTTGGGCTGGTGGGGAG
GCCTAGTTTGGGTGCAAGTAGGTCTGATTGAGCTTGTGTTGTGCTGAAGGGACAGCCCTGGGTCTAGGGGAGAGA
GTCCCTGAGTGTGAGACCCGCCTTCCCCGGTCCCAGCCCCTCCCAGTTCCCCCAGGGACGGCCACTTCCTGGTCC
CCGACGCAACC**ATG**GCTGAAGAACAACCGCAGGTCGAATTGTTCGTGAAGGCTGGCAGTGATGGGGCCAAGATTG
GGAACTGCCCATTCTCCCAGAGACTGTTCATGGTACTGTGGCTCAAGGGAGTCACCTTCAATGTTACCACCGTTG
ACACCAAAAGGCGGACCGAGACAGTGCAGAAGCTGTGCCCAGGGGGGCAGCTCCCATTCCTGCTGTATGGCACTG
AAGTGCACACAGACACCAACAAGATTGAGGAATTTCTGGAGGCAGTGCTGTGCCCTCCCAGGTACCCCAAGCTGG
CAGCTCTGAACCCTGAGTCCAACACAGCTGGGCTGGACATATTTGCCAAATTTTCTGCCTACATCAAGAATTCAA
ACCCAGCACTCAATGACAATCTGGAGAAGGGACTCCTGAAAGCCCTGAAGGTTTTAGACAATTACTTAACATCCC
CCCTCCCAGAAGAAGTGGATGAAACCAGTGCTGAAGATGAAGGTGTCTCTCAGAGGAAGTTTTTGGATGGCAACG
AGCTCACCCTGGCTGACTGCAACCTGTTGCCAAAGTTACACATAGTACAGGTGGTGTGTAAGAAGTACCGGGGAT
TCACCATCCCCGAGGCCTTCCGGGGAGTGCATCGGTACTTGAGCAATGCCTACGCCCGGGAAGAATTCGCTTCCA
CCTGTCCAGATGATGAGGAGATCGAGCTCGCCTATGAGCAAGTGGCAAAGGCCCTCAAA**TAA**GCCCCTCCTGGGA
CTCCCTCAACCCCCTCCATTTTCTCCACAAAGGCCCTGGTGGTTTCCACATTGCTACCCAATGGACACACTCCAA
AATGGCCAGTGGGCAGGGAATCCTGGAGCACTTGTTCCGGGATGGTGTGGTGGAAGAGGGGATGAGGGAAAGAAA
TGGGGGGCCTGGGTCAGATTTTTATTGTGGGGTGGGGTGAGTAGGACAACATATTTCAGTAATAAAATACAGAAT
AAAAATCAAGTGTTTTTAAAAAAAA

FIGURE 444

MAEEQPQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPGGQLPFLLYGTEVHT
DTNKIEEFLEAVLCPPRYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPE
EVDETSAEDEGVSQRKFLDGNELTLADCNLLPKLHIVQVVCKKYRGFTIPEAFRGVHRYLSNAYAREEFASTCPD
DEEIELAYEQVAKALK

FIGURE 445

GATATCAATTCCGCCGGGAACTGGAGGAAGGAGACCCTGGCTTCGCAGGGGCCCCGGCTGGGGCAGAGGCGAGGG
GCCTGGGGGGGCGCTGGCTTTGGCCCCGCCTGGGGCAGG**ATG**GTGAATCTGGAGTCCATGCACACAGATATCAAG
ATGAGTGGGGATGTAGCCGATTCCACGGATGCTCGCAGCACTCTCAGCCAGGTGGAGCCAGGAAATGATCGAAAT
GGCCTAGATTTCAACAGGCAGATTAAAACCGAAGATCTCAGTGACTCCCTGCAGCAGACCCTCTCCCATCGGCCA
TGCCACCTGAGTCAAGGACCTGCCATGATGTCCGGAAACCAAATGTCTGGGCTAAATGCCAGCCCATGTCAGGAC
ATGGCTTCCCTCCATCCGCTCCAGCAGCTTGTGCTGGTTCCCGGCCACTTACAGTCTGTATCCCAGTTCCTGCTA
TCTCAGACCCAGCCTGGGCAGCAAGGTCTGCAGCCAAATCTCCTCCCCTTTCCACAGCAACAAAGCGGTCTCCTC
CTCCCACAGACTGGGCCGGGACTGGCATCCCAGGCATTTGGGCGCCCTGGGCTGCCAGGATCCTCTTTAGAACCC
CACCTGGAAGCATCCCAGCATCTCCCAGTGCCCAAGCATCTACCCAGCTCTGGAGGGGCCGATGAGCCCAGTGAC
CTCGAGGAGCTGGAGAAGTTTGCCAAGACCTTCAAGCAGAGGCGCATTAAGCTGGGCTTCACACAGGGAGATGTG
GGGCTGGCGATGGGAAAGCTGTATGGCAACGACTTCAGCCAGACCACCATCTCACGATTTGAGGCCCTCAACCTG
AGCTTCAAGAACATGTGCAAGCTCAAGCCCCTGCTGGAGAAGTGGCTGAATGATGCAGAGTCCTCTCCGTCAGAC
CCCTCAGTGAGCACGCCCAGCTCCTACCCCAGCCTCAGTGAAGTATTTGGTAGGAAGAGAAAGAAACGGACCAGC
ATCGAGACCAACATCCGCCTGACTCTGGAGAAGAGGTTTCAAGATAACCCAAAACCCAGCTCGGAGGAGATCTCC
ATGATTGCAGAGCAGTTGTCCATGGAGAAGGAGGTGGTGAGGGTCTGGTTCTGCAACCGACGCCAAAAGGAGAAG
CGAATCAACTGCCCTGTGGCCACACCCATCAAACCACCTGACTACAACTCCCGGCTGGTATCTCCCTCAGGGTCT
CTGGGCCCCCTCTCTGTCCCTCCTGTCCACAGTACCATGCCTGGAACAGTAACGTCATCCTGTTCCCCTGGGAAC
AACAGCAGGCCTTCATCTCCTGGCTCAGGACTCCACGCCAGCAGCCCCACTGCATCTCAAAATAACTCCAAAGCA
GCAGTGAACTCCGCCTCCAGTTTTAACTCTTCAGGATCTTGGTACCGATGGAATCATTCCACCTACCTCCAC**TGA**

GACCAAAAAGTTTCTCCTACTCCAGCTGGCCCTGTATTCCCCCTGGAAGGAAGGGAATCATGCCTTCTATATACA
GACAGATTGCCTTCAGAAGAGTGGAAGAAAATCTCCACTATCAATGAACCCAGACTCTTGTCTTCTTCAAGAGCA
AGGGCCTCCGGAGATCCAAACTGTGATTGAACCAAGTGCAGACTCCTAATGCTCTTGAAATACACAGCCCCTCCT
AGGAGCTTACCATTTTCACCTTCCTTGCCTATGCCCTTGCCTTCTAGTTCCAAATATTTTAGCCAGCTTCACTGT
GGCAATAGTCTTTCAGAGAAAAGACTTCTTGCTGTTATTCTCCAACTCATCCGTGGGCTTCTGGGGACAGCCATT
TGGCTGGGGTGCCAAACACCAGAAGGGGAGATAATAGTTTTGACTCTGAACTTGGCCACAACCCCTGAACTGATC
CCAAAATCTGTGAAAAGATTTGAATCTGATATCTCCACCAAAGCCTTGATGTTTTCTCTGTACAGCTAAGTTTTC
TGATGGAATCTTCATCTCACCCCATTTTCTTTTTAACCTCGCCCCCTTTTCTACAATCAAATCCATTCATTATTG
CGCCCTCCAGGTCCCCTCCTTTTTGCAGAAGGTGTAAAAGAGCTGCCCTTGGTGGGTGCCCTGGGCATGTTGCAA
CGCCTGCTGGTGCCCTTCTGTCTGTCCACGTCTGCCTAGGGCTCAGGAGTGCTTGTTCTTTCCCTTCCTCCCTGT
GTTTCTCTTTATCCTGTCCCCTCTCCTTTCTCCTGGCAGCAGAAAAGGAAGAACACAAGAGCAAACACACAACAA
TGATGGTGGCAAAGTACCTGTATATAGCCCTTTCCCATTTTTTGCATTATGTTCTTAACTCCTTAATGTGGAATT
TTCCAGCGAAATGTTTAACTCAGGTGTGATTTTTG

FIGURE 446

MVNLESMHTDIKMSGDVADSTDARSTLSQVEPGNDRNGLDFNRQIKTEDLSDSLQQTLSHRPCHLSQGPAMMSGN
QMSGLNASPCQDMASLHPLQQLVLVPGHLQSVSQFLLSQTQPGQQGLQPNLLPFPQQQSGLLLPQTGPGLASQAF
GRPGLPGSSLEPHLEASQHLPVPKHLPSSGGADEPSDLEELEKFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFS
QTTISRFEALNLSFKNMCKLKPLLEKWLNDAESSPSDPSVSTPSSYPSLSEVFGRKRKKRTSIETNIRLTLEKRF
QDNPKPSSEEISMIAEQLSMEKEVVRVWFCNRRQKEKRINCPVATPIKPPDYNSRLVSPSGSLGPLSVPPVHSTM
PGTVTSSCSPGNNSRPSSPGSGLHASSPTASQNNSKAAVNSASSFNSSGSWYRWNHSTYLH

FIGURE 447

CAGGAAGGATTCAGACAACTCTGCCTGGGAGTGAGGGCTCTGCTCAGCGGCCTAGACCTGGGCACAACGGAGCAG
GCCACTCCGTTTCTCATCACAGACCTGAAGGCAGATGGCCTGGGCGTCGGGCTTCCTCTGCTCTCTGGCGGGGCG
ATTTTCACGGTCACCAGGCTGCGGACAGGCTGTGGGGGTGGCGGGCGGTCCAAAGCCACCGCTTCACGTAGGCCA
GGGGAGCCTTGGAGAAATCAGGCCTGATGTTGCTCAGCAGCGGCAGCCTGTTGGGAAAGCACCTCCAGGCCTCGG
GGACCATCTCTCTCAGGACGCGGATGCGGGCGGGGACCATCTCTCTCTGGATGCAGATGCGGGTGTAGTCCCAGC
TGGGAGGAGTGGTGCGGAGGGGCCGGATGCGGACCCAGTGCTTCCTGTGGAAGTAGGTGACCTTGCAGTTCTCCT
GGACCTGGGAGCTGAGGAAGGGCCTGGACTGCAGAACCCAGTGCTTTTGGGCGGGGCGCAGCTTTCTGGCAAGCG
GCTTGGGCCTTCCAGTAGACACTGGGCTGCCAGAAGTTTCCGAAATCTGCGGTCAAGGCCAGAGATCAAATGTCA
GGGCTCAGTGACTAGCGACGGTTGGCATCAAAATGTTGGAAAGTGCACAAGGCGCCGTGTGCCAGGTACGGTCTG
TCCACCAACTGTTGCATGGGGCAGGAGGCCACGGCCAGGCCACAGCTTTGCCGCGCGCAGCTGCAGAAGGGGCAA
GTAGCGCCCCATGCTGTCTGGAGGACCAAGGAGGCTCAAGCCTGTCCTTCCCACTCATGGTCCCAGACACTTAGC
TCTGGGCAGAGGGGCCTGGCAGCTGTCTCTGCTTTTGTACCTGACCTTTAAAGGCAGAACATAGAAGAATTTCTG
CCAGGTCCTGAAAACTGCAGATACCTGTTGACAGAAGGGTGCTCTCTTTGATCAGTGTGAAAATGATCACAATAC
ACTTGGAGGCTCTTTTAAGGAAAAACAAATCATTTGCTCATATTCGTCTAGGATGACTGTTAATATCACTTTTTG
CAATTTTGCTCTTAAGAAAACGGTGAAAGCCATCAGGATTTATGTTTTAGTACCTGTAATGCTGATTTTATGTTG
ACCCTCATAATTTTCAGTGTTCACACAGCCATATATACATAATCTTCTCTAAACACTAATGCCATTTCTGTCCTT
TCATTTCTATTGGTAATCCTGGAGTAGAGTGAGGCACATTTTCCACTAATAGCTGAAAAGATCTAACTTCAAAAA
CAAAGAATCCAAAGGCTGCTTAGTAACTGTAGTGCCTAAGTTTAGAGTCTGTTCAAGGTGGTGTGAAAAGTTTTT
TGGGGGGGGGGCATTTCCCTCAAAAGCACGTGGAGAAGGAACCTATTGACCCTCTGGAATGCCAGAATCGGGAAG
AGACAAAAAAGTCGCAACCAATTGAAGATTGGGCAATAGATTTGGCCCAGACTGAGGCAGATGGGTGAATAGTAA
AAACAATAATTTGGAAAAACCCATGAAGGTAACTAACGGAAGGAAAAACTAAGAGAATGAAAAGTATTTGCCTCT
GGAAAGAACAACTGGCAGGACTGTTGTTTTCATTGTAAGACTTTTGGAGCCATTTAATTGTACTTAACCATTTTC
ATCTATTTCTTTAATAAGAACAATTCCATCTTAATAAAGAGTTACACTTGTTAATAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAGCG

FIGURE 448

MAWASGFLCSLAGRFSRSPGCGQAVGVAGGPKPPLHVGQGSLGEIRPDVAQQRQPVGKAPPGLGDHLSQDADAGG
DHLSLDADAGVVPAGRSGAEGPDADPVLPVEVGDLAVLLDLGAEEGPGLQNPVLLGGAQLSGKRLGPSSRHWAAR
SFRNLRSRPEIKCQGSVTSDGWHQNVGKCTRRRVPGTVCPPTVAWGRRPRPGHSFAARSCRRGK

FIGURE 449

ACCACCCCAGTGAAACCCACAGAACCATGTACACCCTCTAAGTCCCGAAGTGCCAGCTCAGAGGAGGCCTCAGAG
TCACCTACAGCCCGGCAGATCCCCCCAGAGGCACGTCGGCTCATAGTGAACAAAAATGCTGGTGAGACCCTCCTG
CAGAGGGCGGCGCGTCTTGGCTATAAGGATGTTGTTCTCTACTGCCTCCAGAAAGACAGTGAAGATGTGAATCAC
CGTGACAATGCTGGCTACACAGCCCTGCATGAGGCTTGTTCCCGGGGCTGGACCGACATCCTGAACATCCTGCTG
GAGCACGGGGCCAACGTGAACTGCAGTGCGCAGGACGGCACGAGGCCAGTTCATGATGCGGTGGTCAATGACAAC
CTGGAGACCATCTGGCTCCTGCTGTCCTATGGGGCCGATCCCACACTGGCTACCTACTCGGGTCAGACAGCC**ATG**

AAGCTGGCCAGCAGCGACACCATGAAGCGCTTTCTCAGTGATCACCTCTCGGATCTTCAGGGCCGGGCAGAGGGT
GATCCCGGTGTATCCTGGGATTTTTACAGCAGTTCTGTGTTGGAGGAAAAAGACGGGTTTGCCTGTGACCTCCTA
CATAATCCTCCTGGGAGCTCAGATCAAGAAGGAGACGATCCGATGGAGGAGGATGATTTCATGTTTGAACTCTCA
GACAAGCCTCTTCTCCCTTGCTACAACCTCCAAGTGTCAGTGTCCCGCGGGCCCTGCAACTGGTTCCTCTTTTCC
GATGTCTTGAAGAGGCTGAAGCTTTCCTCGAGGATCTTTCAGGCCCGGTTCCCGCACTTTGAAATCACCACCATG
CCCAAGGCCGAGTTCTACAGGCAGGTGGCCTCCAGTCAGCTGCTGACCCCTGCCGAGAGGCCTGGAGGCTTGGAC
GACAGATCCCCCCCAGGCTCCTCTGAGACTGTGGAGCTGGTGCGGTACGAGCCAGACCTACTTCGGCTCCTAGGG
TCCGAGGTGGAATTCCAGTCTTGCAACAGT**TGA**CCGGGAAAACAGCCCCTCCTCTTCTTTCTCCTTCCGAGTTCG
CCCTTCCCCCACCTCCTTGTCTTTCCCCGACCGAGCACCAGACTGCAGAATGAGGCAATAATACGGACCAACAAG
AAGCCGCCTTATCAATGCCAGCATTAGCGACTGGACTGTTTTTGTTTTTTTGGTTACAATTAGTTCTCATCTCCC
TGTCGTCGTCATTGTTATCGTGGTTGCTGATGGGGGTGGAAAGTTGAACTCCATGTCTGAGGACAAGAGGTCCCG
GGGGTGGTGGGAGGTGGCGCCGGGGTCCCTTGGACTGGCCTCCTTGTTCATGACCAAGACCAAACCTGGGCCCTG
GATGGCCTTGGCCTGTCCCGAGGAGAAATGAGAAAATCCCAGATCTCTGAGCGCCCCCCAACTCCATTCCCCTGT
GTTCTTCTGTCTTCTGTAGTATTTATTTTATTAGTATTTAATTTGTATTGTTTCATTGGTTTCTGATAAGTCTGT
ATCACTGTGACGATTTGAGACAACTTGTTGTATTGAGGGACTTTCTGTACCTCCTTTTCTTTTTCTTTGTTGATG
AGCTCTGACAAAGCTATTCCCTGGTGTTTTTTTCCCCCACTGGGGAGGGGGTGAGGTGGAATGGGGTGGGGGAAC
ATGGACTTGTGACTAACGAAGCTGGTTGCTGCTGGCCCAGGGCTGGGGGCTTGGGGGTAAATCCTGAGGCTTTGG
TGCTCCCCCACCCACCCATTCCCGCCCTTTGCAGCAGCCCCGCTATCTTGAGATTAGTGTTGACAGGGAGGGGAG
GATTGTGAGGTGAGGGGTTAATAAGTTACTCTAATAAAGGAGCGTGGAGAAGGGATCTGAGGGGTGAGGGTGGCC
CCCCTCCTCACGCCTTCTTCACTGCCCCCCTCAGAGTGCACAATACGAGTTTGTTCCTGCCTCCACTCTCCCACC
CCGTTCTGGCCTCCCTGTCTCAAGATACTGAGCCTCTCACCTCCCAGCCCTCAGCCACCCCCATCCCTGCCCCTT
CTGAGACTCACAGCACCCCTTTCCTTCCTCTCCTCCCACCTCCTCCCTCAGCCCCTCATTCTCCTTGGGAATCTG
CAGAGGGCTCTGGGACTCACTGCCGGATGTGAAATCCAGGCGTCAGCTGTTTGCTAGGCAAGGGCAGGAAAGTGG
TCTCCAGCCCTTGCTCCACTCATGCCTGGGGGCCTGGGGCTGAGTGGTATCCCTACCTGGCCTCCCCCTGGCCTC
TGGGCCTCCAGCGCTGGGTTTGTCGAGTGAGAGAGAGAGAGGAGCTTGGGTTGCTTCCCTGTCCCCGCCCCCTCT
GTGGCATTGTCCCTCCCACTCTTATTTTTCTACCAATTGCTATTTTTCCGAACAATCCTTGTAGAGTATGTACCA
TCCAAAGGCAGGAGGGCCTCGCCGTGGCCGGCTCTGGTTGGAGATGGTACAGTTTTATTGTACAGGTGCTAAAAC
AACAACAACAAAAAAGAAAATGG

FIGURE 450

MKLASSDTMKRFLSDHLSDLQGRAEGDPGVSWDFYSSSVLEEKDGFACDLLHNPPGSSDQEGDDPMEEDDFMFEL
SDKPLLPCYNLQVSVSRGPCNWFLFSDVLKRLKLSSRIFQARFPHFEITTMPKAEFYRQVASSQLLTPAERPGGL
DDRSPPGSSETVELVRYEPDLLRLLGSEVEFQSCNS

FIGURE 451

ATCGAATAGGAGCCATCCGAGACAACCTGAGTGAAACGGCCAGCACCATGGCACTAGCTGGAGCCAGTATAACGG
GGAGTCTGTCAGGAAGTGCCATGGTAAACTGTTTTAACAGGTTGGAAGTACAAGCAGATGTACAGAAAGAACGGT
ACAGTCTAAGTGGAGAATCTGGCACAGTCAGCTTGGGAACAGTTAGTGATAATGCCAGCACCAAAGCAATGGCAG
GATCCATTCTGAATTCCTACATCCCATTGGACAAAGAAGGCAACAGTATGGAGGTGCAAGTAGATATTGAGTCAA
AGCCATCCAAATTCAGGCACAACAGTGGAAGCAGTAGTGTGGATGATGGCAGTGCCACCCGAAGTCATGCTGGCG
GTTCATCCAGTGGCTTGCCTGAAGGTAAATCTAGTGCCACCAAGTGGTCCAAAGAAGCAACAGCAGGGAAAAAAT
CAAAAAGTGGTAAACTGAGGAAAAAGGGTAACATGAAGATAAATGAGACGAGAGAGGACATGGATGCACAGTTGT
TAGAACAACAAAGCACGAACTCAAGTGAATTTGAGGCTCCATCCCTCAGTGACAGTATGCCTTCTGTAGCAGATT
CTCACTCTAGTCATTTTTCTGAATTTAGTTGTTCTGACCTAGAAAGCATGAAAACTTCTTGTAGTCATGGTTCCA
GTGATTATCACACCCGCTTTGCTACTGTTAACATTCTTCCTGAGGTAGAAAATGACCGTCTGGAAAATTCCCCAC
ATCAGTGTAGCATTTCTGTGGTTACCCAAACTGCTTCCTGTTCAGAAGTTTCACAGTTGAATCATATTGCTGAAG
AACATGGTAACAATGGAATAAAACCTAATGTTGATTTATATTTGGCGATGCACTAAAAGAAACAAATAACAACC
ACTCACATCAGACAATGGAATTAAAAGTTGCAATTCAGACTGAAATTTAGGCCCATAAATGCTGCAGAATAATTA
CCACTGTACAACCGTGTTTGGAGCTGGTTGAACTACATGTGACTACTTAAGTTTCAGGTTACCAGCAAAAGCCGG
GTTTCATTATCATAATGCAGATACATTTTCTGTGTTCAGCAAGGCATTGTGTGTCATGTGGATCTTAGTTACCAA
ACTATGAAGTGAAGGCTTTAAAAGTGCATTATTTTAAGGATAATAAATTTGAAGAGCAAAGCATGTTTTGTGTGT
TTGCCACAAAACATTGCTTGAAGCACATACTTAGATAGAAATTGGTCTTAATTTATATAATCAATATAAAATACT
AATGCAATTCTACAGCATTCAAATGAAGAAAACTTGAGGCTTTAGGGATAAGTGGTTAGTGATATTTTATTGAAA
CCACTAAAGAGATAAGTTTAAAAGAACTGCATAGGTTACTCTCAGTATATGATACTCTGTAACATTTCTATTTAT
ATCGGCATAAATTTCATTTTTTTCTTCATATGCAATGTGGTTATATAAAGCTTAATGCAGCTCATTTGCTACCA
TTTGGATACTTAGACACTTTGAGCAAGATTGTGGCAGTTTTGCACAACTTTGAAATAGAAATACCTGGTACTCT
ATCTTGTTTATTGTTGATGCCATCTTAGAGGAAAAAATGTAAAGGTAAGTAATTAAGCATATGACAGCAACAAAT
AAGATACATAAAACTACAAAATAAAGTCCCATTAGGTTATAAGTATTACAAAAAATCCACCTTTCTCTAAGGGGA
AGTTTGTACCCCATTGATTCTTGGTGCCTTTGGGATCGACTGGGTTTTAATGGCCTAGTTATTTGAGGATTTTGC
TGTGTTGTTTTCCATGTCTTCTCTGGTCACCTTGGATTATATATAAAAATACAGGAAATAGATAAACATGAATGT
GATTAATAATGCTGAAAAAGTATTAGCCTACCAAAGACACACTCAGGCTTTAGTGAATAACTTTACATAACCTCA
GTTTTTAACACATGCATATCTTCTCCAACCATGAAATCAAAGCACGGTGCAGAACTTGTACCAAGTACAAAAGGT
CCATGTATGATTAGCATTATTTTCTTTTGCTTTTGTTTATGGACAATGTTCAGCTGACATAAGCAGAAGTTGGCC
AAAATACTGCCTGTACTGTTAATTTCCTGTATAATTCACTTAAATAAAAGCAGGTTAACCTCAATGATAGCAGTT
AAAATGTTCTATCTTATGTATTTCTTTTAAGT

FIGURE 452

RIGAIRDNLSETASTMALAGASITGSLSGSAMVNCFNRLEVQADVQKERYSLSGESGTVSLGTVSDNASTKAMAG
SILNSYIPLDKEGNSMEVQVDIESKPSKFRHNSGSSSVDDGSATRSHAGGSSSGLPEGKSSATKWSKEATAGKKS
KSGKLRKKGNMKINETREDMDAQLLEQQSTNSSEFEAPSLSDSMPSVADSHSSHFSEFSCSDLESMKTSCSHGSS
DYHTRFATVNILPEVENDRLENSPHQCSISVVTQTASCSEVSQLNHIAEEHGNNGIKPNVDLYFGDALKETNNNH
SHQTMELKVAIQTEI

FIGURE 453

CACGAGGCCGCGGGGGCAAGGCCTGGAGCTGTGGTTCGAATTTGTGCAGGCAGCGGGTGCTGGCTTTTAGGGTCC
GCCGCCTCTCTGCCTA**ATG**AGCTGCACCAGAATGATCCAGGTTTTAGATCCACGTCCTTTGACAAGTTCGGTCAT
GCCCGTGGATGTGGCCATGAGGCTTTGCTTGGCACATTCACCACCTGTGAAGAGTTTCCTGGGCCCGTACGATGA
ATTTCAACGACGACATTTTGTGAATAAATTAAAGCCCCTGAAATCATGTCTCAATATAAAACACAAAGCCAAATC
ACAGAATGACTGGAAGTGCTCACACAACCAAGCCAAGAAGCGCGTTGTGTTTGCTGACTCCAAGGGCCTCTCTCT
CACTGCGATCCATGTCTTCTCCGACCTCCCAGAAGAACCAGCGTGGGATCTGCAGTTTGATCTCTTGGACCTTAA
TGATATCTCCTCTGCCTTAAAACACCACGAGGAGAAAAACTTGATTTTAGATTTCCCTCAACCTTCAACCGATTA
CTTAAGTTTCCGGAGCCACTTTCAGAAGAACTTTGTCTGTCTGGAGAACTGCTCATTGCAAGAGCGAACAGTGAC
AGGGACTGTTAAAGTCAAAAATGTGAGTTTTGAGAAGAAAGTTCAGATCCGTATCACTTTCGATTCTTGGAAAAA
CTACACTGACGTAGACTGTGTCTATATGAAAAATGTGTATGGTGGCACAGATAGTGATACCTTCTCATTTGCCAT
TGACTTACCCCCTGTCATTCCAACTGAGCAGAAAATTGAGTTCTGCATTTCTTACCATGCTAATGGGCAAGTCTT
TTGGGACAACAATGATGGTCAGAATTATAGAATTGTTCATGTTCAATGGAAGCCTGATGGGGTGCAGACACAGAT
GGCACCCCAGGACTGTGCATTCCACCAGACGTCTCCTAAGACAGAGTTAGAGTCAACAATCTTTGGCAGTCCGAG
GCTGGCTAGTGGGCTCTTCCCAGAGTGGCAGAGCTGGGGGAGAATGGAGAACTTGGCCTCTTATCGA**TGA**ATTAA
GCAACAATGTAACTGGTCTTGACTTGTCATATTCCCCCATGCAATCCTAGGTCTGTATTGCTCAATTTTAGGAAG
CCTTTGCTACTCCATCAGTAGGTTTAGATTTGA

FIGURE 454

MSCTRMIQVLDPRPLTSSVMPVDVAMRLCLAHSPPVKSFLGPYDEFQRRHFVNKLKPLKSCLNIKHKAKSQNDWK
CSHNQAKKRVVFADSKGLSLTAIHVFSDLPEEPAWDLQFDLLDLNDISSALKHHEEKNLILDFPQPSTDYLSFRS
HFQKNFVCLENCSLQERTVTGTVKVKNVSFEKKVQIRITFDSWKNYTDVDCVYMKNVYGGTDSDTFSFAIDLPPV
IPTEQKIEFCISYHANGQVFWDNNDGQNYRIVHVQWKPDGVQTQMAPQDCAFHQTSPKTELESTIFGSPRLASGL
FPEWQSWGRMENLASYR

FIGURE 455A

CGACTCCTTAGAGCATGGCATGGCTCAGAGGTGCTGGTAAAACTGATGGGGGTTTTTGCTGTCCCTCCCCTCAGC
GCCGACACC**ATG**TGGATCCAGGTTCGGACCATGGACGGGAGGCAGACCCACACGGTGGACTCGCTGTCCAGGCTG
ACCAAGGTGGAGGAGCTGAGGCGGAAGATCCAGGAGCTGTTCCACGTGGAGCCAGGCCTGCAGAGGCTGTTCTAC
AGGGGCAAACAGATGGAGGACGGCCATACCCTCTTCGACTACGAGGTCCGCCTGAATGACACCATCCAGCTCCTG
GTCCGCCAGAGCCTCGTGCTCCCCCACAGCACCAAGGAGCGGGACTCCGAGCTCTCCGACACCGACTCCGGCTGC
TGCCTGGGCCAGAGTGAGTCAGACAAGTCCTCCACCCACGGCGAGGCGGCCGCCGAGACTGACAGCAGGCCAGCC
GATGAGGACATGTGGGATGAGACGGAATTGGGGCTGTACAAGGTCAATGAGTACGTCGATGCTCGGGACACGAAC
ATGGGGGCGTGGTTTGAGGCGCAGGTGGTCAGGGTGACGCGGAAGGCCCCCTCCCGGGACGAGCCCTGCAGCTCC
ACGTCCAGGCCGGCGCTGGAGGAGGACGTCATTTACCACGTGAAATACGACGACTACCCGGAGAACGGCGTGGTC
CAGATGAACTCCAGGGACGTCCGAGCGCGCGCCCGCACCATCATCAAGTGGCAGGACCTGGAGGTGGGCCAGGTG
GTCATGCTCAACTACAACCCCGACAACCCCAAGGAGCGGGGCTTCTGGTACGACGCGGAGATCTCCAGGAAGCGC
GAGACCAGGACGGCGCGGGAACTCTACGCCAACGTGGTGCTGGGGGATGATTCTCTGAACGACTGTCGGATCATC
TTCGTGGACGAAGTCTTCAAGATTGAGCGGCCGGGTGAAGGGAGCCCCATGGTTGACAACCCCATGAGACGGAAG
AGCGGGCCGTCCTGCAAGCACTGCAAGGACGACGTGAACAGACTCTGCCGGGTCTGCGCCTGCCACCTGTGCGGG
GGCCGGCAGGACCCCGACAAGCAGCTCATGTGCGATGAGTGCGACATGGCCTTCCACATCTACTGCCTGGACCCG
CCCCTCAGCAGTGTTCCCAGCGAGGACGAGTGGTACTGCCCTGAGTGCCGGAATGATGCCAGCGAGGTGGTACTG
GCGGGAGAGCGGCTGAGAGAGAGCAAGAAGAAGGCGAAGATGGCCTCGGCCACATCGTCCTCACAGCGGGACTGG
GGCAAGGGCATGGCCTGTGTGGGCCGCACCAAGGAATGTACCATCGTCCCGTCCAACCACTACGGACCCATCCCG
GGGATCCCCGTGGGCACCATGTGGCGGTTCCGAGTCCAGGTCAGCGAGTCGGGTGTCCATCGGCCCCACGTGGCT
GGCATACACGGCCGGAGCAACGACGGAGCGTACTCCCTAGTCCTGGCGGGGGGCTATGAGGATGACGTGGACCAT
GGGAATTTTTTCACATACACGGGTAGTGGTGGTCGAGATCTTTCCGGCAACAAGAGGACCGCGGAACAGTCTTGT
GATCAGAAACTCACCAACACCAACAGGGCGCTGGCTCTCAACTGCTTTGCTCCCATCAATGACCAAGAAGGGGCC
GAGGCCAAGGACTGGCGGTCGGGGAAGCCGGTCAGGGTGGTGCGCAATGTCAAGGGTGGCAAGAATAGCAAGTAC
GCCCCCGCTGAGGGCAACCGCTACGATGGCATCTACAAGGTTGTGAAATACTGGCCCGAGAAGGGGAAGTCCGGG
TTTCTCGTGTGGCGCTACCTTCTGCGGAGGGACGATGATGAGCCTGGCCCTTGGACGAAGGAGGGGAAGGACCGG
ATCAAGAAGCTGGGGCTGACCATGCAGTATCCAGAAGGCTACCTGGAAGCCCTGGCCAACCGAGAGCGAGAGAAG
GAGAACAGCAAGAGGGAGGAGGAGGAGCAGCAGGAGGGGGGCTTCGCGTCCCCCAGGACGGGCAAGGGCAAGTGG
AAGCGGAAGTCGGCAGGAGGTGGCCCGAGCAGGGCCGGGTCCCCGCGCCGGACATCCAAGAAAACCAAGGTGGAG
CCCTACAGTCTCACGGCCCAGCAGAGCAGCCTCATCAGAGAGGACAAGAGCAACGCCAAGCTGTGGAATGAGGTC
CTGGCGTCACTCAAGGACCGGCCGGCGAGCGGCAGCCCGTTCCAGTTGTTCCTGAGTAAAGTGGAGGAGACGTTC
CAGTGTATCTGCTGTCAGGAGCTGGTGTTCCGGCCCATCACGACCGTGTGCCAGCACAACGTGTGCAAGGACTGC
CTGGACAGATCCTTTCGGGCACAGGTGTTCAGCTGCCCTGCCTGCCGCTACGACCTGGGCCGCAGCTATGCCATG
CAGGTGAACCAGCCTCTGCAGACCGTCCTCAACCAGCTCTTCCCCGGCTACGGCAATGGCCGG**TGA**TCTCCAAGC
ACTTCTCGACAGGCGTTTTGCTGAAAACGTGTCGGAGGGCTCGTTCATCGGCACTGATTTTGTTCTTAGTGGGCT
TAACTTAAACAGGTAGTGTTTCCTCCGTTCCCTAAAAAGGTTTGTCTTCCTTTTTTTTTATTTTTATTTTTCAAA
TCTATACATTTTCAGGAATTTATGTATTCTGGCTAAAAGTTGGACTTCTCAGTATTGTGTTTAGTTCTTTGAAAA
CATAAAAGCCTGCAATTTCTCGACAAAACAACACAAGATTTTTAAAGATGGAATCAGAAACTACGTGGTGTGGA
GGCTGTTGATGTTTCTGGTGTCAAGTTCTCAGAAGTTGCTGCCACCAACTCTTTAAGAAGGCGACAGGATCAGTC
CTTCTCTAGGGTTCTGGCCCCCAAGGTCAGAGCAAGCATCTTCCTGACAGCATTTTGTCATCTAAAGTCCAGTGA
CATGGTTCCCCGTGGTGGCCCGTGGCAGCCCGTGGCATGGCGTGGCTCAGCTGTCTGTTGAAGTTGTTGCAAGGA
AAAGAGGAAACATCTCGGGCCTAGTTCAAACCTTTGCCTCAAAGCCATCCCCCACCAGACTGCTTAGCGTCTGAG
ATCCGCGTGAAAAGTCCTCTGCCCACGAGAGCAGGGAGTTGGGGCCACGCAGAAATGGCCTCAAGGGGACTCTGC
TCCACGTGGGGCCAGGCGTGTGACTGACGCTGTCCGACGAAGGCGGCCACGGACGGACGCCAGCACACGAAGTCA
CGTGCAAGTGCCTTTGATTCGTTCCTTCTTTCTAAAGACGACAGTCTTTGTTGTTAGCACTGAATTATTGAAAAT
GTCAACCAGATTCTAGAAACTGCGGTCATCCAGTTCTTCCTGACACCGGATGGGTGCTTGGGAACCGTTTGAGCC
TTATAGATCATTTACATTCAATTTTTTTAACTCAGCAAGTGAGAACTTACAAGAGGGTTTTTTTTTAATTTTTTT
TTCTCTTAATGAACACATTTTCTAAATGAATTTTTTTTGTAGTTACTGTATATGTACCAAGAAAGATATAACGTT
AGGGTTTGGTTGTTTTTGTTTTTGTATTTTTTTTCTTTTGAAAGGGTTTGTTAATTTTTCTAATTTTACCAAAGT

FIGURE 455B

TTGCAGCCTATACCTCAATAAAACAGGGATATTTTAAATCACATACCTGCAGACAAACTGGAGCAATGTTATTTT
TAAAGGGTTTTTTTCACCTCCTTATTCTTAGATTATTAATGTATTAGGGAAGAATGAGACAATTTTGTGTAGGCT
TTTTCTAAAGTCCAGTACTTTGTCCAGATTTTAGATTCTCAGAATAAATGTTTTTCACAGATTGAAAAAAAAAAA
AAA

FIGURE 456

MWIQVRTMDGRQTHTVDSLSRLTKVEELRRKIQELFHVEPGLQRLFYRGKQMEDGHTLFDYEVRLNDTIQLLVRQ
SLVLPHSTKERDSELSDTDSGCCLGQSESDKSSTHGEAAAETDSRPADEDMWDETELGLYKVNEYVDARDTNMGA
WFEAQVVRVTRKAPSRDEPCSSTSRPALEEDVIYHVKYDDYPENGVVQMNSRDVRARARTIIKWQDLEVGQVVML
NYNPDNPKERGFWYDAEISRKRETRTARELYANVVLGDDSLNDCRIIFVDEVFKIERPGEGSPMVDNPMRRKSGP
SCKHCKDDVNRLCRVCACHLCGGRQDPDKQLMCDECDMAFHIYCLDPPLSSVPSEDEWYCPECRNDASEVVLAGE
RLRESKKKAKMASATSSSQRDWGKGMACVGRTKECTIVPSNHYGPIPGIPVGTMWRFRVQVSESGVHRPHVAGIH
GRSNDGAYSLVLAGGYEDDVDHGNFFTYTGSGGRDLSGNKRTAEQSCDQKLTNTNRALALNCFAPINDQEGAEAK
DWRSGKPVRVVRNVKGGKNSKYAPAEGNRYDGIYKVVKYWPEKGKSGFLVWRYLLRRDDDEPGPWTKEGKDRIKK
LGLTMQYPEGYLEALANREREKENSKREEEEQQEGGFASPRTGKGKWKRKSAGGGPSRAGSPRRTSKKTKVEPYS
LTAQQSSLIREDKSNAKLWNEVLASLKDRPASGSPFQLFLSKVEETFQCICCQELVFRPITTVCQHNVCKDCLDR
SFRAQVFSCPACRYDLGRSYAMQVNQPLQTVLNQLFPGYGNGR

FIGURE 457

CTGGGTCCTGTGTGTGCCACAGGGGTGGGGTGTCCAGCGAGCGGTCTCCTCCTCCTGCTAGTGCTGCTGCGGCGT
CCCGCGGCCTCCCCGAGTCGGGCGGGAGGGGAGAGCGGGTGTGGATTTGTCTTGACGGTAATTGTTGCGTTTCCA
CGTCTCGGAGGCCTGCGCGCTGGGTTGCTCCTTCTTCGGGAGCGAGCTGTTCTCAGCGATCCCACTCCCAGCCGG
GGCTCCCCACACACACTGGGCTGCGTGCGTGTGGAGTGGGACCCGCGCACACGCGTGTCTCTGGACAGCTACGGC
GCCGAAAGAACTAAAATTCCAG**<u>ATG</u>**GCAAACTCAATGAATGGCAGAAACCCTGGTGGTCGAGGAGGAAATCCCCG
AAAAGGTCGAATTTTGGGTATTATTGATGCTATTCAGGATGCAGTTGGACCCCCTAAGCAAGCTGCCGCAGATCG
CAGGACCGTGGAGAAGACTTGGAAGCTCATGGACAAAGTGGTAAGACTGTGCCAAAATCCCAAACTTCAGTTGAA
AAATAGCCCACCATATATACTTGATATTTTGCCTGATACATATCAGCATTTACGACTTATATTGAGTAAATATGA
TGACAACCAGAAACTTGCCCAACTCAGTGAGAATGAGTACTTTAAAATCTACATTGATAGCCTTATGAAAAAGTC
AAAACGGGCAATAAGACTCTTTAAAGAAGGCAAGGAGAGAATGTATGAAGAACAGTCACAGGACAGACGAAATCT
CACAAAACTGTCCCTTATCTTCAGTCACATGCTGGCAGAAATCAAAGCAATCTTTCCCAATGGTCAATTCCAGGG
AGATAACTTTCGTATCACAAAAGCAGATGCTGCTGAATTCTGGAGAAAGTTTTTTGGAGACAAAACTATCGTACC
ATGGAAAGTATTCAGACAGTGCCTTCATGAGGTCCACCAGATTAGCTCTAGCCTGGAAGCAATGGCTCTAAAATC
AACAATTGATTTAACTTGCAATGATTACATTTCAGTTTTTGAATTTGATATTTTTACCAGGCTGTTTCAGCCTTG
GGGCTCTATTTTGCGGAATTGGAATTTCTTAGCTGTGACACATCCAGGTTACATGGCATTTCTCACATATGATGA
AGTTAAAGCACGACTACAGAAATATAGCACCAAACCCGGAAGCTATATTTTCCGGTTAAGTTGCACTCGATTGGG
ACAGTGGGCCATTGGCTATGTGACTGGGGATGGGAATATCTTACAGACCATACCTCATAACAAGCCCTTATTTCA
AGCCCTGATTGATGGCAGCAGGGAAGGATTTTATCTTTATCCTGATGGGAGGAGTTATAATCCTGATTTAACTGG
ATTATGTGAACCTACACCTCATGACCATATAAAAGTTACACAGGAACAATATGAATTATATTGTGAAATGGGCTC
CACTTTTCAGCTCTGTAAGATTTGTGCAGAGAATGACAAAGATGTCAAGATTGAGCCTTGTGGGCATTTGATGTG
CACCTCTTGCCTTACGGCATGGCAGGAGTCGGATGGTCAGGGCTGCCCTTTCTGTCGTTGTGAAATAAAAGGAAC
TGAGCCCATAATCGTGGACCCCTTTGATCCAAGAGATGAAGGCTCCAGGTGTTGCAGCATCATTGACCCCTTTGG
CATGCCGATGCTAGACTTGGACGACGATGATGATCGTGAGGAGTCCTTGATGATGAATCGGTTGGCAAACGTCCG
AAAGTGCACTGACAGGCAGAACTCACCAGTCACATCACCAGGATCCTCTCCCCTTGCCCAGAGAAGAAAGCCACA
GCCTGACCCACTCCAGATCCCACATCTAAGCCTGCCACCCGTGCCTCCTCGCCTGGATCTAATTCAGAAAGGCAT
AGTTAGATCTCCCTGTGGCAGCCCAACAGGTTCACCAAAGTCTTCTCCTTGCATGGTGAGAAAACAAGATAAACC
ACTCCCAGCACCACCTCCTCCCTTAAGAGATCCTCCTCCACCGCCACCTGAAAGACCTCCACCAATCCCACCAGA
CAATAGACTGAGTAGACACATCCATCATGTGGAAAGCGTGCCTTCCAGAGACCCGCCAATGCCTCTTGAAGCATG
GTGCCCTCGGGATGTGTTTGGGACTAATCAGCTTGTGGGATGTCGACTCCTAGGGGAGGGCTCTCCAAAACCTGG
AATCACAGCGAGTTCAAATGTCAATGGAAGGCACAGTAGAGTGGGCTCTGACCCAGTGCTTATGCGGAAACACAG
ACGCCATGATTTGCCTTTAGAAGGAGCTAAGGTCTTTTCCAATGGTCACCTTGGAAGTGAAGAATATGATGTTCC
TCCCCGGCTTTCTCCTCCTCCTCCAGTTACCACCCTCCTCCCTAGCATAAAGTGTACTGGTCCGTTAGCAAATTC
TCTTTCAGAGAAAACAAGAGACCCAGTAGAGGAAGATGATGATGAATACAAGATTCCTTCATCCCACCCTGTTTC
CCTGAATTCACAACCATCTCATTGTCATAATGTAAAACCTCCTGTTCGGTCCTGTGATAATGGTCACTGTATGCT
GAATGGAACACATGGTCCATCTTCAGAGAAGAAATCAAACATCCCTGACTTAAGCATATATTTAAAGGGTACGTA
TAGAATA**<u>TAA</u>**TTTCCTTTGTGATGTACATCTTAATGGTCAGAATTTAAAGGCAAAATTTCATGCCATTGTACTGA
AAATACATTAAGGTTTTGTGTTATCCTCTAGGAGATGTTTTTGATTCAGCCTCTGATCCCGTGCCATTACCACCT
GCCAGGCCTCCAACTCGGGACAATCCAAAGCATGGTTCTTCACTCAACAGGACGCCCTCTGATTATGATCTTCTC
ATCCCTCCATTAGGTTGAAACCTTTAAAAAAGTTTTGAACAACCCACCCCTCCTTCTTTTAATTTCAGAATTTTC
AGAATTCAGAGTTCAGTATAACACAGACTCACTGGGTTGTGAATTTGCCTGAAATTTGAATGGGTTCTCCAGGTG
CCGGTGACTCCCAAGTTCACGAGACCATTACTCCATGTAGATGATTAAGGTAGTAGTGTAGTAGTTGGGCATCAG
TCAGGTTTTAAGCAAGTTGTTTTGTCCATACTAAATGTAGTCTAAAAACACATGAGAGCTTTGTGCTCTAGTAGT
TTTGAAGTGATGACTTGAAGTGTTGAGATTTTCTTTAAGTATAATAATTCTTAATAAATATGAACTTGCTTTTCT
TGCAGCATGAGCACCAGTTCCACTTACGCTAATTAAATTATGCAAAATTAAATAGTTGTATGTAGAGAACTGATA
ATAAATTCTGTTTTATTCTAATCATTACAACTGTAACACATTCAAAAAAAAAAA

FIGURE 458

MANSMNGRNPGGRGGNPRKGRILGIIDAIQDAVGPPKQAAADRRTVEKTWKLMDKVVRLCQNPKLQLKNSPPYIL
DILPDTYQHLRLILSKYDDNQKLAQLSENEYFKIYIDSLMKKSKRAIRLFKEGKERMYEEQSQDRRNLTKLSLIF
SHMLAEIKAIFPNGQFQGDNFRITKADAAEFWRKFFGDKTIVPWKVFRQCLHEVHQISSSLEAMALKSTIDLTCN
DYISVFEFDIFTRLFQPWGSILRNWNFLAVTHPGYMAFLTYDEVKARLQKYSTKPGSYIFRLSCTRLGQWAIGYV
TGDGNILQTIPHNKPLFQALIDGSREGFYLYPDGRSYNPDLTGLCEPTPHDHIKVTQEQYELYCEMGSTFQLCKI
CAENDKDVKIEPCGHLMCTSCLTAWQESDGQGCPFCRCEIKGTEPIIVDPFDPRDEGSRCCSIIDPFGMPMLDLD
DDDDREESLMMNRLANVRKCTDRQNSPVTSPGSSPLAQRRKPQPDPLQIPHLSLPPVPPRLDLIQKGIVRSPCGS
PTGSPKSSPCMVRKQDKPLPAPPPPLRDPPPPPPERPPPIPPDNRLSRHIHHVESVPSRDPPMPLEAWCPRDVFG
TNQLVGCRLLGEGSPKPGITASSNVNGRHSRVGSDPVLMRKHRRHDLPLEGAKVFSNGHLGSEEYDVPPRLSPPP
PVTTLLPSIKCTGPLANSLSEKTRDPVEEDDDEYKIPSSHPVSLNSQPSHCHNVKPPVRSCDNGHCMLNGTHGPS
SEKKSNIPDLSIYLKGTYRI

FIGURE 459

CTGCCCTGACTTCTCATATCTTGCCTAGGAACTCCAGGCTTGTCTTGGCTCCAAATGGATCCCAACTGCTCCTGC
ACCACAGGTGGCTCCTGTGCCTGCGCCGGCTCCTGCAAGTGCAAAGAGTGCAAATGTACCTCCTGCAAGAAGTGC
TGCTGCTCTTGCTGCCCCGTGGGCTGTGCCAAGTGTGCCCAGGGCTGTGTCTGCAAAGGCTCATCAGAGAAGTGC
CGCTGCTGTGCCTGATGTTGGGAGAGCCCTGCTCCCAGACA**TAA**ATAGAGCAACCAGTACTAACCTGGATTTTTT
TTTTAACTACCCTGACCGGTTTGCTACATTCTTTTTTCTATTCAATATGTGAAAGACAATAAAACACGTTTGACT
TGAAAAAAGGCATAACATTACCTGGAAGGGATTTCCCAAAAATATGAAAACCTCGGGGGCGGACCCCCCTAGTCT
ATTCAGCCCACCGGATATTTACTCCGCCGATGAAAACCGGGCCAAAAAACTTTCTCAAAACTAGGGCCCGGAGAG
ACCTTGCCGTCTATCTTGGCCGAATGCTTGGCATCCAGCC

FIGURE 460

ALTSHILPRNSRLVLAPNGSQLLLHHRWLLCLRRLLQVQRVQMYLLQEVLLLLLPRGLCQVCPGLCLQRLIREVP
LLCLMLGEPCSQT

FIGURE 461A

GAAGGTTGCAGTGAGCCGAGATCATGCCATTGTGCTCTACCCTGGGCAACAGAGCAAGACTCCTTCTCAAAAAAA
AAAAAAAAAATCTAATCGTTAAACTTTCAGGAATTTTGTGAGCTGATTGTAAACATAACAGTTATTACAAATTAA
AGTATATAAATGCACAAGTACATAAATGATCATATTTAATACATCATTTCCTACTTAATACATCATTTCCTACTA
TCTGTGCACTTGAGGTTATTTGCATCTATTGGTAGAAATACTATTAATACATAATAGTGTCCTGCTGCAGTATTG
ATAGAACATTACCCCATTGTAATCAGTAAAATACAAACTAGAATTTGATTTATTATTTGTTGATTAAACTTAAGA
AAGTGAAGGATAGAATGTTAATGCAGATTAAATTTCAAAGTGTGATGTGTCTCTGCTAGACTAAATGCAATACAA
AAAAATTGAGGAAGTTGCTTTGCAATATTCCAAAACTCGGCCAGGCATGGTGGCTCACACCTGTAATCCCAGCAC
TTTGGGAGGCCAAGGCTGGCAGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAGTATAGTGAAACCTCA
TCTCTACCAAAGATACAAAAACTAGCCGGGCGTGGTGGTGCATGCCTATAGTCCCAACTAATTAGCCAGGTGTCG
TGGCACGTGCCTGTAATTTCAGCTACTTGGGAGGCAGAGACATGAGAATTGCTTGAACCCGGGAGGTGGAGTTTA
CGGTGAGCTGAGATCGCGCCACTGCACTCCAGCTTGGGTGACAGAGCGAGACTCCGTCTCAAAAAAAAAATTTTT
TTTTAAACTCTTCATTAGTTCGGAAAGATGTTGATGTCATTGATGAATGAGCGAAACTCTAATATATGTCTTTAT
TGTTTCACTTTCATCTTATTCATTAATGTAATTGAAAATATTATCCACCCTTCATGTTGCTACTACAGTCAGCCC
TTCATATACTGTGGGTTCCACATCCGTGGATTCACCCAACTGTAGATGGAAAATATTTTTTTAAATAATAAAAAT
ACAATAATAAACACATTAAAAAGTAATACATTATAAAAACTTTTATGGCATTGATATTATATTAGGTATTAAAAA
TAATCTAGAAATGACCTCAAGTATAGAGGAGGATATGCAAAGGTTGAGTGCAAATACTTCATTTTATACAAGGGA
CTTGAGCATGGGAGGATTTTGGTATGGGGAGGTGCAAATAGCATACTCATTTGCGAAACATATGACCAACCATTT
TGCTAATTGGATGATAATTCATAGTCAAATTTTGTGAAACTGTTGTTGGTTGTAGAATTTTAAAAACTAATAGTG
GGTTTTTCAAGAAATAGCAAGTCATATTGATATTATAGATATAAACTGAAAATCAGGTTAAATATTTAAGTTTAA
AATGTATTTCCAAAATTAGATAATCACTAAGAGAACTTTTTACATTGACCCTTAAAGTGTTATGAATTTTACTTA
CATATGTAAAATTATTTTTCAGATTCTGTTTCCTAAAATGCCAAAACGACAGGGTGATTTTTTGCATTTTTTAAA
TGTGAAGAAGGTGAAAACAGACACAGAAAATAATGAAGTGAGCAAAAATCACTGCAGATTGTCTAAGGCAAAGGA
ACCACATTTCGAGTATATTGAACAACCAATCATTGAAGAAAAGCCATCACTTTCATCAAAGAAAGAAATAGATAA
TCTTGTGCTTCCAGATTGTTGGAATGAAAAACAAGCATTTATGTTTACAGAACAATACAAATGGCTTGAAATAAA
AGAAGGTAAATTAGGATGTAAGGATTGTTCAGCAGTTCGGCATTTGGGATCGAAAGCAGAAAAGCATGTCCATGT
GTCCAAGGAATGGATTGCATATTTAGTAACCCCTAATGGCAGTAATAAAACTACTAGGCAAGCTTCTCTACGAAA
AAAAATTAGGGAACATGATGTTTCTAAAGCCCATGGTAAAATTCAGGATTTGTTAAAGGAATCAACTAATGATTC
AATTTGTAATTTAGTGCATAAACAAAATAATAAAAATATTGATGCTACTGTAAAAGTTTTCAATACTGTTTACAG
TTTAGTAAAACATAACAGACCTTTATCTGATATTGAGGGGGCAAGAGAATTACAGGAAAAAAATGGAGAGGTAAA
TTGTTTAAATACACGTTACAGTGCAACAAGAATAGCAGAACATATTGCAAAAGAAATGAAGATGAAGATATTTAA
GAATATTATAGAAGAGAATGCCAAAATCTGTATCATAATTGATGAGGCATCTACAGTTTCAAAGAAAACCACCCT
AGTGATTTATCTCCAGTGCACAATTCAGTCAGCTCCTGCACCTGTTATGTTATTTGTGGCTTTAAAAGAATTGGT
GTCAACTATAGCAGAGTGTATTGTCAATACATTATTGACTACTTTAAATGATTGTGGTTTTACAAATGAATATTT
GAAAGCAAATTTAATTGCATTTTGTTCTGATGGTGCTAATACAATCCTGGGAAGAAAGTCTGGAGTAGCTACAAA
ATTGTTAGAAAATTTTCCTGAAATCATCATTTGGAACTGTTTAAATCATCGATTACAATTGTCACTTGATGATTC
TATATCCGAAATAAAACAAATTAATCATTTAAAAATATTTATTGATAAAATTTATTCTATTTATCATCAACCTAA
TAAAAATCAAACCAAGCTTCTAGGAACTGTAGCTAAAGAACTTGAAACTGAAATTATTAAAATTGGTCGAGTAAT
GGGACCAAGATGGGCGGCATGTAGTTTACAAGCTGCTACTGCTGTATGGCATGCATATCCTATATTATATATGCA
TTTTTCTCATTCTTACTCTGGTTTGGCGAAGAGATTAGCTAACATTAATTTCTTACAAGACCTTGCTTTAATGAT
TGACATTCTTGAAGAATTTTCAGTACTTTCAACTGCATTACAGTCAAGATCAACTAATATTAAGAAAGCACAAAA
ATTGATCAAACGTACCATAAGAGCTTTGGAAAATTTAAAAATTGGTACTGGAAAGTATGAATCTCAAATTGAAGA
TTTGATCAAGTCAGATAAGTTTAAAGATATTCCATTTAATAAAAACAATAAATTTAATGCTCTTCCTAGGAGTAT
ATTACTAGACAATATAATTCAGCACATGAACCTACGCCTTTTATCTGACAGAAATCATGAAGATATTTTTAATTA
CTTTGATTTGCTGGAACCTTCCACATGGCCTTATGAAGAAATAACTTCACCATGGATAGCTGGTGAAAAAACATT
ATTTCATTTGTGTAAAATTTTAAAATATGAAGTTGATTTGAATGATTTTCGGGAATTTGTAAATAATAATATAAA
ATCAAACAATGTTTCAATTCCTACAACTATATACAAAGCTAAAAAGATAGTTAGCACCATTGCAATCAATAGTGC
TGAAGCTGAAAGGGGTTTCAATTTAATGAACATAATTTGTACAAGGGTGAGAAATAGTTTAACAATAGATCATGT
ATCAGATTTAATGACAATAAATTTACTGGGGAAAGAATTAGCAGATTGGGATGCAACACCGTTTGTAAAATCTTG

FIGURE 461B

GTCAAATTGCAACCACAGGTTGGCTACAGATACAAGAGTTCGGCAAAAGTCAACAAAAGTCTTCCATGAGAATCA
ATTGGCTATATGGAACTTAAAA**TAG**AATATTGTATACGTTTTTTGTCATCTGTAAATTATGTACTACACATCCTT
TATATACATAAAGGTCTTTTTTTTTTTTTGGAAAGCCAGTTAAACTTTTATCAGCATGTTGCTGTTTAAAAGGCG
TTCTTTAAGAAGATAATCTTGAAGATTGGTTTTAGAAGCTATAGTTTTTTAGAGATTGGCCCATGTTTGCTAGAG
TGGGTCATAATACATATTCCATGAAGTTCTGTACAGAACAAACACCGTTTATAATTTTGTACTGTTTTACTTTAA
GTAAGGATGCAAAAAAATAGCAGGACTCAGCTAAGTTCTAAGCCCTGGAGGTTATATTAAATAAAAGAGAAATGGA
ATAAAAACTGT

FIGURE 462

SVMNFTYICKIIFQILFPKMPKRQGDFLHFLNVKKVKTDTENNEVSKNHCRLSKAKEPHFEYIEQPIIEEKPSLS
SKKEIDNLVLPDCWNEKQAFMFTEQYKWLEIKEGKLGCKDCSAVRHLGSKAEKHVHVSKEWIAYLVTPNGSNKTT
RQASLRKKIREHDVSKAHGKIQDLLKESTNDSICNLVHKQNNKNIDATVKVFNTVYSLVKHNRPLSDIEGARELQ
EKNGEVNCLNTRYSATRIAEHIAKEMKMKIFKNIIEENAKICIIIDEASTVSKKTTLVIYLQCTIQSAPAPVMLF
VALKELVSTIAECIVNTLLTTLNDCGFTNEYLKANLIAFCSDGANTILGRKSGVATKLLENFPEIIIWNCLNHRL
QLSLDDSISEIKQINHLKIFIDKIYSIYHQPNKNQTKLLGTVAKELETEIIKIGRVMGPRWAACSLQAATAVWHA
YPILYMHFSHSYSGLAKRLANINFLQDLALMIDILEEFSVLSTALQSRSTNIKKAQKLIKRTIRALENLKIGTGK
YESQIEDLIKSDKFKDIPFNKNNKFNALPRSILLDNIIQHMNLRLLSDRNHEDIFNYFDLLEPSTWPYEEITSPW
IAGEKTLFHLCKILKYEVDLNDFREFVNNNIKSNNVSIPTTIYKAKKIVSTIAINSAEAERGFNLMNIICTRVRN
SLTIDHVSDLMTINLLGKELADWDATPFVKSWSNCNHRLATDTRVRQKSTKVFHENQLAIWNLK

FIGURE 463

CGTACATACAATGCCTCCATCACGCTACAGCAGCAGCTAAAAGAACTGACAGCCCCGGATGAGAACATCCCAGCG
AAGATCCTTTCTTATAACCGTGCCAATCGAGCTGTTGCAATTCTTTGTAACCATCAGAGGGCACCACCAAAAACT
TTTGAGAAGTCTATGATGAACTTGCAAACTAAGATTGATGCCAAGAAGGAACAGCTAGCAGATGCCCGGAGAGAC
CTGAAAAGTGCTAAGGCTGATGCCAAGGTCATGAAGGATGCAAAGACGAAGAAGGTAGTAGAGTCAAAGAAGAAG
GCTGTTCAGAGACTGGAGGAACAGTTGATGAAGCTGGAAGTTCAAGCCACAGACCGAGAGGAAAATAAACAGATT
GCCCTGGGAACCTCCAAACTCAATTATCTGGACCCTAGGATCACAGTGGCTTGGTGCAAGAAGTGGGGTGTCCCA
ATTGAGAAGATTTACAACAAAACCCAGCGGGAGAAGTTTGCCTGGGCCATTGACATGGCTGATGAAGACTATGAG
TTTTAGCCAGTCTCAAGAGGCAGAGTTCTGTGAAGAGGAACAGTGTGGTTTGGGAAAGATGGATAAACTGAGCCT
CACTTGCCCTCGTGCCTGGGGGAGAGAGGCAGCAAGTCTTAACAAACCAACATCTTTGCGAAAAGATAAACCTGG
AGATATTATAAGGGAGAGCTGAGCCAGTTGTCCTATGGACAACTTATTTAAAAATATTTCAGATATCAAAATTCT
AGCTGTATGATTTGTTTTGAATTTTGTTTTTATTTTCAAGAGGGCAAGTGGATGGGAATTTGTCAGCGTTCTACC
AGGCAAATTCACTGTTTCACTGAAATGTTTGGATTCTCTTAGCTACTGTATGCAAAGTCCGATTATATTGGTGCG
TTTTTACAGTTAGGGTTTTGCAATAACTTCTATATTTTAATAGAAATAAATTCCTAAACTCCCTTCCCTCTCTCC
CATTTCAGGAATTTAAAATTAAGTAGAACAAAAAACCCAGCGCACCTGTTAGAGTCGTCACTCTCTATTGTCATG
GGGATCAATTTTCATTAAACTTGAAGCAGTCGTGGCTTTGGCAGTGTTTTGGTTCAGACACCTGTTCACAGAAAA
AGCATGATGGGAAAATATTTCCTGACTTGAGTGTTCCTTTTTAAATGTGAATTTTTATTTCTTTTTAATTATTTT
AAAATATTTAAACCTTTTTCTTGATCTTAAAGATCGTGTAGATTGGGGTTGGGGAGGGATGAAGGGCGAGTGAAT
CTAAGGATAATGAAATAATCAGTGACTGAAACCATTTTCCCATCATCCTTTGTTCTGAGCATTCGCTGTACCCTT
TAAGATATCCATCTTTTTCTTTTTAACCCTAATCTTTCACTTGAAAGATTTTATTGTATAAAAAGTTTCACAGGT
CAATAAACTTAGAGGAAAATGAGTATTTGGTCCAAAAAAAGGAAAAATAATCAAGATTTTAGGGCTTTTATTTTT
TCTTTTGTAATTGTGTAAAAAATGGAAAAAAACATAAAAAGCAGAATTTTAATGTGAAGACATTTTTTGCTATAA
TCATTAGTTTTAGAGGCATTGTTAGTTTAGTGTGTGTGCAGAGTCCATTTCCCACATCTTTCCTCAAGTATCTTC
TATTTTTATCATGAATTCCCTTTTAATCAACTGTAGGTTATTTAAAATAAATTCCTACAACTTAATGGAAAAAAA
AAAAAAAA

FIGURE 464

RTYNASITLQQQLKELTAPDENIPAKILSYNRANRAVAILCNHQRAPPKTFEKSMMNLQTKIDAKKEQLADARRD
LKSAKADAKVMKDAKTKKVVESKKKAVQRLEEQLMKLEVQATDREENKQIALGTSKLNYLDPRITVAWCKKWGVP
IEKIYNKTQREKFAWAIDMADEDYEF

FIGURE 465

ATGCCTGAGGAAGTGCACCATGGAGAGGAGGAGGTGGAGACTTTTGCCTTTCAGGCAGAAATTGCCCAACTCATG
TCCCTCATCATCAATACCTTCTATTCCAACAAGGAGATTTTCCTTCGGGAGTTGATCTCTAATGCTTCTGATGCC
TTGGACAAGATTCGCTATGAGAGCCTGACAGACCCTTCGAAGTTGGACAGTGGTAAAGAGCTGAAAATTGACATC
ATCCCCAACCCTCAGGAACGTACCCTGACTTTGGTAGACACAGGCATTGGCATGACCAAAGCTGATCTCATAAAT
AATTTGGGAACCATTGCCAAGTCTGGTACTAAAGCATTCATGGAGGCTCTTCAGGCTGGTGCAGACATCTCCATG
ATTGGGCAGTTTGGTGTTGGCTTTTATTCTGCCTACTTGGTGGCAGAGAAAGTGGTTGTGATCAGAAAGCACAAC
GATGATGAACAGTATGCTTGGGAGTCTTCTGCTGGAGGTTCCTTCACTGTGCGTGCTGACCATGGTGAGCCCATT
GGCATGGGTACCAAAGTGATCCTCCATCTTAAAGAAGATCAGACAGAGTACCTAGAAGAGAGGCGGGTCAAAGAA
GTAGTGAAGAAGCATTCTCAGTTCATAGGCTATCCCATCACCCTTTATTTGGAGAAGGAACGAGAGAAGGAAATT
AGTGATGATGAGGCAGAGGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGATGAAGAAAAGCCCAAGATC
GAAGATGTGGGTTCAGATGAGGAGGATGACAGCGGTAAGGATAAGAAGAAGAAAACTAAGAAGATCAAAGAGAAA
TACATTGATCAGGAAGAACTAAACAAGACCAAGCCTATTTGGACCAGAAACCCTGATGACATCACCCAAGAGGAG
TATGGAGAATTCTACAAGAGCCTCACTAATGACTGGGAAGACCACTTGGCAGTCAAGCACTTTTCTGTAGAAGGT
CAGTTGGAATTCAGGGCATTGCTATTTATTCCTCGTCGGGCTCCCTTTGACCTTTTTGAGAACAAGAAGAAAAAG
AACAACATCAAACTCTATGTCCGCCGTGTGTTCATCATGGACAGCTGTGATGAGTTGATACCAGAGTATCTCAAT
TTTATCCGTGGTGTGGTTGACTCTGAGGATCTGCCCCTGAACATCTCCCGAGAAATGCTCCAGCAGAGCAAAATC
TTGAAAGTCATTCGCAAAAACATTGTTAAGAAGTGCCTTGAGCTCTTCTCTGAGCTGGCAGAAGACAAGGAGAAT
TACAAGAAATTCTATGAGGCATTCTCTAAAAATCTCAAGCTTGGAATCCACGAAGACTCCACTAACCGCCGCCGC
CTGTCTGAGCTGCTGCGCTATCATACCTCCCAGTCTGGAGATGAGATGACATCTCTGTCAGAGTATGTTTCTCGC
ATGAAGGAGACACAGAAGTCCATCTATTACATCACTGGTGAGAGCAAAGAGCAGGTGGCCAACTCAGCTTTTGTG
GAGCGAGTGCGGAAACGGGGCTTCGAGGTGGTATATATGACCGAGCCCATTGACGAGTACTGTGTGCAGCAGCTC
AAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTACCAAGGAGGGTCTGGAGCTGCCTGAGGATGAGGAGGAGAAG
AAGAAGATGGAAGAGAGCAAGGCAAAGTTTGAGAACCTCTGCAAGCTCATGAAAGAAATCTTAGATAAGAAGGTT
GAGAAGGTGACAATCTCCAATAGACTTGTGTCTTCACCTTGCTGCATTGTGACCAGCACCTACGGCTGGACAGCC
AATATGGAGCGGATCATGAAAGCCCAGGCACTTCGGGACAACTCCACCATGGGCTATATGATGGCCAAAAAGCAC
CTGGAGATCAACCCTGACCACCCCATTGTGGAGACGCTGCGGCAGAAGGCTGAGGCCGACAAGAATGATAAGGCA
GTTAAGGACCTGGTGGTGCTGCTGTTTGAAACCGCCCTGCTATCTTCTGGCTTTTCCCTTGAGGATCCCCAGACC
CACTCCAACCGCATCTATCGCATGATCAAGCTAGGTCTAGGTATTGATGAAGATGAAGTGGCAGCAGAGGAACCC
AATGCTGCAGTTCCTGATGAGATCCCCCCTCTCGAGGGCGATGAGGATGCGTCTCGCATGGAAGAAGTCGAT**TAG**

GTTAGGAGTTCATAGTTGGAAAACTTGTGCCCTTGTATAGTGTCCCCATGGGCTCCCACTGCAGCCTCGAGTGCC
CCTGTCCCACCTGGCTCCCCCTGCTGGTGTCTAGTGTTTTTTTCCCTCTCCTGTCCTTGTGTTGAAGGCAGTAAA
CTAAGGGTGTCAAGCCCCATTCCCTCTCTACTCTTGACAGCAGGATTGGATGTTGTGTATTGTGGTTTATTTTAT
TTTCTTCATTTTGTTCTGAAATTAAAGTATGCAAAATAAAGAATATGCCGTTTTTATAC

FIGURE 466

MPEEVHHGEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLTDPSKLDSGKELKIDI
IPNPQERTLTLVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVVVIRKHN
DDEQYAWESSAGGSFTVRADHGEPIGMGTKVILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREKEI
SDDEAEEEKGEKEEEDKDDEEKPKIEDVGSDEEDDSGKDKKKKTKKIKEKYIDQEELNKTKPIWTRNPDDITQEE
YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKKNNIKLYVRRVFIMDSCDELIPEYLN
FIRGVVDSEDLPLNISREMLQQSKILKVIRKNIVKKCLELFSELAEDKENYKKFYEAFSKNLKLGIHEDSTNRRR
LSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANSAFVERVRKRGFEVVYMTEPIDEYCVQQL
KEFDGKSLVSVTKEGLELPEDEEEKKKMEESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWTA
NMERIMKAQALRDNSTMGYMMAKKHLEINPDHPIVETLRQKAEADKNDKAVKDLVVLLFETALLSSGFSLEDPQT
HSNRIYRMIKLGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDASRMEEVD

FIGURE 467A

GACCGCGGCTGCAGGAACGGAGGCGGAAGGGGCCCTGCGGCGACGACGTCGTCGACGGGGGTGGCCGTGGGAGCT
GAGCACGGAGAAGACTCCCTCTCTCGGAAGCCGGATCCCGAGCCGGGCAGGATGGATCACCACCAGCCGGGGACT
GGGCGCTACCAGGTGCTTCTTAATGAAGAGGATAACTCAGAATCATCGGCTATAGAGCAGCCACCTACTTCAAAC
CCAGCACCGCAGATTGTGCAGGCTGTGTCTTCAGCACCAGCACTTGAAACTGACTCTTCCCCTCCACCATATAGT
AGTATTACTGTGGAAGTACCTACAACTTCAGATACAGAAGTTTACGGTGAGTTTTATCCCGTGCCACCTCCCTAT
AGCGTTGCTACCTCTCTTCCTACATACGATGAAGCTGAGAAGGCTAAAGCTGCTGCAATGGCAGCTGCAGCAGCA
GAAACATCTCAAAGAATTCAGGAGGAAGAGTGTCCACCAAGAGATGACTTCAGTGATGCAGACCAGCTCAGAGTG
GGGAATGATGGCATTTTCATGCTGGCATTTTTCATGGCATTTATTTCAACTGGCTTGGATTTTGTTTATCCTTC
TGTATCACCAATACCATAGCTGGAAGGTATGGTGCTATCTGCGGATTTGGCCTTTCCTTGATCAAATGGATCCTT
ATTGTCAGGTTTTCTGATTATTTTACTGGATATTTCAATGGACAGTATTGGCTTTGGTGGATATTTCTTGTACTT
GGCCTGCTCCTTTTCTTCAGAGGATTTGTTAATTATCTAAAAGTCAGAAACATGTCTGAAAGTATGGCAGCTGCT
CATAGAACAAGGTATTTCTTCTTATTG**TAG**AGACTGCATCAACCCGACATTCCTTTCTTATACCAATGTGAAATT
TCCAGATCATCTGTAAACCTACAACTTTAATAGAAGACTACTAATAACAGAAGACAAATTAGTGAAGAAAAGACG
GAGTTTCGAAATTGAATGGCAGGGTGGTTTTTGCTTACAAGCCATTTCTGTTCATTCTTTAAGTATCTATATTTC
ATTTGTTTTGCACATATGCATATGTGCCCATTTAAGATATTTGCATATACTTGATAGAAACCATAAAGTTGTAGC
AGTTAAGTCCAGTCACATTTGGTTAATCAGTGTTTGATATAATTGAAAGAGTTGAGTGGATAAACAGTCTTCCAG
CTTGTAAATGCCATTGACTTCTGACCTGACATTTAGTATAATAAAAATGAAATTCTTAACCATGTCAAATGATTT
AGTTTCTGGCTCTTAGACTCATCTGGCAGTTCTACACATGAAACATCTTTTGTTATATAAGGTGTATTGAAACCT
GCAGTGCTGATTATTAGAAAGGATTTGTCGGATTTTTGAACATGATATTTACATTATTATTTAGGAAAACTCTTC
CTGTAAATAACCATGCATAACTTACTTTCTGCAATGTTTTCTTAGAAATTGTGTCCAGATAGCTTTCACTAATTT
TAAATTAAGTGAACTAAATATATATGTGTATATGTATACACATATATATACACACACACATATATATATTTAGAA
ACGTGAGTGTTAAAGATAGAATTTGTTTTAGGACAAATTTTAAGAAAATGTGGGAATACCAAATGTCCTTTATAA
GAAAAATAAATTTTGTTTTAAGGGACATACCAGTTTTAGGGATTTTCAGATGGGAAGCTGCATTTTTAGGATTGC
CCATCTTAAGAGATCTTGCAGGAAGAGATTGTATTAGATATTATATTTATTTCATTTAAGATAATTTTCAAAGTT
AATTTTCTAAATAAGATAATTCTCATTTGTGTTTGTCTTTTAAAAGGCCAATAAAATATCTTTCAGTATCATTGT
AATAATTTTTTAGAGTTTAATTTGTAAAGCTTAGCAAATAAAATCTTGTACTATGAATAGCTTCTTGCTTTATGA
CTTTAGGATTAACTTGTAAAAAACATATCCTGAACTGAGATATGCAAAATACTCATTTTCAAGTTATGGAAATGT
GTTTGTGGCATATAGGACTGTGGGGTCTGTGTGTGTAGTGAGAGTGTGTAGCCACTATTATAACTGGAATTTAAT
TTACATTCATAAACTACTATATTTCCCATCTTGCAAATCATTTTATGTCTCATCTGTTTTTCCTTTCGGTTATAT
CTTTGGTTTTGAATACCAACATTTAAAATGATGGTATTTTATCTTTTAAACTTAAAAATTATTTAATACAGCTAT
ATGGACCTTATAAAATTGATTTCTTATTTATTATTAGACATTACTACTAAAAGGTACATCTAACTATTCAGGGAC
ATTTTTCCATTTCCAAAAAATAAAATTTATTATGCTTTATAACCTCTTCTGTATTTTCTAATTTTTTCATTGTCT
TTGATAAATAAAACAGTTTTGTTTTGCTAATATAGCCTATTTTTTGTTTTGTCTCATTCAGTTTACTTTCCTGCG
TAGAATTTTTATTGTTATATTAAAATTTTTATTGTTGTATTAAAGTACCTGTGTTACACCCCTTGAAGTAAGACA
GTAGCATGGGGTAAAGAAAAAAATATTTAGTTTAGTTGCCTAATTTGGAAGTTAATTAAAATTAAACTGTACTAAT
AACATATTCAAACTCATGCTGGATCTCTTTCATATTAATTTCTTATAGACCTGTACTTTATTCTTTCAATAATTT
TTAAATGAAATTAAGCTTTGCTACATGGTAATTAAATAATTACTAGGAAGCTTAGCTATCAAACATCGACTTACT
AAAATTTCATTTTAGCTTTTATGGTATATGTGCTTGTTTTCTGAATATGGATACATGTTACTTTTGATCCAGCAT
CAAAACTTCACTTTTTGTTTTGACTTTTCCCCCCAAATCTGTAAGGTTCAAGTATACATATTACTGAATCCTCTA
TAATTGGCATAATTCAATGGTAGCCTTAAATCTCATCATGTAAGCAGGGGAATCAGAATGTTATTTTCAAGAACT
TAATGTTCCCTTCAGATATATAAAATCCTGCATACTTCATTTCCTGTGAGCTTGAACAGCTGCTGTTGTGTTTTG
GGGATGCTTGATCATCTTTGCACTCTGCCTTAAAGATTGAAAAATCAAAACTCTTGTTAGGGTATCTAAACATTT
TTGAGTGTGAACTGGGGATTGGAAGTTAATACAAAAAAAATTTCAAATTATTTCTATTGTAAATGAATAAGCTAGT
CATGGCTAGGATAATCCATTTTCATGTATTTATGCAATAAACTGAATTTTAAGGCAAAAACAACACTTTTCTATA
TAGTGTATGCAGGACAGATTTTAGAAACTTAGATTAAAATACAAATCCCATTACATTTGGTTAAAATGAATCTCT
GCTTAATGGAAAAAAATACTAATCTTTAGCCTATTTTGAGTCTATAAGATATATTTCATTTTAGACATGCCTTCTA
AGTTGTTCACAGATTTTTACCTGCTAAAACAATATTATTTCCAGTAAAACCTCTCCTAACAGGAAAAGTGGAGTT
CAAAATATCCAATTGGAGAAAAATTCAGAGTTCCTTCATTAAATATAATTTTTTTCATCTAGTATGTACTATTTC

FIGURE 467B

AAGAAGTGCAAAAAGTAATGATAGTGAATGTGATACCATACTTAACTAAGGTAATATATATCCTTAGTTTGCTCA
AAAGAGTCCTGGTTATTCCTGTTTTCTCAGCTTAATAGTGCCTCATCGTACTCTCAAAAGTGTTCTAATTTGGAG
GATAAGTTATATGATCATCCTGTGTATAATTGTAGACTGTACCAAGAAGCAACTACCTTAGCTCCACTGCCCTTT
GAGGGATGGAACTGGGGTAAGGGCAGGAGCCAGTTATTATTGCCACAGTGTTTTCTAATGAACCATTTGGCCTGT
AGAAGAGGAATAGTATTTTTTTTAATAGTTGTATTTGAATGATTCCAGCTTATCGTAAATACTAAACTGAATGGC
TTTTATATTTTTAACTGCTGTTAAATGTTATTTTAGCATTTATTAGTTGTTTATTATTTAATTCTTCAAATAGTC
ATATGAAAACATATATTTGATAAAGGTCAATTGTTAGATGATAATGTGCCATTCATTATCATAGGAATGTCCTTG
CCCATATATAAAACATGCTGGCATGTATTTTACTTGTTAATAAAGTTGTATAGATGTGGAAGTGTGAACCTGTGA
TGCATCCTTTTCAAAATCAGTTTAAGATTCGCATATTATCATGACTGTGACCTCACTAAACTGTTTATGTGACAA
ACCTTTCAAGATTGGAGATGAAAACAACACTTGTGAAATTAGGTTGGGGTTGCAACATCTTTTAACTTCTCAGTT
ATTTGTATGTCAGGAAACAGATTGTGGTTTAATTTTAATAAACAAAATATCATCTTTTTGAAAAT

FIGURE 468

DRGCRNGGGRGPAATTSSTGVAVGAEHGEDSLSRKPDPEPGRMDHHQPGTGRYQVLLNEEDNSESSAIEQPPTSN
PAPQIVQAVSSAPALETDSSPPPYSSITVEVPTTSDTEVYGEFYPVPPPYSVATSLPTYDEAEKAKAAAMAAAAA
ETSQRIQEEECPPRDDFSDADQLRVGNDGIFMLAFFMAFIFNWLGFCLSFCITNTIAGRYGAICGFGLSLIKWIL
IVRFSDYFTGYFNGQYWLWWIFLVLGLLLFFRGFVNYLKVRNMSESMAAAHRTRYFFLL

FIGURE 469

GGCTGAGGCAGTGGCTCCTTGCACAGCAGCTGCACGCGCCGTGGCTCCGGATCTTCTTCGTCTTTGCAGCGTAGC
CCGAGTCGGTCAGCGCCAGAGGACCTCAGCAGCC**ATG**TCGAAGCCCCATAGTGAAGCCGGGACTGCCTTCATTCA
GACCCAGCAGCTGCACGCAGCCATGGCTGACACATTCCTGGAGCACATGTGCCGCCTGGACATTGATTCACCACC
CATCACAGCCCGGAACACTGGCATCATCTGTACCATTGGCCCAGCTTCCCGATCAGTGGAGACGTTGAAGGAGAT
GATTAAGTCTGGAATGAATGTGGCTCGTCTGAACTTCTCTCATGGAACTCATGAGTACCATGCGGAGACCATCAA
GAATGTGCGCACAGCCACGGAAAGCTTTGCTTCTGACCCCATCCTCTACCGGCCCGTTGCTGTGGCTCTAGACAC
TAAAGGACCTGAGATCCGAACTGGGCTCATCAAGGGCAGCGGCACTGCAGAGGTGGAGCTGAAGAAGGGAGCCAC
TCTCAAAATCACGCTGGATAACGCCTACATGGAAAAGTGTGACGAGAACATCCTGTGGCTGGACTACAAGAACAT
CTGCAAGGTGGTGGAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCTCCAGGTGAAGCAGAAAGG
TGCCGACTTCCTGGTGACGGAGGTGGAAAATGGTGGCTCCTTGGGCAGCAAGAAGGGTGTGAACCTTCCTGGGGC
TGCTGTGGACTTGCCTGCTGTGTCGGAGAAGGACATCCAGGATCTGAAGTTTGGGGTCGAGCAGGATGTTGATAT
GGTGTTTGCGTCATTCATCCGCAAGGCATCTGATGTCCATGAAGTTAGGAAGGTCCTGGGAGAGAAGGGAAAGAA
CATCAAGATTATCAGCAAAATCGAGAATCATGAGGGGGTTCGGAGGTTTGATGAAATCCTGGAGGCCAGTGATGG
GATCATGGTGGCTCGTGGTGATCTAGGCATTGAGATTCCTGCAGAGAAGGTCTTCCTTGCTCAGAAGATGATGAT
TGGACGGTGCAACCGAGCTGGGAAGCCTGTCATCTGTGCTACTCAGATGCTGGAGAGCATGATCAAGAAGCCCCG
CCCCACTCGGGCTGAAGGCAGTGATGTGGCCAATGCAGTCCTGGATGGAGCCGACTGCATCATGCTGTCTGGAGA
AACAGCCAAAGGGGACTATCCTCTGGAGGCTGTGCGCATGCAGAACCTGATTGCCCGTGAGGCAGAGGCTGCCAT
CTACCACTTGCAATTATTTGAGGAACTCCGCCGCCTGGCGCCCATTACCAGCGACCCCACAGAAGCCACCGCCGT
GGGTGCCGTGGAGGCCTCCTTCAAGTGCTGCAGTGGGGCCATAATCGTCCTCACCAAGTCTGGCAGGTCTGCTCA
CCAGGTGGCCAGATACCGCCCACGTGCCCCCATCATTGCTGTGACCCGGAATCCCCAGACAGCTCGTCAGGCCCA
CCTGTACCGTGGCATCTTCCCTGTGCTGTGCAAGGACCCAGTCCAGGAGGCCTGGGCTGAGGACGTGGACCTCCG
GGTGAACTTTGCCATGAATGTTGGCAAGGCCCGAGGCTTCTTCAAGAAGGGAGATGTGGTCATTGTGCTGACCGG
ATGGCGCCCTGGCTCCGGCTTCACCAACACCATGCGTGTTGTTCCTGTGCCG**TGA**TGGACCCCAGAGCCCCTCCT
CCAGCCCCTGTCCCACCCCCTTCCCCCAGCCCATCCATTAGGCCAGCAACGCTTGTAGAACTCACTCTGGGCTGT
AACGTGGCACTGGTAGGTTGGGACACCAGGGAAGAAGATCAACGCCTCACTGAAACATGGCTGTGTTTGCAGCCT
GCTCTAGTGGGACAGCCCAGAGCCTGGCTGCCCCATCATGTGGCCCCACCCAATCAAGGGAAGAAGGAGGAATGC
TGGACTGGAGGCCCCTGGAGCCAGATGGCAAGAGGGTGACAGCTTCCTTTCCTGTGTGTACTCTGTCCAGTTCCT
TTAGAAAAAATGGATGCCCAGAGGACTCCCAACCCTGGCTTGGGGTCAAGAAACAGCCAGCAAGAGTTAGGGGCC
TTAGGGCACTGGGCTGTTGTTCCATTGAAGCCGACTCTGGCCCTGGCCCTTACTTGCTTCTCTAGCTCTCTAGGC
CTCTCCAGTTTGCACCTGTCCCCACCCTCCACTCAGCTGTCCTGCAGCAAACACTCCACCCTCCACCTTCCATTT
TCCCCCACTACTGCAGCACCTCCAGGCCTGTTGCCGC

FIGURE 470

MSKPHSEAGTAFIQTQQLHAAMADTFLEHMCRLDIDSPPITARNTGIICTIGPASRSVETLKEMIKSGMNVARLN
FSHGTHEYHAETIKNVRTATESFASDPILYRPVAVALDTKGPEIRTGLIKGSGTAEVELKKGATLKITLDNAYME
KCDENILWLDYKNICKVVEVGSKIYVDDGLISLQVKQKGADFLVTEVENGGSLGSKKGVNLPGAAVDLPAVSEKD
IQDLKFGVEQDVDMVFASFIRKASDVHEVRKVLGEKGKNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIE
IPAEKVFLAQKMMIGRCNRAGKPVICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLEAV
RMQNLIAREAEAAIYHLQLFEELRRLAPITSDPTEATAVGAVEASFKCCSGAIIVLTKSGRSAHQVARYRPRAPI
IAVTRNPQTARQAHLYRGIFPVLCKDPVQEAWAEDVDLRVNFAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTM
RVVPVP

FIGURE 471

GCAAGAGTGACACACAGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAG
CCTCAGGGGCGGGCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCC
CGCGGGTTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCACTTCGGAGGATTGCTCAACAACC**ATG**CT
GGGCATCTGGACCCTCCTACCTCTGGTTCTTACGTCTGTTGCTAGATTATCGTCCAAAAGTGTTAATGCCCAAGT
GACTGACATCAACTCCAAGGGATTGGAATTGAGGAAGACTGTTACTACAGTTGAGACTCAGAACTTGGAAGGCCT
GCATCATGATGGCCAATTCTGCCATAAGCCCTGTCCTCCAGGTGAAAGGAAAGCTAGGGACTGCACAGTCAATGG
GGATGAACCAGACTGCGTGCCCTGCCAAGAAGGGAAGGAGTACACAGACAAAGCCCATTTTTCTTCCAAATGCAG
AAGATGTAGATTGTGTGATGAAGGACATGGCTTAGAAGTGGAAATAAACTGCACCCGGACCCAGAATACCAAGTG
CAGATGTAAACCAAACTTTTTTTGTAACTCTACTGTATGTGAACACTGTGACCCTTGCACCAAATGTGAACATGG
AATCATCAAGGAATGCACACTCACCAGCAACACCAAGTGCAAAGAGGAAGGATCCAGATCTAACTTGGGGTGGCT
TTGTCTTCTTCTTTTGCCAATTCCACTAATTGTTTGGGTGAAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCA
CAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGT
TGACTTGAGTAAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCGAAAGAA
TGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACT
GCTTCGTAATTGGCATCAACTTCATGGAAAGAAAGAAGCGTATGACACATTGATTAAAGATCTCAAAAAAGCCAA
TCTTTGTACTCTTGCAGAGAAAATTCAGACTATCATCCTCAAGGACATTACTAGTGACTCAGAAAATTCAAACTT
CAGAAATGAAATCCAAAGCTTGGTC**TAG**AGTGAAAAACAACAAATTCAGTTCTGAGTATATGCAATTAGTGTTTG
AAAAGATTCTTAATAGCTGGCTGTAAATACTGCTTGGTTTTTTACTGGGTACATTTTATCATTTATTAGCGCTGA
AGAGCCAACATATTTGTAGATTTTTAATATCTCATGATTCTGCCTCCAAGGATGTTTAAAATCTAGTTGGGAAAA
CAAACTTCATCAAGAGTAAATGCAGTGGCATGCTAAGTACCCAAATAGGAGTGTATGCAGAGGATGAAAGATTAA
GATTATGCTCTGGCATCTAACATATGATTCTGTAGTATGAATGTAATCAGTGTATGTTAGTACAAATGTCTATCC
ACAGGCTAACCCCACTCTATGAATCAATAGAAGAAGCTATGACCTTTTGCTGAAATATCAGTTACTGAACAGGCA
GGCCACTTTGCCTCTAAATTACCTCTGATAATTCTAGAGATTTTACCATATTTCTAAACTTTGTTTATAACTCTG
AGAAGATCATATTTATGTAAAGTATATGTATTTGAGTGCAGAATTTAAATAAGGCTCTACCTCAAAGACCTTTGC
ACAGTTTATTGGTGTCATATTATACAATATTTCAATTGTGAATTCACATAGAAAACATTAAATTATAATGTTTGA
CTATTATATATGTGTATGCATTTTACTGGCTCAAAACTACCTACTTCTTTCTCAGGCATCAAAAGCATTTTGAGC
AGGAGAGTATTACTAGAGCTTTGCCACCTCTCCATTTTTGCCTTGGTGCTCATCTTAATGGCCTAATGCACCCCC
AAACATGGAAATATCACCAAAAAATACTTAATAGTCCACCAAAAGGCAAGACTGCCCTTAGAAATTCTAGCCTGG
TTTGGAGATACTAACTGCTCTCAGAGAAAGTAGCTTTGTGACATGTCATGAACCCATGTTTGCAATCAAAGATGA
TAAAATAGATTCTTATTTTTCCCCCACCCCCGAAAATGTTCAATAATGTCCCATGTAAAACCTGCTACAAATGGC
AGCTTATACATAGCAATGGTAAAATCATCATCTGGATTTAGGAATTGCTCTTGTCATACCCCCAAGTTTCTAAGA
TTTAAGATTCTCCTTACTACTATCCTACGTTTAAATATCTTTGAAAGTTTGTATTAAATGTGAATTTTAAGAAAT
AATATTTATATTTCTGTAAATGTAAACTGTGAAGATAGTTATAAACTGAAGCAGATACCTGGAACCACCTAAAGA
ACTTCCATTTATGGAGGATTTTTTTGCCCCTTGTGTTTGGAATTATAAAATATAGGTAAAAGTACGTAATTAAAT
A

FIGURE 472

MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCHKPCPPGERKARDCTV
NGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVCEHCDPCTKCE
HGIIKECTLTSNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLS
DVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK
ANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV

FIGURE 473

ATGGCTTCTCTGGACGACCCAGGGGAAGTGAGGGAGGGCTTCCTCTGCCCTCTGTGCCTGAAGGATCTGCAGTCT
TTCTATCAGCTTCACTCACATTACGAGGAAGAACACTCAGGGGAAGACCGTGATGTCAAAGGGCAAATTAAAAGT
CTTGTCCAGAAGGCTAAAAAAGCAAAGGACAGGTTGTTGAAACGAGAAGGGGATGATCGAGCAGAGTCAGGGACC
CAAGGATATGAGTCTTTCAGCTATGGAGGGGTTGATCCTTACATGTGGGAACCCCAGGAGCTTGGTGCTGTGAGG
AGCCATCTTTCCGACCTCAAAAAACACCGAGCTGCTAGAATTGACCACTATGTTGTGGAAGTCAATAAACTAATA
ATCAGGTTAGAGAAGCTCACTGCATTTGACAGAACAAATACTGAGTCTGCAAAGATTCGAGCAATAGAAAAGTCT
GTGGTGCCTTGGGTCAACGACCAGGATGTCCCTTTCTGTCCAGACTGTGGGAATAAGTTCAGCATCCGGAACCGC
CGCCACCACTGCCGCCTCTGCGGGTCTATTATGTGCAAGAAGTGTATGGAGCTCATCAGCCTTCCCTTGGCAAAC
AAGCTCACCAGTGCCAGCAAGGAGTCCCTGAGCACCCACACCAGCCCCAGCCAGTCACCCAACAGTGTCCATGGC
TCCCGCCGAGGCAGCATCAGCAGCATGAGCAGTGTCAGCTCGGTCCTGGATGAGAAGGACGATGACCGGATCCGC
TGCTGTACACACTGCAAGGACACGCTGCTCAAGAGAGAGCAGCAGATTGATGAGAAGGAGCACACACCTGACATC
GTGAAGCTCTACGAGAAATTACGACTTTGCATGGAGAAAGTTGACCAGAAAGCTCCAGAATACATCAGGATGGCA
GCATCATTAAATGCTGGGGAGACAACCTACAGTCTGGAACATGCCAGTGACCTTCGAGTGGAAGTGCAGAAAGTG
TATGAGCTGATAGACGCTTTAAGTAAGAAGATCTTAACCTTGGGCTTGAACCAGGACCCTCCACCACATCCAAGC
AATTTGCGGCTGCAGAGAATGATCAGATACTCAGCTACACTTTTTGTGCAGGAAAAGTTGCTTGGTTTGATGTCA
CTGCCGACCAAAGAACAGTTTGAGGAACTGAAAAAGAAAAGGAAGGAGGAAATGGAGAGGAAGAGGGCCGTGGAG
AGACAAGCTGCTCTGGAGTCCCAGCGAAGGCTTGAGGAAAGGCAGAGTGGCCTGGCTTCTCGAGCGGCCAACGGG
GAGGTGGCATCTCTCCGCAGGGGCCCTGCCCCCTTGAGAAAGGCTGAGGGCTGGCTCCCACTGTCAGGAGGTCAG
GGGCAGAGTGAGGACTCAGACCCGCTCCTCCAGCAGATCCACAACATCACATCATTCATCAGGCAGGCCAAGGCC
GCGGGCCGCATGGATGAAGTGCGCACTCTGCAGGAGAACCTGCGGCAGCTGCAGGACGAGTATGACCAGCAGCAG
ACAGAGAAGGCCATCGAGCTGTCCCGGAGGCAGGCTGAGGAGGAGGACCTGCAGCGGGAACAGCTGCAGATGTTG
CGTGAACGGGAGTTGGAACGAGAAAGGGAGCAGTTTCGGGTGGCATCCCTGCACACACGGACTCGGTCCCTGGAC
TTCAGAGAAATCGGCCCTTTTCAGCTGGAGCCCAGCAGAGAGCCTCGCACCCACCTTGCTTATGCTTTGGATCTA
GGCTCTTCCCCAGTTCCAAGCAGCACAGCTCCCAAGACCCCTTCACTTAGCTCAACTCAACCCACCAGAGTGTGG
TCTGGGCCCCCAGCCGTTGGCCAGGAGCGCTTACCCCAGAGCAGCATGCCACAGCAACATGAGGGGCCCTCCTTA
AACCCCTTTGATGAGGAAGACCTCTCCAGCCCCATGGAAGAGGCCACTACTGGTCCTCCTGCTGCAGGGGTTTCC
TTAGACCCTTCAGCCCGCATCCTGAAGGAGTACAATCCTTTCGAGGAAGAGGACGAGGAGGAGGAAGCAGTGGCA
GGGAATCCATTCATTCAGCCAGACAGCCCAGCTCCTAACCCCTTCAGTGAGGAAGACGAACATCCCCAGCAGAGG
CTCTCAAGCCCTCTGGTTCCTGGTAACCCCTTTGAGGAACCCACCTGTATCAACCCCCTTGAGATGGACAGTGAC
AGTGGGCCAGAGGCTGAGGAGCCCATAGAGGAAGAGCTCCTCCTGCAGCAGATCGATAACATCAAGGCATACATC
TTTGATGCCAAGCAGTGCGGCCGCCTGGATGAGGTAGAGGTGCTGACAGAGAATCTGCGGGAGCTGAAGCACACC
CTGGCCAAGCAGAAGGGGGGCACTGAC**TGA**

FIGURE 474

MASLDDPGEVREGFLCPLCLKDLQSFYQLHSHYEEEHSGEDRDVKGQIKSLVQKAKKAKDRLLKREGDDRAESGT
QGYESFSYGGVDPYMWEPQELGAVRSHLSDLKKHRAARIDHYVVEVNKLIIRLEKLTAFDRTNTESAKIRAIEKS
VVPWVNDQDVPFCPDCGNKFSIRNRRHHCRLCGSIMCKKCMELISLPLANKLTSASKESLSTHTSPSQSPNSVHG
SRRGSISSMSSVSSVLDEKDDDRIRCCTHCKDTLLKREQQIDEKEHTPDIVKLYEKLRLCMEKVDQKAPEYIRMA
ASLNAGETTYSLEHASDLRVEVQKVYELIDALSKKILTLGLNQDPPPHPSNLRLQRMIRYSATLFVQEKLLGLMS
LPTKEQFEELKKKRKEEMERKRAVERQAALESQRRLEERQSGLASRAANGEVASLRRGPAPLRKAEGWLPLSGGQ
GQSEDSDPLLQQIHNITSFIRQAKAAGRMDEVRTLQENLRQLQDEYDQQQTEKAIELSRRQAEEEDLQREQLQML
RERELEREREQFRVASLHTRTRSLDFREIGPFQLEPSREPRTHLAYALDLGSSPVPSSTAPKTPSLSSTQPTRVW
SGPPAVGQERLPQSSMPQQHEGPSLNPFDEEDLSSPMEEATTGPPAAGVSLDPSARILKEYNPFEEEDEEEAVA
GNPFIQPDSPAPNPFSEEDEHPQQRLSSPLVPGNPFEEPTCINPLEMDSDSGPEAEEPIEEELLLQQIDNIKAYI
FDAKQCGRLDEVEVLTENLRELKHTLAKQKGGTD

FIGURE 475

GAAAGAGACAAAGCAGCAATTAAAGTCAGCCCAGCACCAACTCCGACGCCAAGCGTTACACTGGAAACTACTTTT
TAAAGCAACAAAAGAGTCTAAAACAAAATACAACATTTCTTAAATACACTGTTTCCAGAAAGAGCTATTTTAACA
GAAGCAACTCAAAGATATCCCTTCGACAGAAGTGGAAGTGCTGAAAAATGCTCATCTCTCACACAGACTTTTGAT
GGACAGGAGTTTCTAAGTATCATGCCTACCAACAAGCTGTAAA**ATG**ATCACCCTGAACAATCAAGATCAACCTGT
CCCTTTTAACAGCTCACATCCAGATGAATACAAAATTGCAGCCCTTGTCTTCTATAGCTGTATCTTCATAATTGG
ATTATTTGTTAACATCACTGCATTATGGGTTTTCAGTTGTACCACCAAGAAGAGAACCACGGTAACCATCTATAT
GATGAATGTGGCATTAGTGGACTTGATATTTATAATGACTTTACCCTTTCGAATGTTTTATTATGCAAAAGATGA
ATGGCCATTTGGAGAGTACTTCTGCCAGATTCTTGGAGCTCTCACAGTGTTTTACCCAAGCATTGCTTTATGGCT
TCTTGCCTTTATTAGTGCTGACAGATACATGGCCATTGTACAGCCGAAGTACGCCAAAGAACTTAAAAACACGTG
CAAAGCCGTGCTGGCGTGTGTGGGAGTCTGGATAATGACCCTGACCACGACCACCCCTCTGCTACTGCTCTATAA
AGACCCAGATAAAGACTCCACTCCCGCCACCTGCCTCAAGATTTCTGACATCATCTATCTAAAAGCTGTGAACGT
GCTGAACCTCACTCGACTGACATTTTTTTTCTTGATTCCTTTGTTCATCATGATTGGGTGCTACTTGGTCATTAT
TCATAATCTCCTTCACGGCAGGACGTCTAAGCTGAAACCCAAAGTCAAGGAGAAGTCCATAAGGATCATCATCAC
GCTGCTGGTGCAGGTGCTCGTCTGCTTTATGCCCTTCCACATCTGTTTCGCTTTCCTGATGCTGGGAACGGGGGA
GAACAGTTACAATCCCTGGGGAGCCTTTACCACCTTCCTCATGAACCTCAGCACGTGTCTGGATGTGATTCTCTA
CTACATCGTTTCAAAACAATTTCAGGCTCGAGTCATTAGTGTCATGCTATACCGTAATTACCTTCGAAGCATGCG
CAGAAAAAGTTTCCGATCTGGTAGTCTACGGTCACTAAGCAATATAAACAGTGAAATGTTA**TGA**ATAATAAGGTT
CTTTCATTTCAATCCCATCAAAATTCACTTCACTAACTACTCTGGCGTCAATGGATATTCTGTATAATACTATCA
AGTCCCTTTTCTCTTGAAAAAATAAATTCATTATCTTCATTTTAAAAAAAAAAAAAAAA

FIGURE 476

MITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFIIGLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTL
PFRMFYYAKDEWPFGEYFCQILGALTVFYPSIALWLLAFISADRYMAIVQPKYAKELKNTCKAVLACVGVWIMTL
TTTTPLLLLYKDPDKDSTPATCLKISDIIYLKAVNVLNLTRLTFFFLIPLFIMIGCYLVIIHNLLHGRTSKLKPK
VKEKSIRIIITLLVQVLVCFMPFHICFAFLMLGTGENSYNPWGAFTTFLMNLSTCLDVILYYIVSKQFQARVISV
MLYRNYLRSMRRKSFRSGSLRSLSNINSEML

FIGURE 477

GGAATTCCAAAAAAAAAAAAATACGACTACACCTGCTCCGGAGCCCGCGGCGGTACCTGCAGCGGAGGAGCTCTGT
CTTCCCCTTCATCTCACGCGAGCCCGGCGTCCCGCCGCGTGCGCCCCGGCGCAGCCCGCCAGTCCGCCCGGAGCC
CGCCCAGTCGCCGCGCTGCACGCCCGGGGTGAACCCTCTGCCCTCGCTGGGACAGAGGGCCCCGCAGCCGTC**ATG**

CTTTCCGCCATCTACACAGTCCTGGCGGGACTGCTGTTCCTGCCGCTCCTGGTGAACCTCTGCTGCCCATACTTC
TTCCAGGACATAGGCTACTTCTTGAAGGTGGCCGCCGTGGGCCGGAGGGTGCGCAGCTACGGGCAGCGGCGGCCG
GCGCGCACCATCCTGCGGGCGTTCCTGGAGAAAGCGCGCCAGACGCCACACAAGGCTTTTCTGCTCTTCCGCGAC
GAGACTCTCACCTACGCGCAGGTGGACCGGCGCAGCAATCAAGTGGCCCGGGCGCTGCACGACCACCTCGGCCTG
CGCCAGGGAGACTGCGTGGCGCTCCTTATGGGTAACGAGCCGGCCTACGTGTGGCTGTGGCTGGGGCTGGTGAAG
CTGGGCTGTGCCATGGCGTGCCTCAATTACAACATCCGCGCGAAGTCCCTGCTGCACTGCTTCCAGTGCTGCGGG
GCGAAGGTGCTGCTGGTGTCGCCAGAACTACAAGCAGCTGTCGAAGAGATACTGCCAAGCCTTAAAAAAGATGAT
GTGTCCATCTATTATGTGAGCAGAACTTCTAACACAGATGGGATTGACTCTTTCCTGGACAAAGTGGATGAAGTA
TCAACTGAACCTATCCCAGAGTCATGGAGGTCTGAAGTCACTTTTTCCACTCCTGCCTTATACATTTATACTTCT
GGAACCACAGGTCTTCCAAAAGCAGCCATGATCACTCATCAGCGCATATGGTATGGAACTGGCCTCACTTTTGTA
AGCGGATTGAAGGCAGATGATGTCATCTATATCACTCTGCCCTTTTACCACAGTGCTGCACTACTGATTGGCATT
CACGGATGTATTGTGGCTGGTGCTACTCTTGCCTTGCGGACTAAATTTTCAGCCAGCCAGTTTTGGGATGACTGC
AGAAAATACAACGTCACTGTCATTCAGTATATCGGTGAACTGCTTCGGTATTTATGCAACTCACCACAGAAACCA
AATGACCGTGATCATAAAGTGAGACTGGCACTGGGAAATGGCTTACGAGGAGATGTGTGGAGACAATTTGTCAAG
AGATTTGGGGACATATGCATCTATGAGTTCTATGCTGCCACTGAAGGCAATATTGGATTTATGAATTATGCGAGA
AAAGTTGGTGCTGTTGGAAGAGTAAACTACCTACAGAAAAAAATCATAACTTATGACCTGATTAAATATGATGTG
GAGAAAGATGAACCTGTCCGAGATGAAAATGGATATTGCGTCAGAGTTCCCAAAGGTGAAGTTGGACTTCTGGTT
TGCAAAATCACACAACTTACACCATTTAATGGCTATGCTGGAGCAAAGGCTCAGACAGAGAAGAAAAAACTGAGA
GATGTCTTTAAGAAAGGAGACCTCTATTTCAACAGTGGAGATCTCTTAATGGTTGACCATGAAAATTTCATCTAT
TTCCACGACAGAGTTGGAGATACATTCCGGTGGAAAGGGGAAAATGTGGCCACCACTGAAGTTGCTGATACAGTT
GGACTGGTTGATTTTGTCCAAGAAGTAAATGTTTATGGAGTGCATGTGCCAGATCATGAGGGTCGCATTGGCATG
GCCTCCATCAAAATGAAAGAAAACCATGAATTTGATGGAAAGAAACTCTTTCAGCACATTGCTGATTACCTACCT
AGTTATGCAAGGCCCCGGTTTCTAAGAATACAGGACACCATTGAGATCACTGGAACTTTTAAACACCGCAAAATG
ACCCTGGTGGAGGAGGGCTTTAACCCTGCTGTCATCAAAGATGCCTTGTATTTCTTGGATGACACAGCAAAAATG
TATGTGCCTATGACTGAGGACATCTATAATGCCATAAGTGCTAAAACCCTGAAACTC**TGA**ATATTCCCAGGAGGA
TAACTCAACATTTCCAGAAAGAAACTGAATGGACAGCCACTTGATATAATCCAACTTTAATTTGATTGAAGATTG
TGAGGAAATTTTGTAGGAAATTTGCATACCCGTAAAGGGAGACTTTTTTAAATAACAGTTGAGTCTTTGCAAGTA
AAAAGATTTAGAGATTATTATTTTTCAGTGTGCACCTACTGTTTGTATTTGCAAACTGAGCTTGTTGGAGGGAAG
GCATTATTTTTTAAAATACTTAGTAAATTAAATGAAC

FIGURE 478

MLSAIYTVLAGLLFLPLLVNLCCPYFFQDIGYFLKVAAVGRRVRSYGQRRPARTILRAFLEKARQTPHKPFLLFR
DETLTYAQVDRRSNQVARALHDHLGLRQGDCVALLMGNEPAYVWLWLGLVKLGCAMACLNYNIRAKSLLHCFQCC
GAKVLLVSPELQAAVEEILPSLKKDDVSIYYVSRTSNTDGIDSFLDKVDEVSTEPIPESWRSEVTFSTPALYIYT
SGTTGLPKAAMITHQRIWYGTGLTFVSGLKADDVIYITLPFYHSAALLIGIHGCIVAGATLALRTKFSASQFWDD
CRKYNVTVIQYIGELLRYLCNSPQKPNDRDHKVRLALGNGLRGDVWRQFVKRFGDICIYEFYAATEGNIGFMNYA
RKVGAVGRVNYLQKKIITYDLIKYDVEKDEPVRDENGYCVRVPKGEVGLLVCKITQLTPFNGYAGAKAQTEKKKL
RDVFKKGDLYFNSGDLLMVDHENFIYFHDRVGDTFRWKGENVATTEVADTVGLVDFVQEVNVYGVHVPDHEGRIG
MASIKMKENHEFDGKKLFQHIADYLPSYARPRFLRIQDTIEITGTFKHRKMTLVEEGFNPAVIKDALYFLDDTAK
MYVPMTEDIYNAISAKTLKL

FIGURE 479

GGTCGCGCAGCTGTGTTCGCGGACTCAGGTGGAAGGAATTTCTTCTCTTCGTTGACGTTGCTGGTGTTCACTGTT
TGGAATTAGTCAAGTTTCGGGAATCACCGTCGCTGCCATCAAC**ATG**TCGGTCCCAAGCGCTCTCATGAAGCAACC
GCCCATTCAGTCTACGGCTGGGGCCGTCCCAGTTCGCAATGAGAAAGGTGAGATTTCAATGGAAAAAGTGAAGGT
AAAGCGTTATGTGTCCGGAAAAAGGCCAGACTATGCCCCTATGGAGTCCTCAGATGAGGAGGATGAAGAATTTCA
GTTCATTAAGAAAGCCAAAGAACAAGAAGCAGAGCCTGAGGAACAGGAGGAGGATTCATCCAGTGACCCCCGGCT
ACGGCGTTTACAGAACCGTATTAGTGAAGATGTGGAAGAGAGATTGGCTCGACATCGAAAAATAGTGGAACCTGA
AGTGGTAGGAGAGAGTGACTCAGAAGTAGAAGGAGATGCTTGGCGCATGGAACGAGAAGACAGCAGTGAAGAAGA
GGAGGAGGAAATTGATGATGAGGAAATAGAGCGGCGGCGTGGCATGATGCGTCAGCGAGCACAGGAGAGAAAAAA
TGAAGAGATGGAAGTCATGGAAGTGGAAGATGAGGGTCGTTCTGGAGAGGAGTCAGAATCAGAGTCTGAGTATGA
AGAGTACACAGACAGTGAAGATGAGATGGAGCCTCGCCTTAAGCCAGTCTTCATTCGAAAGAAGGACCGAGTGAC
AGTTCAAGAACGTGAAGCCGAAGCATTGAAACAGAAGGAGCTGGAGCAGGAAGCCAAACGCATGGCTGAGGAAAG
GCGCCAGTACACACTCCAGATTGTCGGAGAGGAAACCCCAAAAGAGCTGGAAGAGAACAAGCGATCCCTGGCTGC
ATTGGATGCACTCAATACTGATGATGAAAATGATGAGGAGGAATATGAGGCATGGAAAGTTCGAGAGCTAAAAAG
AATCAAGAGGGACAGAGAAGATCGAGAAGCGCTTGAGAAGGAGAAAGCAGAAATTGAACGCATGCGAAACCTGAC
TGAGGAAGAGAGGAGAGCTGAACTTCGGGCAAACGGCAAAGTCATTACCAACAAAGCTGTTAAGGGCAAATACAA
GTTCTTACAGAAGTATTATCACCGGGGTGCCTTCTTCATGGATGAGGATGAAGAAGTATACAAGAGAGATTTCAG
CGCTCCTACCCTGGAGGATCATTTCAATAAAACCATTCTTCCTAAAGTCATGCAGGTCAAGAACTTTGGACGCTC
AGGTCGCACCAAATACACTCACCTTGTGGATCAAGATACCACCTCCTTTGACTCAGCTTGGGGCCAAGAGAGTGC
CCAGAACACAAAGTTCTTCAAACAAAAGGCAGCTGGGGTACGAGATGTATTTGAGCGGCCATCTGCCAAGAAGCG
GAAAACTACC**TAG**GGTCCAACTGCTTATTCTTCCAACTGTGGAACACAAGGGGAGTCTCAGCATCTGGTCCTTGA
TTGGGTTTTTTCATTGTTTCCTTGGCCCCTGTATCCAGATATTGGACTTACTGCTATACTTGTGATACTGGGTAG
CCCAGACTTTGAAGGTGCTTTGTGAGGTTTGGACTCATGCTGAGAAACCCACAGGAAAGCACTGTCCAGGTAGGA
TTAGAGGCTTCCCACTTAAAACTATTTCTGAGAAATCTTAGGTTTTATCACTGCTATGGTTTCCCATATTTACTT
GGGACTGTTCTGACTTTCTTTTTCCAGCCCTTAGCTTGGGTTAGAAAAGTGGACATGTAAGTGAACAATGCATTA
CTTCTACCTTAGGTTTAGGAGTAATATACCCGGAAATCTAAGCTCATGGAAACATGTTTTCCATTTGGGGTTGGA
GTCCGTTTTTCTAGTTGTACATACTTGXGGATCCATATATGTGTGCATGTCAWGAAATAAAAGAATCACACAACA
AAAAA

FIGURE 480

MSVPSALMKQPPIQSTAGAVPVRNEKGEISMEKVKVKRYVSGKRPDYAPMESSDEEDEEFQFIKKAKEQEAEPEE
QEEDSSSDPRLRRLQNRISEDVEERLARHRKIVEPEVVGESDSEVEGDAWRMEREDSSEEEEEEIDDEEIERRRG
MMRQRAQERKNEEMEVMEVEDEGRSGEESESESEYEEYTDSEDEMEPRLKPVFIRKKDRVTVQEREAEALKQKEL
EQEAKRMAEERRQYTLQIVGEETPKELEENKRSLAALDALNTDDENDEEEYEAWKVRELKRIKRDREDREALEKE
KAEIERMRNLTEEERRAELRANGKVITNKAVKGKYKFLQKYYHRGAFFMDEDEEVYKRDFSAPTLEDHFNKTILP
KVMQVKNFGRSGRTKYTHLVDQDTTSFDSAWGQESAQNTKFFKQKAAGVRDVFERPSAKKRKTT

FIGURE 481

GCGACCCGGGGCGTTTGCAGCGGTGCCGAGGAAGAGGACGGGAACGGTGTTACGATTGCCTGCGTTTAGGAGGTG
GCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTCAGAGTAGTTCAC
AACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAACAACAAAAAACTTAAGCTTTAATTTCATCTGGAA
TTCCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGC
TCTCCGACTACTCACCCCGAGTGTAAAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGG**ATG**GCCTCGGCTC
TCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTT
TCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAACTGGATGTACTTCTATGAGT
ATGAGCCGATTTACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAACTGCTCTCATCAAAATCCATTTC
TGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAA
AGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGG
CATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATAACC
TGACCTTGAAAACCATTATGGCATTCAGGTGGGTAACTGAGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAG
ACACTGATGTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTTTTCA
CAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTTCTTACCAGGAGTATC
CTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAATGTCCAGAGATTTGGTGCCAAGGATCTATG
AAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAAAGTGA
ACATTCATATTCCAGAAGACACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTG
TGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACCACATGCC
ATTAT**TAA**

FIGURE 482

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHFTLREHSNCSH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLLGQEAEKEDKMLALSLEDEHLLYGDIIRQDFLD
TYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

FIGURE 483

CGAAAGGCCGGCCTTGGCTGCGACAGCCTGGGTAAGAGGTGTAGGTCGGCTTGGTTTTCTGCTACCCGGAGCTGG
GCAAGCGGGTTGGGAGAACAGCGAAGACAGCGTGAGCCTGGGCCGTTGCCTCGAGGCTCTCGCCCGGCTTCTCTT
GCCGACCCGCCACGTTTGTTTGGATTTAATCTTACAGCTGGTTGCCGGCGCCCGCCCGCCCGCTGGCCTCGCGGT
GTGAGAGGGAAGCACCCGTGCCTGTGGCTGGTGGCTGGCGCCTGGAGGGTCCGCACACCCGCCCGGCCGCGCCGC
TTTGCCCGCGGCAGCCGCGTCCCTGAACCGCGGAGTCGTGTTTGTGTTTGACCCGCGGGCGCCGGTGGCGCGCGG
CCGAGGCCGGTGTCGGCGGGGCGGGGCGGTCGCGGCGGAGGCAGAGGAAGAGGGAGCGGGAGCTCTGCGAGGCCG
GGCGCCGCC**ATG**GAACTGGGCCCGAGCCCCGCACCGCGCCGCCTGCTCTTCGCCTGCAGCCCCCCTCCCGCGTCG
CAGCCCGTCGTGAAGGCGCTATTTGGCGCTTCAGCCGCCGGGGGACTGTCGCCTGTCACCAACCTGACCGTCACT
ATGGACCAGCTGCAGGGTCTGGGCAGTGATTATGAGCAACCACTGGAGGTGAAGAACAACAGTAATCTGCAGAGA
ATGGGCTCCTCCGAGTCAACAGATTCAGGTTTCTGTCTAGATTCTCCTGGGCCATTGGACAGTAAAGAAAACCTT
GAAAATCCTATGAGAAGAATACATTCCCTACCTCAAAAGCTGTTGGGATGTAGTCCAGCTCTGAAGAGGAGCCAT
TCTGATTCTCTTGACCATGACATCTTTCAGCTCATCGACCCAGATGAGAACAAGGAAAATGAAGCCTTTGAGTTT
AAGAAGCCAGTAAGACCTGTATCTCGTGGCTGCCTGCACTCTCATGGACTCCAGGAGGGTAAAGATCTCTTCACA
CAGAGGCAGAACTCTGCCCAGCTCGGAATGCTTTCCTCAAATGAAAGAGATAGCAGTGAACCAGGGAATTTCATT
CCTCTTTTTACACCCCAGTCACCTGTGACAGCCACTTTGTCTGATGAGGATGATGGCTTCGTGGACCTTCTCGAT
GGAGAGAATCTGAAGAATGAGGAGGAGACCCCCTCGTGCATGGCAAGCCTCTGGACAGCTCCTCTCGTCATGAGA
ACTACAAACCTTGACAACCGATGCAAGCTGTTTGACTCCCCTTCCCTGTGTAGCTCCAGCACTCGGTCAGTGTTG
AAGAGACCAGAACGTTCTCAAGAGGAGTCTCCACCTGGAAGTACAAAGAGGAGGAAGAGCATGTCTGGGGCCAGC
CCCAAAGAGTCAACTAATCCAGAGAAGGCCCATGAGACTCTTCATCAGTCTTTATCCCTGGCATCTTCCCCCAAA
GGAACCATTGAGAACATTTTGGACAATGACCCAAGGGACCTTATAGGAGACTTCTCCAAGGGTTATCTCTTTCAT
ACAGTTGCTGGGAAACATCAGGATTTAAAATACATCTCTCCAGAAATTATGGCATCTGTTTTGAATGGCAAGTTT
GCCAACCTCATTAAAGAGTTTGTTATCATCGACTGTCGATACCCATATGAATACGAGGGAGGCCACATCAAGGGT
GCAGTGAACTTGCACATGGAAGAAGAGGTTGAAGACTTCTTATTGAAGAAGCCCATTGTACCTACTGATGGCAAG
CGTGTCATTGTTGTGTTTCACTGCGAGTTTTCTTCTGAGAGAGGTCCCCGCATGTGCCGGTATGTGAGAGAGAGA
GATCGCCTGGGTAATGAATACCCCAAACTCCACTACCCTGAGCTGTATGTCCTGAAGGGGGGATACAAGGAGTTC
TTTATGAAATGCCAGTCTTACTGTGAGCCCCCTAGCTACCGGCCCATGCACCACGAGGACTTTAAAGAAGACCTG
AAGAAGTTCCGCACCAAGAGCCGGACCTGGGCAGGGGAGAAGAGCAAGAGGGAGATGTACAGTCGTCTGAAGAAG
CTC**TGA**GGGCGGCAGGACCAGCCAGCAGCAGCCCAAGCTTCCCTCCATCCCCCTTTACCCTCTTTCCTGCAGAGA
AACTTAAGCAAAGGGGACAGCTGTGTGACATTTGGAGAGGGGGCCTGGGACTTCCATGCCTTAAACCTACCTCCC
ACACTCCCAAGGTTGGAGCCCAGGGCATCTTGCTGGCTACGCCTCTTCTGTCCCTGTTAGACGTCCTCCGTCCAT
ATCAGAACTGTGCCACAATGCAGTTCTGAGCACCGTGTCAAGCTGCTCTGAGCCACAGTGGGATGAACCAGCCGG
GGCCTTATCGGGCTCCAGCATCTCATGAGGGGAGAGGAGACGGAGGGGAGTAGAGAAGTTTACACAGAAATGCTG
CTGGCCAAATAGCAAAGAG

FIGURE 484

MELGPSPAPRRLLFACSPPPASQPVVKALFGASAAGGLSPVTNLTVTMDQLQGLGSDYEQPLEVKNNSNLQRMGS
SESTDSGFCLDSPGPLDSKENLENPMRRIHSLPQKLLGCSPALKRSHSDSLDHDIFQLIDPDENKENEAFEFKKP
VRPVSRGCLHSHGLQEGKDLFTQRQNSAQLGMLSSNERDSSEPGNFIPLFTPQSPVTATLSDEDDGFVDLLDGEN
LKNEEETPSCMASLWTAPLVMRTTNLDNRCKLFDSPSLCSSSTRSVLKRPERSQEESPPGSTKRRKSMSGASPKE
STNPEKAHETLHQSLSLASSPKGTIENILDNDPRDLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVLNGKFANL
IKEFVIIDCRYPYEYEGGHIKGAVNLHMEEEVEDFLLKKPIVPTDGKRVIVVFHCEFSSERGPRMCRYVRERDRL
GNEYPKLHYPELYVLKGGYKEFFMKCQSYCEPPSYRPMHHEDFKEDLKKFRTKSRTWAGEKSKREMYSRLKKL

FIGURE 485

GGAGAAGGGGTTTGAGATAGTGAATTCCTAAGAAGAAAATAATGGATTGCATATTAGTTGTTCTCTAAGTGGACT
CAACAGTGTGCAAGCTTGTTGGAAAAGCCAAAAGAAG**ATG**GCAACTCCTTATGTCCCAGTTCCTATGCCCATAGG
AAACTCTGCTTCCAGTTTTACAACAAACAGAAATCAAAGAAGTTCTTCTTTTGGCAGTGTCTCAACAAGCTCAAA
TTCTTCTAAGGGCCAGTTAGAAGACTCAAATATGGGTAATTTTAAACAGACAAGTGTTCCTGATCAAATGGATAA
TACTTCATCTGTCTGTAGCAGTCCCCTCATTAGGACTAAATTTACAGGTACAGCTTCTTCCATTGAGTATTCTAC
TAGACCAAGAGACACTGAAGAACAAAATCCGGAAACAGTGAATTGGGAAGATAGACCATCTACACCTACTATACT
GGGTTATGAAGTGATGGAAGAAAGAGCTAAATTTACTGTATATAAAATACTAGTAAAGAAAACCCCAGAAGAAAG
CTGGGTAGTTTTCAGAAGATACACTGACTTCTCTAGGCTTAATGACAAATTAAAAGAGATGTTTCCAGGTTTTCG
ATTAGCACTTCCTCCAAAACGCTGGTTTAAAGATAATTACAATGCTGACTTTTTAGAAGACAGACAATTAGGATT
ACAAGCGTTTCTTCAAAATTTAGTAGCTCACAAGGACATTGCTAACTGCCTTGCAGTGAGAGAATTTCTTTGTTT
GGATGATCCACCGGGTCCATTTGATAGCCTAGAAGAAAGCAGGGCATTCTGTGAAACTTTAGAAGAGACAAACTA
CCGCTTACAGAAAGAACTACTTGAAAAACAAAAGGAGATGGAATCACTAAAGAAACTGCTCAGTGAGAAGCAACT
TCATATAGACACTTTAGAGAACAGAATCAGAACATTGTCTTTAGAACCTGAAGAATCACTGGATGTGTCAGAAAC
AGAAGGTGAACAGATCCTAAAGGTGGAGTCCTCTGCACTTGAGGTTGATCAAGATGTCTGGATGAGATCTAGAGC
TGATAATAAACCATGCTTAAGTTTTAGTGAACCTGAAAATGCTGTATCAGAGATAGAAGTAGCAGAAGTGGCATA
TGATGCTGAAGAAGAC**TAA**TGTATCACAAGCAGTTCCCTCCATTTAGACTATTCAAAAATTTAGAAGAGTGGCAA
ATACTATTTTAAAAGAAGAACCAAGAACTGTAAAACATATAGAAAAGAGCAAGAATGCACATGTATAAAGTTTAC
ATAAAGAGTTTTTTTAGTTATTGAGATAGGAAATATATTCACTGCTGCTTTTAATTGTATTTTATCCAATTACAT
TTAATACACTAAAAAAAATCTTGTTGGAATTCTGTTATCAAGGCCCACATTCTTAAATACTGTGCATAAATTATT
ATGGTGTTTTGCCTATATATTGCTCCAAACTACTGTGTATATATGTATGTGTGTTAAATCACCAATTATATTAAT
CAAATGGAAATTAATTCGATGTTCATATCTGGGTGATATATTCTTCTTTATATCTCTGACATGACATATTTTCAT
TAATAGTTTAAATCAGTGACCATCATAATAAAGATAAAATTTAGTTGAGTTTTTAATGTTTACATGTTTACATCT
CTAAATAAAATTTGCTTATTTGAAATGTTAATGCTCTTTAGAAAAATGACTTTCTAGTACCAAAGGAAAACTACT
TGAAAGAGCTGTAATCATATAGCTAAAGTGATAAGATAGCCTTGATTTTAAAAGCTGATTCATTAATATCAAAAT
ACTTTAATAAGTGTCACAGTTATTAATATGTAACATTTGTTTAGTTTCCACGTAATCTTTATCTCTACCTAGATT
TAGTGAGTTTGCCTCTTTCAGAATACTACCTCCTTTTGTTA

FIGURE 486

MATPYVPVPMPIGNSASSFTTNRNQRSSSFGSVSTSSNSSKGQLEDSNMGNFKQTSVPDQMDNTSSVCSSPLIRT
KFTGTASSIEYSTRPRDTEEQNPETVNWEDRPSTPTILGYEVMEERAKFTVYKILVKKTPEESWVVFRRYTDFSR
LNDKLKEMFPGFRLALPPKRWFKDNYNADFLEDRQLGLQAFLQNLVAHKDIANCLAVREFLCLDDPPGPFDSLEE
SRAFCETLEETNYRLQKELLEKQKEMESLKKLLSEKQLHIDTLENRIRTLSLEPEESLDVSETEGEQILKVESSA
LEVDQDVWMRSRADNKPCLSFSEPENAVSEIEVAEVAYDAEED

FIGURE 487

CCCTTTCGCTGCGGCCTTTCCCCAACCCGGACCCGGCACTTCTCGGGTTCCGCGACTGCCGATCGCCCCGGCGCG
GCACCGCTCCCTCAGGAGTCGCCTAGGCCGCGCAGTCTCCCGACTTCTCGTCAGGCTTTCGCGCCGGCGCTCCAG
CAATCACTGGCTGGAGAAGGTGGGCGTTCCGGCTCGAGAGGACCCTGCCGCGGCTCCGGAAGAGCCTCGTCCTGG
GCGGCGGTGGTGCGGCGGTCGCCGTTATGGCCACTGGGCTGGGCGGCTGACCGCGGGCTAGGAAAGGGCCCAGGG
CCCGAATCTCGGTGGCCGCTGCTCCAGCGCGGCCTGCGCC**ATG**GCCTCCTCCGCCGCCTCCTCGGAGCATTTCGA
GAAGCTGCACGAGATCTTCCGCGGCCTCCATGAAGACCTACAAGGGGTGCCCGAGCGGCTGCTGGGGACGGCGGG
GACCGAAGAAAAGAAGAAATTGATCAGGGATTTTGATGAAAAGCAACAGGAAGCAAATGAAACGCTGGCAGAGAT
GGAGGAGGAGCTACGTTATGCACCCCTGTCTTTCCGAAACCCCATGATGTCTAAGCTTCGAAACTACCGGAAGGA
CCTTGCTAAACTCCATCGGGAGGTGAGAAGCACACCTTTGACAGCCACACCTGGAGGCCGAGGAGACATGAAATA
TGGCATATATGCTGTAGAGAATGAGCATATGAATCGGCTACAGTCTCAAAGGGCAATGCTTCTGCAGGGCACTGA
AAGCCTGAACCGGGCCACCCAAAGTATTGAACGTTCTCATCGGATTGCCACAGAGACTGACCAGATTGGCTCAGA
AATCATAGAAGAGCTGGGGGAACAACGAGACCAGTTAGAACGTACCAAGAGTAGACTGGTAAACACAAGTGAAAA
CTTGAGCAAAAGTCGGAAGATTCTCCGTTCAATGTCCAGAAAAGTGACAACCAACAAGCTGCTGCTTTCCATTAT
CATCTTACTGGAGCTCGCCATCCTGGGAGGCCTGGTTTACTACAAATTCTTTCGCAGCCAT**TGA**ACTTCTATAGG
GAAGGGTTTGTGGACCAGAACTTTGACCTTGTGAATGCATGATGTTAGGGATGTGGATAGAATAAGCATATTGCT
GCTGTGGGCTGACAGTTCAAGGATGCACTGTATAGCCAGGCTGTGGGAGGAGGGAGGAAAGATGAAAAACCACTT
AAATGTGAAGGAACAACAGCAACAAGACCAGTATGATATACCAAGGTAATAAATGCTGTTTATGACTTCTTTAAA
AAAAAAAAAAAA

FIGURE 488

MASSAASSEHFEKLHEIFRGLHEDLQGVPERLLGTAGTEEKKKLIRDFDEKQQEANETLAEMEEELRYAPLSFRN
PMMSKLRNYRKDLAKLHREVRSTPLTATPGGRGDMKYGIYAVENEHMNRLQSQRAMLLQGTESLNRATQSIERSH
RIATETDQIGSEIIEELGEQRDQLERTKSRLVNTSENLSKSRKILRSMSRKVTTNKLLLSIIILLELAILGGLVY
YKFFRSH

FIGURE 489

TGCCTATCATCTGGCCACATGAGGCTGTCAAGCAAAAGAATAGGAGTGTAGTTGAGTAGCTGGTTGGCCCTACAT
CTCTGAGAAGTGACGGCACACTGGGTTGGCATAAGATATCCTAAAATCACGCTGGAACCTTGGGCAAGGAAGAAT
GTGAGCAAGAGTAGAGAGAGTGCCTGGATTTCATGTCAGTGAAGCCAAGTCACCATATCATATTTTTGAATGAAC
TCTGAGTCAGTTGAAATAGGGTACCATCTAGGTCAGTTTAAGAAGAGTCAGCTCAGAGAAAGCAAGCATAAGGGA
AA**ATG**TCACGTAAACTAGATCAGGGAACAAAATCCTCTCCTTGTGGAAATATCCCATGCAGTTTGTTGATACAAC
TTAGTATCTTATTGCCTAAAAAAAAATTTCTTATCATTGTTTCAAAAAAGCAAAATCATGGAAAATTTTTGTTGT
CCAGGCAAATAAAAGGTCATTTTAATTTAGCTGC

FIGURE 490

MSRKLDQGTKSSPCGNIPCSLLIQLSILLPKKKFLIIVSKKQNHGKFLLSRQIKGHFNLA

FIGURE 491

ACAGCAGTTACACTGCGGCGGGCGTCTGTTCTAGTGTTTGAGCCGTCGTGCTTCACCGGTCTACCTCGCTAGC**<u>AT</u>**
<u>G</u>TCGGGCCGCGGCAAGACTGGCGGCAAGGCCCGCGCCAAGGCCAAGTCGCGCTCGTCGCGCGCCGGCCTCCAGTT
CCCAGTGGGCCGTGTACACCGGCTGCTGCGGAAGGGCCACTACGCCGAGCGCGTTGGCGCCGGCGCGCCAGTGTA
CCTGGCGGCAGTGCTGGAGTACCTCACCGCTGAGATCCTGGAGCTGGCGGGCAATGCGGCCCGCGACAACAAGAA
GACGCGAATCATCCCCCGCCACCTGCAGCTGGCCATCCGCAACGACGAGGAGCTCAACAAGCTGCTGGGCGGCGT
GACGATCGCCCAGGGAGGCGTCCTGCCCAACATCCAGGCCGTGCTGCTGCCCAAGAAGACCAGCGCCACCGTGGG
GCCGAAGGCGCCCTCGGGCGGCAAGAAGGCCACCCAGGCCTCCCAGGAGTAC**<u>TAA</u>**GAGGGCCCGCGCCGCGGCCG
GCCGCCCCAGCTCCCCATGCCACCACAAAGGCCCTTTTAAGGGCCACCACCGCCCTCATGGAAAGAGCTGAGCCG
CTTCAGACTGCGGGGCAAGCGGGCCGCGGCTCCCTTCCCCTCCCCTCCCCTCGCCCGCCTTCGCCGCCCGGCCTC
GAGTCCCCGCCCGCCCCCGCTCCCGTCCCGCACCGCCTGCCGCGTCGGCCTCGGGCCTGCCCTGTCCGCCGTCCG
CCCTCCGGTAGGGTTCGGGCCTTCCGGATGCGGCTTGGGCGCTCTTCGGGGACCTCCGTGGCGCGGAAGACCCGA
GCCTGCCGGGGGGAGGCCGGCGGCGCCGCACCTGCCCGCCTCGGCGTTCGTGACTCAGCCGCCCCATCCCGAGTC
GCTAAGGGGCTGCGGGGAGGCCGCAGCACCTTCTGGAAGACTTGGCCTTCCGCTCTGACGCAGGGCCGAGGTGGG
CAGTCCAGGCCGAGAGCCGGCGGCCCTGAAGGTGAGTGAGGCCCTCGGCAGCTGCAGCCGGGGTGTCTGGTACCC
CCCCGGCGTGGTGCTTAGCCCAGGACTTTCAGACGGCCGCTGGCCGGGAGGCTTTGGTGGGAGAGACGCGATCGC
CGATTTCGGTCTGGCGCCCCTTCTGCGGCCGGGACCCAGGCCTTTCACATCAGCTCTCCCTCCATCTTCATTCAT
AGGTCTGCGCTGGGGCCGGGACGAAGCACTTGGTAACAGGCACATCTTCCTCCCGAGTGACTGCCTCCTAGGAGG
ACATTTAGGGGAGGGCAGAGGCCTGCAGTTTGGCTTCACGGCTGGCTATGTGGACAGCAAGAGTCGTTTTGCGGA
ACGCGACTGGCAGCCAGGCCTGTCGGGCCCCCGACGCCGCCCCATTTCCCTTCCAGCAAACTCAACTCGGCAATC
CAAGCACCTAGATACCAGCACAAGTCGGTTAATCCCTGTCTGGACTGAGCCTCCGTTGGCTTCTGAACTGGAATT
CTGCAGCTAACCCTTCCACGACTAGAACCTTAGGCATTGGGGAGTTTTAGATGGACTAATTTTATTAAAGGATTG
TTTTTTTTTT

FIGURE 492

MSGRGKTGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGHYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNK
KTRIIPRHLQLAIRNDEELNKLLGGVTIAQGGVLPNIQAVLLPKKTSATVGPKAPSGGKKATQASQEY

FIGURE 493

GATGACAATAAGGAAGTTCCTTTCCTTTGGGATTATTTCTGCCTGAAAGCTCAAGACTTTTAGCCACATCATTGT
CTGGGCTCCACGGGAAGGCAGTGCCACATGCTGAGGCATGCTGGGAAAAGACTTTGTTCCATCCTGTTTTGTTGA
CATGCTCTTCATTTTTAAGCCTGAAACCGAAGCTTCCTGCTAAGAATTCAAACCATGGAGAAAAACGCAGCCATG
ATAACGGCCACTACTTCCTGAGCCTCCAGTGTTCCCTGTGCTTGGGGATCCATATATGTCACTTAACCTTAACCT
TCACAACACCAGGGCAGCCTCCATTTTCACAAGTGAAGAAATGGAGGCCCAGAGTCACTTAGAAGATGCTCGAAG
GTGCACAGCTGCTAAGTGGTGGTGCTGGGATTTGTCCTCAGGTCCTCAAGAGTCCTGACTCTTATGTGCTGGCTC
CCCACGGAGGCGTGGAGTCTTGTTTGCTGGGCATTTGACAGAAATGTTTCTGCTCATCTTCTGCCACAGGTTGGT
CCTTCAGCGTCAAGATTCCTGGGCCACTTATTAATAGAAGGCACCAGGACACAGGTGCAGGGATGCAGAGCTGGA
TGCTGCCTTCTCAATAGGAGAAGCCAAGAAACGCAGATGCCGATGCTTAATCAACTCCGTCTCTCCCTCTAGTGA
CTCGGGGATAGCTGCCCTGATGCCAAGGCGATTGTCTTCTGGAAGCAGCCACGCCGTGTGAGGTTCCTCATCACT
GCCCTGCATCTCCCTGCGAGCTCTCGGGGATAATTGCAAAATCACGTTTGATTCCAGGGGAGCAGAAAGCAGCAG
GAGCCGTGAATTCTCCAACTCTTAACTGGTCCTCGACTGGAGCCACTTTTCCCTGCCCACCCATCCCTGTGGCGG
ATTCATTACAGTTATCCAAAGCCGGTTTTAACTTTGCTCCCCCTGGGCTCAGAAGTCTGTCAGTGGGTCCTGAGC
GGCTTCACCATTCAAGTTTATTCCTATCAGCCTGGAATACA**ATG**CTCTATCTGGCTCCGGTTGCTTCTCCAAACC
TTCTCTC

FIGURE 494

MLYLAPVASPNLL

FIGURE 495

AAAAAAAAGAAAAAAAAAGATATATATATTCCTACTCTTATTAAATGAATATAGCATTTCT**TAG**CAACTTCTTTT
GATTTGTGAGTATATATTTTCTTGGCCTCAAAATTAAAGTAAAAAGTATCCTCTTACTCAGAGGAGGACAGGGGC
AAGAGCCTGGGACCTTATTTGCTAATTAAAATGNNNNNNNNNNNNNNNNNNNNNNNNGACAGACAATTTTGAGAGC
CATTTTAATATAATTGCCTCCCTAGAAACATACCTTTTAGGGAATTTTTATCACTAAACCACATGTTATTTAAAT
ACGTACATGTTTAACATAAATACATACATAAAATTCACATGCATACTTAACACTTATGTTAAATATATTCAATGT
ATATACATATGTACACAATATATGCATATATACATGTGGGTATGTGGTATGTGTGCATGTGTGTGTATGGCCAGC
TACATAATTGGGGGGGACTAGGGGCAAAATGAAACTGTACGGCCCTCGTTCAAAAATTAGGTGTGGGGTGCTTCT
AAGCACAGTCTTGTGCAACTGCACAGGTTGCATGTCCATGAAGCCATCCTGTGTGTGTGCACATATGTGTATGAA
TATGTATTTTATATAATACATATATATGCATGTATGTATCTGAGAAGAAATGTTTAAAAGGCTACATACAAGCTT
TTCCAGGTCTCTACTATCTGTTAACTAACTAGAGACATAACTCACAATATGCAGTCCCCACTGAGTGTTCACCAT
AATTTGAGATTCTTGGCATGTTAACTTTTCATTATGGAATATTGAATAATTTCAATATTATTCATACATTTCTTG
ATGTTCAAACATACACAAAAATAGAATAATGAAACTCTACCCATCACCCAGCCTGGGTGACAAGAGCAAAACTCA
GTTTCNNNNNNNNNNNNNNNNNNNNNNNNNNNNTATATATTCCTACTCTTATTAAATGAATATAGCATTTCTTAGCA
ACTTCTTTTGATTTGTGAGTATATATTTTCTTGGCCTCAAAATTAAAGTAAAAAGTATCCTCTTACTCAGAGGAG
GACAGGGGCAAGAGCCTGGGTGACAAGAGCAAAACTCAGTCTCAAAAA

FIGURE 496

KKRKKKIYIFLLLLNEYSIS

FIGURE 497

CCTGCCGGCAGAACTCTATGCGGTGCTTTTACAAGAGATTATCGTCACAATGTACTAAACTGTCAGGTACTTATT
ACAGTGCCGGAATGTTTTGAAATCCTGTTGCTTGCTCCTCATCGCCAAAAATGGGTGGAAAGGATCAGATATGTT
ATATTTGATGAGGCTTCCCACTGGCCAAACCCAGTAGAAGCTAGAGGGCTAAGGAGGCTGGGTGAGCCAATTCCC
AAGGTCAGACTCATTGGCCAGAGAGGAAGGTGGCGAATGGTG<u>**TAG**</u>ATCTGGAAGGACATAGCTATGTTATTATCA
AAATGAATGGAAAGAACTGTAAATAGAATTCAAGCTTTGTATTTTGTTGCTTCAAGGAATTTTCAACTTAAAGGA
AAACTAGGTCCATTATCTTGGCAGAGAAGTTGGAGCAAAATTTTGGGAGCTCCTCCTTGTCATTATTCGATGTCC
CTTTTTGGTTCTTTCAGCTACCATAAATAACCCAAATCTTCTCACCAAGTGGCTGCAATCAGTAAAACAGTACTG
GAAACAGGCAGACAAGATTATGGAAGAGAAATGTATTTCTGAAAAACAGGCTGACAAATGTCTCAACTTTCTCCA
AGACCATTCATATAAAAAATCAATCATATTGAAGTTAGACTTGTGCTCTGTGGAGAGAGATACCATGATTTAGAG
AAGCATATATGTTCAGTAAAACATGATGATGTTTATTTTGATCATTTTCATCCCTGTGCTGCGCTAACGACAGAT
ATTATTGAAAAGTATGGATTCCCACCTGATCTTACCCTCACCCCTCAAGAAAGCATCCAGCTTTATGATACCATG
GCTCAAGTCTGGGAAACTTGGCCCAGGGCTCAGGAATTGTGTCCAGAGGAATTCATTCTTTTTAAGAATAAGATA
GTCATTAAGAAGTTGGATGCTAGAAAATATGAAGAAAACTTAAAGGCAGAATTGACAAATTGGATTAAAAATGGC
CAAGTGAAGAAGGTCAAAAGAGTACTGAAGAACCTTAGTCCGGATTCATTGTCTAGTTCAAAAGATATGGTGAAA
ATGTTTCCTCTTCTTGTTTAAAAGTTAAGACAAATGGATAAGTTGCCTGCAATATTTTTTTTGTTTAAGAATGAT
GATGTGGGAAAAAGAGCTGGAAGTGTGTGCACTTTTCTGGAGAAGACAGAGACAAAAAGCCATCCCCACACTGAA
TGTCATAGTTATGTCTTTGCAATAGATGAAGTACTTGAAAAAGTGAGGAAGACACAGAAAAGGATCACTAAAAAA
AACCCAAAGAAGGCTGAAAAACTGGAAAGAAAAAAAGTGTATAGGAGCTGAATATATTAATTTCCTGGAGAATCT
GAAGATTCTGGA

FIGURE 498

PAGRTLCGAFTRDYRHNVLNCQVLITVPECFEILLLAPHRQKWVERIRYVIFDEASHWPNPVEARGLRRLGEPIP
KVRLIGQRGRWRMV

FIGURE 499

AGAGGCCACATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGCTGGTGTCTCCTCCTGATCTGGGCCCAGG
GGCTGAGGCAGGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAACGGGGAACATTTCTGCAGAGA
AAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCCACCACGGCACAAGTGACCCAGGTCAACTGGGAGCAGC
AGGACCAGCTTCTGGCCATTTGTAATGCTGACTTGGGGTGGCACATCTCCCCATCCTTCAAGGATCGAGTGGCCC
CAGGTCCCGGCCTGGGCCTCACCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACA
CCTACCCTGATGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGCTCAGTGGCTGAGCACGGTGCCA
GGTTCCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCTGGTGGTCATCTGCACAGCAGTCATCGTGGTGGTCG
CGTTGACTAGAAAGAAGAAAGCCCTCAGAATCCATTCTGTGGAAGGTGACCTCAGGAGAAAATCAGCTGGACAGG
AGGAATGGAGCCCCAGTGCTCCCTCACCCCCAGGAAGCTGTGTCCAGGCAGAAGCTGCACCTGCTGGGCTCTGTG
GAGAGCAGCGGGGAGAGGACTGTGCCGAGCTGCATGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGGTAACT
GCAGCTTCTTCACAGAGACTGGT**TAG**CAACCAGAGGCATCTTCTGGAAGATACACTTTTGTCTTTGCAATTATAG
ATGAATATATAAGCAGCTGTACTCTCCATCAGTGC

FIGURE 500

RPHLLPVGPLGRSMRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQ
DQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGAR
FQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLRRKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCG
EQRGEDCAELHDYFNVLSYRSLGNCSFFTETG

FIGURE 501

AACGGTCTAAGGTAGCCAGGCGGGTTAGGGCTCAGGCAGGGCTTGAGCGGGACGAGGGGGCGGGCTCCGAGGCGG
GCTAGATGCCTGGGCTGGATGAAGTCCGAGTCTGGGAAGAGAACCGTGTTGTGGCGGGAGGAGGCGGTGATTGGG
GTGGTGGGGCTAAGCGCGGGGGCAGGGCTCGAGCGAGGGGGGCGGGGTAGCACCTCCGCCTGTCGGTGGTGGGGC
GGAGGCTGGAGGGGGTGGGCCTAGGATGCGTGAGGCGGCAGCTCGCGTGGGGGCGTGACCATGCCTGGCGGGGGC
GGGGCCGGAGGCGGGCGGTTTAGAGAGCGGGGCGGTCCTGCGGGGTGGGGGCGGGGCCTGGTGGGGGCGGGGCCT
GTGCGGTCTGCGGCGCGGAGCCGAGTGGGCTGCGGGGATGCGGGGGACCAGCTGCGTGGGCGGCGGCGCCGAGAG
CCCCGGAGGCGCGGGGCTGAGCGAGGGCCCGCGGGGGCGCTGGCTGCGCTTGGCTCCGGTATGCGCCTACTTCCT
CTGCGTCTCGCTAGCTGCCGTGCTGCTCGCCGTGTACTACGGTCTCATCTGGGTACCCACGCGGTCTCCCGCGGC
ACCCGCCGGCCCACAGCCCAGCGCGCCGTCCCCTCCGTGTGCTGCCCTCCCGGGCGTGCCGCCTGTCCCGGCGCC
CGCCGCTGCCTCCCTCTCCTGCCTCCTGGGAGTCCCCGGCGGGCCGCGACCCCAGCTCCAGCTGCCGCTGAGCCG
CCGCCGCCGCTACAGCGACCCTGACCGCCGTCCGAGCCGCCAGACACCCAGAGAGACGCCAGAGGCCGCGGAGGG
GCGAAGACCCGGGTAACTCTCCCTTCCACCCCAACCCGGATCGCCAGCCCTCGAGAGCTCTGTGCTCCACGCCGA
GGATGCACCGTCTCTGGATTGGTCCGGCCTTCTTCCTAATGACATCGCTCAGCGTCTCTGGAGCCGTCATCCCGC
GGAATGGGGGCCCAGGGGGTGTCAGCTCGGGGCCTTGCCTCTTGCAGCTACTCTGTGGTCAGGCCGGGTCCTCCA
CCATCAGGAAGATCCCATCCTGAGCTCTGTCTCCTGCCCCTCCTGCTGTGGGATGCTGAGCACAGAGCCCACAGC
CCATCTGCCTCTTCACCTCCCTGAATCCGTGTCCATCTGCAATAAACGACAGCCTCGGCTGCCTCGTGCTGTGTC
AAAAAAATCTATGTCGGGTGCGGAGAAAGAGGTA**ATG**AAATGGCAGGAATTCGATATCAGCTTATCGATAC

FIGURE 502

MKWQEFDISLS

FIGURE 503

TTTACGATATCCAAATAAACTGGACACCATCACATGGACGTGGCAAGGACCTGGAGCGCTGGAAATCCTGTGGCT
CACGCTGTGTCAGTTTCACAACCAAGTGGAAATCGAGTTCCTTCCTGTGTACAGCCCTTCTGAGGAGGAGAAGAG
GAACCCCGCGCTGTATGCCAGCAACGTGCGGCGAGTC**ATG**GCCGAGGCCTTGGGTGTCTCCGTGACTGACTACAC
GTTCGAGGACTGCCAGCTGGCCCTGGCGGAAGGACAGCTCCGTCTCCCCGCTGACACTTGCCTTTTAGAATTTGC
CAGGCTCGTGCGGGGCCTCGGGCTAAAACCAGAAAAGCTTGAAAAAGATCTGGACAGATACTCAGAAAGAGCCAG
GATGAAGGGAGGAGAGAAGATAGGTATTGCGGAGTTTGCCGCCTCCCTGGAAGTCCCCGTTTCTGACTTGCTGGA
AGACATGTTTTCACTGTTCGACGAGAGCGGCAGCGGCGAGGTGGACCTGCGAGAGTGTGTGGTTGCCCTGTCTGT
CGTCTGCCGGCCGGCCCGGACCCTGGACACCATCCAGCTGGCTTTCAAGACGTACGGAGCGCAAGAGGACGGCAG
CGTCGGCGAAGGTGACCTGTCCTGCATCCTCAAGACGGCCCTGGGGGTGGCAGAGCTCACCGTGACCGACCTATT
CCGAGCCATTGACCAAGAGGAGAAGGGGAAGATCACATTCGCTGACTTCCACAGGTTTGCAGAAATGTACCCTGC
CTTCGCAGAGGAATACCTGTACCCGGATCAGACACATTTCGAAAGCTGTGCAGAGACCTCACCTGCGCCAATCCC
AAACGGCTTCTGTGCCGATTTCAGCCCGGAAAACTCAGACGCTGGGCGGAAGCCTGTTCGCAAGAAGCTGGAT**TA**
GGACCCAGGGTTGCGGAGAGACGCGGCCCCTCCCGCGTGGACATCACCGCCATGAGCCTCTTTGCGAGTGACCTC
TGGGCTCCGCTCCTCACTCCTGCTGTACAGGCACTGTCTTCAGCCCGAGTTCCAGGGGCCTCGGGGGCTGTTTGT
ATCTTGTTCCTTTGTGAAGTGTGTTGCAGAACCGACGCTTACTGTGCGAGAATCGGAGGGCGCGCACGCGGATCC
CCCGCCTGGCCTGGACCCCGTGGGGTCAGGTTCCCTGCCGGGCGGGGGGCACCGGTGCCGCCCCGTGTTCTCCCA
CGGGGCCCTGGTTTCGAGTCTCTGTCACAGCCTCTTCCGGCGGCAGCGTGCACCGGGCGGGCCTCCGTGCACACT
CAGCACACGCCTGCCACACAGCGTGCGCTTGCGTGTCACTCTGGCACGAAACCTGTCTGCCTCTGTGGATCCACA
GCCTGGCAGAGCCGAGCCGTCACCTGATTTTTCAGTGTTTCTACCTGTGTGCTGGAGCTCATGAGTATTTTATAA
ACTCCATTTAGGTACTTCAGGAAACATGCAGCATTTTTTAAAAAATGAAAATTGTTTTTCTACTTCATTTTTCCT
TTTAGAGTCAAAGGATATTTATTTATAGGCCTTTTTTTTTTAATATAGAATCTGAGGCTGTTTGGGCTTTGACTT
AAATTTCCATCAGGCCTCTCTCCAGCAGGTAATCCCTCTGCTTCCGCTGGGTCCCCTGGGGAGGTGTGAACTCAA
GGGCCTAGCCCCAAAACACTTTTTCTGCTTTTCTTAATCCTTTTCCAGTCCGCTCTTTTTTTATAAACGTTGGCA
GTTTGATGTTTCTGTTTCGGCATAACGTAATCCATTTCACTGTAGCCTAAACTCCAGTCCGAGGTTGGATATTGT
TCAAATGAGCAGGGCCCGAGCTGGAAGCGCAAGGCAGCCGCCGCCGTGCCGCTCCTCCCTTGCCCTCAGGCCAGG
TCCCTGCTGGAAGCGGCTGCATCTTCCTGTCAGCCCTGGTTTCCATGGTGACTGGCGTGACGCAGCCACCTGAGT
ATGGCTGACCTTCCTGCAGAGAGAGGAGCCGCAGTCTTTTGCTTGTGGAAGGAGACGCTGGGCTGTGCGGTGCGG
AGGGTGATGAGGATGTCTGGTGACAGCCGTGCGGACACCACTCCTCTCTGCAGCACTGCCTCCCAGCGCCAGGGT
CGCGGGCACATCCCACTGAGAGCGGGGGTCCTGCCCCATCTTAGAGTCAAAGGCAGAGGGGCTTCCAGGCCCTGG
ATGGGGTATTTTGGTGTCACCTGAAGTCCCTCTGACATCACCTTGTTTCATCATTTTTTATGACAGAATTAGAAA
CCCATCCTTCAAGCACAATAATCATCACAGACTTGAGTTTGCTTCCTAAAGCAAAGGCTCCGGGTTTGTTTGGAA
AATTTTTTTGATTTCTGAAATGAATTGATTTTTATATTTGGGGCATCTCTATAGAAAGTGACCACCAAGGCCAGT
AAGTACGGGAAAAAATGTTTACTAACTTCCTCAGAGATTCGTGATACGCGTTTCTCCACTGACAGACATTTAAAA
ACAACCTTCAGCTCCGTTTCAATCAATCACCTCGACTTGTTTTTAGCATGGACACTGCCAGCAGGACAGACAGG
GATGGAGTAAACCGAAGTCAATTTCAGGGCTCTTGGCGTGTTGGACACAGAAGAAATCCTAGTGCAGCCTTTGGT
AGCTAACAGTCACTGATTTTATAATTGGAGAATGCGTAAAGATTCATTTTTCAAGGAGAAGAGCCTGCAAATGGC
CAATGAAGGAGGTAAATAAACTAAGATATTCCGAGGGAAGGGACCCAGGCCACCTCCCTTCCGCAGGTCTGCAGA
TGAAGGGTTTTTTGAATGAAATGCCACTGCGCATTTTCAGAAAAAAAAATCTCTGATAAACAGACTTTGAATGGA
TGTTTGTTCCTCCTGATTCTCTTTTCTCTTCGTGGCGACTTAGAGTTGGCGGATATTCGGAACTGTGAATGTACA
TAGCGTTGAGTTAAACCCCTTGTGTGTGAGACAGGACGCAGCGGGCCCCTGGTGGCCTGGGGGCCAGACCCGTGG
GCAGGTGGGGCATGGGCCCTGGCCTGCGGGGACCTGCTGGGGTGTGAGGGCAGAGGGAGGGTTGCCATGAAGGAA
CTTGGGATTTTCAATGGAATAAATAAAACATAAAGTCTATACTTGGG

FIGURE 504

MAEALGVSVTDYTFEDCQLALAEGQLRLPADTCLLEFARLVRGLGLKPEKLEKDLDRYSERARMKGGEKIGIAEF
AASLEVPVSDLLEDMFSLFDESGSGEVDLRECVVALSVVCRPARTLDTIQLAFKTYGAQEDGSVGEGDLSCILKT
ALGVAELTVTDLFRAIDQEEKGKITFADFHRFAEMYPAFAEEYLYPDQTHFESCAETSPAPIPNGFCADFSPENS
DAGRKPVRKKLD

FIGURE 505

CGTCAGTATAGGGAGTGTGTGTATAGGGAGGTGGCATCCGGGAGCCCAGCCCAGCAGTGTCTCTGGGCACAGTGA
TTTCAGGGGGATGGCCAGCAGTTGTGAAAGACAGAATGATCTGGAATGTCTCATTGGGAAGACCAAACCCCCTTC
TCGCTGCAGATACCAGATAAGCACCCATCTTCACTGTCCACTGTGCAGCCCAGTCCCCTCCAGACAGCCCCAGCA
CAGCATGAAGAAGGCACATGAGCACCGGCGACAGGCTTACAGGACAGGGTGCAGCGGCCAGCATCCCAGGCATCA
GGGACATGTGGGATCTTCCCACACACCTGGGATGACATCGAAT**<u>TAA</u>**CATGATGAGAAAATTGCATCTTACTGCTA
ATCCCAGTACAGAACCACTATGGGCAAATTTATAAAACTAATCTGCAGAGAGGCAATAACTCTGTCTAAAAAGAA
AACTTGTCCCGTGTGATTACAAAAACAGGAAAAGGCTCCAAGCTAGGAAATGAGATTTGAGGTATGGAGAACATT
CTCACCTGATGGAAGCATCCTGTTCCTGTACAGGAGGAGGAGCTGGTGCAAGCCCTAGGCCACATATGTCACAGT
TGTTTTGGACCCTCCGTAGCTTTTATACTCATAAAATATTAAAGTTGCCCCTTTCATATTTGGGTCATTGAAAGA
GCCCACCGTACTCTAGGTTCCTGCTCACTATGCACAACATCTCAGAAGATGGCGTACAAAACTATTTTTCTAACT
ATAGCACGGGTAATGTGGGGGTGGGGAGGCTTGGGATATACCTAAATGTGGCAAATGATTTATCTTCCACCTTGA
GGGATGAAAAGGAAACTATGCACTTGAATTTTAATTAAAATTTTAATTTAATTCATTGGATAGCTTGTGCCAGAA
AGAACAGTCAATATTCAAGAAGCAAAACTGACGATTAGCTCAGTTTCGGGCCTCCCTGTCGGGGGAGTTTTCTTG
TCTGGAACACAAACACCTACAAGTAGAGTGTGAGCTGGTTCTTGACAATCAGATCTCATCAACCCTTTGAAATGT
TCTGGGCAGCACAGCTCCTTGGTCTGCATGGTTGGTGTAAGTATAATCAAGTAGTGAAATTGTATGGTATATACC
TATATGCCAACAGTGTACACCCGTATGTGCAGAATTTGCTAATATAACCATTTCAATAAAAACCTATTGAAAAAG
CTGATTTGACCACATGGAGTATTGTTGGTGGTGACGTGTATCACTGAGGACTCTCTTGGTTACAAATGACAGAAA
ACCCAGCAAAACTGGCTAACACAAAAGGGAATGTCATGGCTCCCAAAAGCCAAAATGCCCAGGGGTGCCTATGTC
AGGCTTGGTGTGATTTCACCCTCAAATGCTGACACCAAGACACATGCCAACTTTG

FIGURE 506

VSIGSVCIGRWHPGAQPSSVSGHSDFRGMASSCERQNDLECLIGKTKPPSRCRYQISTHLHCPLCSPVPSRQPQH
SMKKAHEHRRQAYRTGCSGQHPRHQGHVGSSHTPGMTSN

FIGURE 507

CACATGCACCTGGCCTCTGCTTTTTTATTTTAAAAGCACAACTAACTGGTAGATAAAGTGATTTGTCTTTAGTAT
TTGATAACTAATGGGTTTTAGAGTGTTATTTATAAGATGTAGTAAATTATCCTCATCATTATTTTTAAGACAAAT
TTATAAGACAAGTGTAATAGAAATAGATCAACAGCACAATAGAAAAAGATGGCAGAAAACATGAATACGTAATTC
ACAG**ATG**AAAGCAAAACAAATGGTCCTTTTATTAAGGGAATGCAAAGTTAAAAATCAACTAGACCCTTTTTTGTT
TGTTTCTTCTTGGATTGGCAAAGAGGAGCACTTAAAAGCTGTATTTTGTTTTGGAGGATTAGTTTGGGTTATGTC
TACTAATGAC**TAA**ATGTGTACATACATTTTGACCCATTAGTTACACTTCAAAGAATTTTTATCCAACAAAAATGT
ACTGAGACACATTGCTTAGTATAATAAGCCATTGGAAGCTTACCCAAATATTCATCAATGAGAAATAGGTTANGA
AAATTATAGTACAACCATACATGNAACTGGATGTAGCTGTAAAAGAAATGGGATCGATTTTTTTTTNGTAATGAT
ATGGAAGGATACTCAAAGTATATCAAGTGAGAAAAGATCTAGGAACAGGANNNNNNNNNNNNNNNNNNNNNNNNN
NNNGTAGGGACAGGGTCTCACCATGTTGCCCAGGCTTAGGAGCAGGATATTAGCTAACTCGTGTTACTTCTGAAA
ATCTTTGAAGCTCCCCCTGCTCTTTTTTCCAGAAGTGTAAAAACAAGCATGTATTTAGTATTACACATTTTTAAA
AAATGAAAAAATGCTGCTGTGTGAATGAAAGAGTATACATCGTGTTGCTCCAGATGGTAAAACTAGAGTAGAATT
TACTAAAATAAAGTTTCAGCACGTAAAGTAAAGCACTTCTCTGCTCTTGGCCATTTAGACACTAACCATCTGGA
GCAACCATGTAACTCTTGCCACTCATAGCTAACTTAATGTAAAGCACTTCTCTGCTCTTGGCCATTTTAGACACT
AACCATCTGGAGCAACCATGTAACTCTTGCCACTCATAGCTAACTTAATGTAAAAAAAAAAAAAATCGCTTGACTT
TCTTAGCACTTCACAAATGCTTGTAAGACTGACACCAGGAGCCCTGTCATCTAAAAGGCACTTTATAGAGTGCTT
TCAATTCTTCTGTTTTTTCATTCATTGCTCAAAATAGATCGTAGTGAGATAAGATAGTCTCTGGCCTTCTTGGTC
TTTGGCACAAGGAAGAGGGTTCCAGAGTTGAGAGTAAGGACTTTGCATCCTTTGCCATAGAATTTGATTAGGGGC
CATAAAAAGGACCATTGTGTTCTAGAATGTGAAGGACTAAGCATACCACTTTATAGTGCAAGGAATAAGTGAAGA
AGTCCTTTTATAAGAAAAACTGCAGTAGAGCAATAACTTGAAATTACACTTATTTATATTTACTTTTCATTAAAT
GTAAATTATTTTCTTTTACCACATTGTACTACTAGAAAGAGAATCAGGAGTTTAGGCATTCAGTCATAGATATTC
GATACCATTGATTTACTTAAGCACTTCTCATGTCAACAAGACTTAAGCCTGCAGATAATTCCTATTTTATCAGTG
TTCGTTATAGCTTCCCTGTTGGTTTTACTTGTGAGTCATAAGCCTAGTATGGTGAATATCTAGGAAATTTCACGG
TAACAGGGCTTGTCTTAGGTTTTGAGAACAGGTGTAACTTGACTTCTCTCTGCTGTTTGTCATCCTACACTTCCC
ACTACATCTGGTCCTTTTTGTAGGGTGTTGAGAACAACATTTTTCTTCATGCAGGGGAAAGTGGAAGTGCATGTT
TTCTAAGAAGGACAAATAGGAATAGAATAAAAGAAAAAGTATATTGG

FIGURE 508

MKAKQMVLLLRECKVKNQLDPFLFVSSWIGKEEHLKAVFCFGGLVWVMSTND

FIGURE 509

CCAGAAACAGACCTGGGAGTGGAACAGCAGCAGTTAGGAGAGGACCCTGCTGGGGTCCAGGAGCCCGCCTGCCTG
GCTGCCCAACCAGCTCCAACACTGCTGGAGGCCTCCATTCTCTGTTCAGGGGAAGGCCCACTGGTTAGCTCAGAG
ATGGCTTCTGCGTGCTTTCTCCCTTCCGTCCTAGAGAACACATATTTCTGTTTCCTCCCTTGCCTTCTCCCACT
TGGACCTGCTCAGAGCCCTGTGTACTCTGGTGTGTGGCCTCTCTCCCCTCTCTCTTTTCCTCCTTCTGGATTCTT
TCCTATCTTCATCCACAATCTCTACCCTTTATCTTGCCGTTACTCTACCCCGAGACTGCCTTCTGCCCTGGGTCC
CACCAAATAGATCCTGTCCTTCCCTTAGTGAAAATGAGGCCACCTCTTGGGGAACAGAAGACGCCCCAGTGAAAA
CAGAGTGCAAACCTGGCCTGGCATGGGAGCCTCCTTCTGGCCAATCAGGCAGGCCAGAGAACAGCAGCGGAGGGC
CCTGTCTTTCAGGCAGACCTCATGGCTGAGTGAGCCTCCCCTGGGCCCAGCACCCCACCTCAGC**ATG**GTCCAAGC
CCATGGGGGGCGCTCCAGAGCACAGCCGTTGACCTTGTCTTTGGGGGCAGCCATGACCCAGCCTCCGCCTGAAAA
AACGCCAGCCAAGAAGCATGTGCGACTGCAGGAGAGGCGGGGCTCCAATGTGGCTCTGATGCTGGACGTTCGGTC
CCTGGGGGCCGTAGAACCCATCTGCTCTGTGAACACACCCCGGGAGGTCACCCTACACTTTCTGCGCACTGCTGG
ACACCCCCTTACCCGCTGGGCCCTTCAGCGCCAGCCACCCAGCCCCAAGCAACTGGAAGAAGAATTCTTGAAGAT
CCCTTCAAACTTTGTCAGCCCCGAAGACCTGGACATCCCTGGCCACGCCTCCAAGGACCGATACAAGACCATCTT
GCCAAATCCCCAGAGCCGTGTCTGTCTAGGCCGGGCACAGAGCCAGGAGGACGGAGATTACATCAATGCCAACTA
CATCCGAGGCTATGACGGGAAGGAGAAGGTCTACATTGCCACCCAGGGCCCCATGCCCAACACTGTGTCGGACTT
CTGGGAGATGGTGTGGCAAGAGGAAGTGTCCCTCATTGTCATGCTCACTCAGCTCCGAGAGGGCAAGGAGAAATG
TGTCCACTACTGGCCCACAGAAGAGGAAACCTATGGACCCTTCCAGATCCGCATCCAGGACATGAAAGAGTGCCC
AGAATACACTGTGCGGCAGCTCACCATCCAGTACCAGGAAGAGCGCCGGTCAGTAAAGCACATCCTCTTTTCGGC
CTGGCCAGACCATCAGACACCAGAATCAGCTGGGCCCCTGCTGCGCCTAGTGGCAGAGGTGGAGGAGAGCCCGGA
GACAGCCGCCCACCCCGGGCCTATCGTAGTCCACTGCAGTGCAGGGATTGGCCGGACGGGCTGCTTCATCGCCAC
GCGAATTGGCTGTCAACAGCTGAAAGCCCGAGGAGAAGTGGACATTCTGGGTATTGTGTGCCAACTGCGGCTAGA
CAGAGGGGGGATGATCCAGACGGCAGAGCAGTACCAGTTCCTGCACCACACTTTGGCCCTGTATGCAGGCCAGCT
GCCTGAGGAACCCAGCCCC**TGA**CCCCTGCCACCCTCCGGTGGCCCAGGTGCCTACCTCCCTCAAGCCTGGGAAGG
TGGGTCTGGGGAAAGTGGGCCGAGTGATCTGGGGGTACCCCTTGGGTTGGTGTGGGGAAGGAGTGCCTCCTTAGT
GGTGCTTGCAGTCACAGGAAGCAGCAGCAGTAAGGACAAGGGGCCGGATTCCAGGTCTTCAACACTGGCCACTCC
TCTGCTTCCTCTGTTGGCCCCAGATGGACAGTAAGGGGAACCTCCAATGTCTCTCTGAACTTAAAGACAGGAGCT
GGCATTTATGACAGACAAAGAAAGAAGCCCAGGTGTCCTGGTGTTCTCTGAGACACTCTTTGTGAGCTTCAGTTT
CCTGTTCTATAACATGAACATAAGTGCTTAGCTGCCATGAGGGAAAAGTAATGAGAGAAGTTTCTAGAAGCCACT
CCAGCCACTCCTTCCTGGGGCTGACAAAAGGGTGATTCCAAGATCATCCTTCACCCGAGGTCCTGCCCAAGCACA
GGCCAGATGCAAGAATGGGGAAAAGTCTGGTCCTGATCTCCAAGTCTCAACATCCTATCAGTGACTCTGCTCCCT
GACCACACATCGGAAGGGCTGGATGACCCCAATCAAAAGAAAGAACAAGGACTCTGGTTACCCTTGCCTCCACCC
ATGTGTCATAAGAGTAGGCTACAGAGGTGACCAGGCCTGGCAGTTGAAATCTCTGGAAGAGGGAACATGTGGGGA
CTACTCAGAGGCAAAGAGGAGCTGCTCCTGCCTCCATGGTTGCTGGCCTCTCCCACCAACTACTCTTAGGGAGGC
TAAGCAGTCTCTGTTTTGCTTCCATGGCTCAAATAATACCCTGGGTATGCAGGACCCACTATACCTTGCATTTGC
TGAGTACACCTAGAGAGCTTGGCTGTTTCCAAAAACAATCAGGGTCATAACCATCCATGCAGACATGGAGGCTCG
GCTGAACCAGGACTCCTCACTGTCTACCTGAGAGAATGAGCACCCCTCATCCATCTCAGCATCAACACAATTTCC
AGGGGACCTCAGGTCTACCTCAGGACTGAACGCCACACCTCAGGATTCCTCCTCCTTGAATCTGAGACTGGCTGC
CCATTCTGAGATGGGGATGAAGGTAAGATGCCGCATCACCAGGCACGCCGCCCCTGACAGCTGCCTTGATACCAG
CTCTCTGTGGAAACCCCCGAGGAGTTGGATCTGGAGAACAGCTGGGCCTCCTCACTCAGGACTTCTCTCCTGAAG
AACACGCAGTGCTAAAACTGAGGATGATTTCCCTAATGCTTCTGCTTGGCCTTATGGAGGAGCTGCTCCTTCCTT
ACAGCCTTGGGGATGGACTTGCCCACACCTCCACCTCCCCTGAGCCCTGTGAGAGGCACGACTGTCTATGCCAAT
GAGGCTCGGTGGGGGGCTCTCAAGTGCCTGATCCTGCCCTGGGCTCAGAGCCAGCCCAGAGGGAAGCAACTGCAC
AGCCCCACAGGCCCTCCTTGGCACTGTCCCCCCAACCCCATCTCAGAGCTCAGAGGGTACAAGCTCCAGAACAGT
AACCAAGTGGGAAAATAAAGACTTCTTGGATGACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 510

MVQAHGGRSRAQPLTLSLGAAMTQPPPEKTPAKKHVRLQERRGSNVALMLDVRSLGAVEPICSVNTPREVTLHFL
RTAGHPLTRWALQRQPPSPKQLEEEFLKIPSNFVSPEDLDIPGHASKDRYKTILPNPQSRVCLGRAQSQEDGDYI
NANYIRGYDGKEKVYIATQGPMPNTVSDFWEMVWQEEVSLIVMLTQLREGKEKCVHYWPTEEETYGPFQIRIQDM
KECPEYTVRQLTIQYQEERRSVKHILFSAWPDHQTPESAGPLLRLVAEVEESPETAAHPGPIVVHCSAGIGRTGC
FIATRIGCQQLKARGEVDILGIVCQLRLDRGGMIQTAEQYQFLHHTLALYAGQLPEEPSP

FIGURE 511

ATGGCGGCGGAGCTGGTGGAGGCCAAAAACATGGTGATGAGTTTTCGAGTCTCCGACCTTCAGATGCTCCTGGGT
TTCGTGGGCCGGAGTAAGAGTGGACTGAAGCACGAGCTCGTCACCAGGGCCCTCCAGCTGGTGCAGTTTGACTGT
AGCCCTGAGCTGTTCAAGAAGATCAAGGAGCTGTACGAGACCCGCTACGCCAAGAAGAACTCGGAGCCTGCCCCA
CAGCCGCACCGGCCCCTGGACCCCCTGACCATGCACTCCACCTACGACCGGGCCGGCGCTGTGCCCAGGACTCCG
CTGGCAGGCCCCAATATTGACTACCCCGTGCTCTACGGAAAGTACTTAAACGGACTGGGACGGTTGCCCGCCAAG
ACCCTCAAGCCAGAAGTCCGCCTGGTGAAGCTGCCGTTCTTTAATATGCTGGATGAGCTGCTGAAGCCCACCGAA
TTAGTCCCACAGAACAACGAGAAGCTTCAGGAGAGCCCGTGCATCTTCGCATTGACGCCAAGACAGGTGGAGTTG
ATCCGGAAATTCCAGGGAATGCAGCCCGGAGTTAAAGCCGTGCAGGTCGTCCTGAGAATCTGTTACTCAGACACC
AGCTGCCCTCAGGAGGACCAGTACCCGCCCAACATCGCTGTGAAGGTCAACCACAGCTACTGCTCCGTCCCGGGC
TACTACCCCTCCAATAAGCCCGGGGTGGAGCCCAAGAGGCCGTGCCGCCCCATCAACCTCACTCACCTCATGTAC
CTGTCCTCGGCCACCAACCGCATCACTGTCACCTGGGGGAACTACGGCAAGAGCTACTCGGTGGCCCTGTACCTG
GTGCGGCAGCTGACCTCATCGGAGCTGCTGCAGAGGCTGAAGACCATTGGGGTAAAGCACCCGGAGCTGTGCAAG
GCACTGGTCAAGGAGAAGCTGCGCCTTGATCCTGACAGCGAGATCGCCACCACCGGTGTGCGGGTGTCCCTCATC
TGTCCGCTGGTGAAGATGCGGCTCTCCGTGCCCTGCCGGGCAGAAACCTGCGCCCACCTGCAGTGCTTCGACGCC
GTCTTCTACCTGCAGATGAACGAGAAGAAGCCCACCTGGATGTGCCCCGTGTGCGACAAGCCAGCCCCCTACGAC
CAGCTCATCATCGACGGGCTCCTCTCGAAGATCCTGAGCGAGTGTGAGGACGCCGACGAGATCGAGTACCTGGTG
GACGGCTCGTGGTGCCCGATCCGCGCCGAAAAGGAGCGCAGCTGCAGCCCGCAGGGCGCCATCCTCGTGCTGGGC
CCCTCGGACGCCAATGGGCTCCTGCCCGCCCCCAGCGTCAACGGGAGCGGTGCCCTGGGCAGCACGGGTGGCGGC
GGCCCGGTGGGCAGCATGGAGAATGGGAAGCCGGGCGCCGATGTGGTGGACCTCACGCTGGACAGCTCATCGTCC
TCGGAGGATGAGGAGGAGGAGGAAGAGGAGGAGGAAGACGAGGACGAAGAGGGGCCCCGGCCCAAGCGCCGCTGC
CCCTTCCAGAAGGGCCTGGTGCCGGCCTGC**TGA**

FIGURE 512

MAAELVEAKNMVMSFRVSDLQMLLGFVGRSKSGLKHELVTRALQLVQFDCSPELFKKIKELYETRYAKKNSEPAP
QPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRLPAKTLKPEVRLVKLPFFNMLDELLKPTE
LVPQNNEKLQESPCIFALTPRQVELIRKFQGMQPGVKAVQVVLRICYSDTSCPQEDQYPPNIAVKVNHSYCSVPG
YYPSNKPGVEPKRPCRPINLTHLMYLSSATNRITVTWGNYGKSYSVALYLVRQLTSSELLQRLKTIGVKHPELCK
ALVKEKLRLDPDSEIATTGVRVSLICPLVKMRLSVPCRAETCAHLQCFDAVFYLQMNEKKPTWMCPVCDKPAPYD
QLIIDGLLSKILSECEDADEIEYLVDGSWCPIRAEKERSCSPQGAILVLGPSDANGLLPAPSVNGSGALGSTGGG
GPVGSMENGKPGADVVDLTLDSSSSSSEDEEEEEEEEEDEDEEGPRPKRRCPFQKGLVPAC

FIGURE 513

GATCGCGGAGTCGGTGCTTTAGTACGCCGCTGGCACCTTTACTCTCGCCGGCCGCGCGAACCCGTTTGAGCTCGG
TATCCTAGTGCACACGCCTTTGCAAGCGACGGCGCC**ATG**AGTCTGACTTCCAGTTCCAGCGTACGAGTTGAATGG
ATCGCAGCAGTTACCATTGCTGCTGGGACAGCTGCAATTGGTTATCTAGCTTACAAAAGATTTTATGTTAAAGAT
CATCGAAATAAAGCTATGATAAACCTTCACATCCAGAAAGACAACCCCAAGATAGTACATGCTTTTGACATGGAG
GATTTGGGAGATAAAGCTGTGTACTGCCGTTGTTGGAGGTCCAAAAAGTTCCCATTCTGTGATGGGGCTCACACA
AAACATAACGAAGAGACTGGAGACAATGTGGGCCCTCTGATCATCAAGAAAAAAGAAACT**TAA**ATGGACACTTTT
GATGCTGCAAATCAGCTTGTCGTGAAGTTACCTGATTGTTTAATTAGAATGACTACCACCTCTGTCTGATTCACC
TTCGCTGGATTCTAAATGTGGTATATTGCAAACTGCAGCTTTCACATTTATGGCATTTGTCTTGTTGAAACATCG
TGGTGCACATTTGTTTAAACAAAAAAAAAAAAAAAA

FIGURE 514

MSLTSSSSVRVEWIAAVTIAAGTAAIGYLAYKRFYVKDHRNKAMINLHIQKDNPKIVHAFDMEDLGDKAVYCRCW
RSKKFPFCDGAHTKHNEETGDNVGPLIIKKKET

FIGURE 515

CCACAAATGTGGGAGGGCGATAACCACTCGTAGAAAGCGTGAGAAGTTACTACAAGCGGTCCTCCCGGCCACCGT
ACTGTTCCGCTCCCAGAAGCCCCGGGCGGCGGAAGTCGTCACTCTTAAGAAGGGACGGGGCCCCACGCTGCGCAC
CCGCGGGTTTGCT**ATG**GCGATGAGCAGCGGCGGCAGTGGTGGCGGCGTCCCGGAGCAGGAGGATTCCGTGCTGTT
CCGGCGCGGCACAGGCCAGAGCGATGATTCTGACATTTGGGATGATACAGCACTGATAAAAGCATATGATAAAGC
TGTGGCTTCATTTAAGCATGCTCTAAAGAATGGTGACATTTGTGAAACTTCGGGTAAACCAAAAACCACACCTAA
AAGAAAACCTGCTAAGAAGAATAAAAGCCAAAAGAAGAATACTGCAGCTTCCTTACAACAGTGGAAAGTTGGGGA
CAAATGTTCTGCCATTTGGTCAGAAGACGGTTGCATTTACCCAGCTACCATTGCTTCAATTGATTTTAAGAGAGA
AACCTGTGTTGTGGTTTACACTGGATATGGAAATAGAGAGGAGCAAAATCTGTCCGATCTACTTTCCCCAATCTG
TGAAGTAGCTAATAATATAGAACAGAATGCTCAAGAGAATGAAAATGAAAGCCAAGTTTCAACAGATGAAAGTGA
GAACTCCAGGTCTCCTGGAAATAAATCAGATAACATCAAGCCCAAATCTGCTCCATGGAACTCTTTTCTCCCTCC
ACCACCCCCCATGCCAGGGCCAAGACTGGGACCAGGAAAGATAATTCCCCCACCACCTCCCATATGTCCAGATTC
TCTTGATGATGCTGATGCTTTGGGAAGTATGTTAATTTCATGGTACATGAGTGGCTATCATACTGGCTATTATAT
GGGTTTCAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTAAAT**TAA**GGAGAAATGCTGGCATAGAGCAG
CACTAAATGACACCACTAAAGAAACGATCAGACAGATCTGGAATGTGAAGCGTTATAGAAGATAACTGGCCTCAT
TTCTTCAAAATATCAAGTGTTGGGAAAGAAAAAAGGAAGTGGAATGGGTAACTCTTCTTGATTAAAAGTTATGTA
ATAACCAAATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAAACCATCTGTAAAAGACTGGGGTGGGGGTGG
GAGGCCAGCACGGTGGTGAGGCAGTTGAGAAAATTTGAATGTGGATTAGATTTTGAATGATATTGGATAATTATT
GGTAATTTTATGGCCTGTGAGAAGGGTGTTGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCATTTAG
GAATGAAGTGTTAGAGTGTCTTAAAATGTTTCAAATGGTTTAACAAAATGTATGTGAGGCGTATGTGGCAAAATG
TTACAGAATCTAACTGGTGGACATGGCTGTTCATTGTACTGTTTTTTTCTATCTTCTATATGTTTAAAAGTATAT
AATAAAAATATTTAATTTTTTTTTA

FIGURE 516

MAMSSGGSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNGDICETSGKPKTTPKRKPA
KKNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIASIDFKRETCVVVYTGYGNREEQNLSDLLSPICEVAN
NIEQNAQENENESQVSTDESENSRSPGNKSDNIKPKSAPWNSFLPPPPPMPGPRLGPGKIIPPPPPICPDSLDDA
DALGSMLISWYMSGYHTGYYMGFRQNQKEGRCSHSLN

FIGURE 517

AAGTGCAAAGCTTTTAACAATAGAAGTTTCAAGGGCTCAGGAAGGACCAGGGGGCCATCTAGGCTCTCCATGAGT
TCACGCTTAACATTATGTTTACGTCTGTCAGATAACAATTTTGGTTTTCCACATCAGGTGCATTGCACTGTTAGA
TGGGTCATCATAAAGGTCATCAATCTAGTGGCATTCATTCAATTTGCACATCCTAACTGTTTCAGCACTATC**TGA**

TTTAGCATGAAAATCTGCCAGGGCAGTCCCTTGATATTCAGGTTCAGCTTTCCATGTATGGGCTTCAATCTTATA
AGAATTTGTTATTTATTTTTCACCTTTACTCAAGATAGCTTGGAACTTATACCAATTTGTGATGGCAACAGGATA
GTAGCAAGTTCATCCACTTGAGTCTGTTTTTAATAGGGGCTCCACTAGAAGTGAGAAACCCTCTTTGTTTCCATA
ACATGCCAAAATTGTGGACTGCAAAGGCATGTATATATACATAGCATGTCTGCTATGTATATAGCATTTTCTGAT
TTCCCTTTAGCTATATGATAAGCTCAAGTGAGAGCAAAAGTTCTGCAGTTTGAGCTGACTGAAACTGGGAAGAGT
CCGCTTTTTATTAACTCATTTTGGGTTTTAATGACATATTTTGCCAAAGAATAATTTCAAATGGGGGCCGGGCGT
CTGTGCT

FIGURE 518

KCKAFNNRSFKGSGRTRGPSRLSMSSRLTLCLRLSDNNFGFPHQVHCTVRWVIIKVINLVAFIQFAHPNCFSTI

FIGURE 519

ACTAGCGGAGCCGCGAGGGAGAGGCCGCGGCCCCTTCCCGTTGCCTGCGGCCACCGGCCGGCATTCAGAGCCCCT
CGCCTGGCGCTAAATTTAAAAACGTAACACGAGCAGCAGGCTGGTCTCGGAAACGAAACGAAATTCGGTCCCTGG
GCCTCCTCCCGGGCGCTGCCGGTCCCTCAGCGCGCCGCGCCACCCGGAACAGACCCTTCTCCCGCCATTTTCGGC
GGGGCTGGGAGACTGAGGCCCGCGGCGCTGAGCCTGCGGCGCCCCGGAAGAGGCGGGCGGC**ATG**GCCGCTGGCGT
GGACTGCGGGGACGGGGTTGGCGCCCGGCAGCACGTGTTCCTGGTTTCAGAATATTTAAAAGATGCTTCAAAGAA
GATGAAAAATGGGCTAATGTTTGTAAAACTGGTTAACCCCTGTTCAGGAGAAGGAGCCATTTACTTGTTCAATAT
GTGTCTACAGCAGCTGCTTGAAGTAAAAGTTTTCAAGGAAAAACACCATTCTTGGTTTATAAATCAATCAGTTCA
ATCAGGAGGTCTTCTCCATTTTGCCACACCTGTGGATCCTCTATTTCTGCTTCTCCACTACCTCATAAAGGCTGA
TAAGGAGGGGAAGTTTCAGCCCCTTGATCAAGTTGTGGTGGATAACGTGTTTCCAAATTGCATCTTGTTGCTGAA
ACTTCCTGGACTTGAGAAGTTACTTCATCATGTGACAGAGGAAAAAGGTAATCCAGAAATAGACAACAAGAAATA
TTACAAGTACAGCAAAGAGAAGACATTAAAGTGGCTGGAAAAAAAGGTTAATCAAACTGTGGCAGCATTAAAAAC
CAATAATGTGAATGTCAGTTCCCGGGTACAGTCAACTGCATTTTTCTCTGGTGACCAAGCTTCCACTGACAAGGA
AGAGGATTATATTCGTTATGCCCATGGTCTGATATCTGACTACATCCCTAAAGAATTAAGTGATGACTTATCTAA
ATACTTAAAGCTTCCAGAACCTTCAGCCTCATTGCCAAATCCTCCATCAAAGAAAATAAAGTTATCAGATGAGCC
TGTAGAAGCAAAAGAAGATTACACTAAGTTTAATACTAAAGATTTGAAGACTGAAAAGAAAAATAGCAAAATGAC
TGCAGCTCAGAAGGCTTTGGCTAAAGTTGACAAGAGTGGAATGAAAAGTATTGATACCTTTTTTGGGGTAAAAAA
TAAAAAAAAAATTGGAAAGGTT**TGA**AACTTTGAAAATAAAATCTAGCAAAAATATTTGCTTTTTACATGTTTCAG
TTTGTCCTTCCTGACTGTTAATGACTACCTTTGGTTGGGGGAAGGAAGAGGCCAATTTCATGTTCTCTTAAACAT
TTCTTTGCATTTGGTTTTTGTGTTCCTGAACAAAATATGGGAAAGTGTCTAACTTCATGGCTATGGCCTTTTGGA
GTCTCATCTGACATAATGAAAAGTAATCACTTGAAGAGAATTAACATATAGCATCATGATTTTCTCAATAAACTG
ATGTGTGACAATGTT

FIGURE 520

MAAGVDCGDGVGARQHVFLVSEYLKDASKKMKNGLMFVKLVNPCSGEGAIYLFNMCLQQLLEVKVFKEKHHSWFI
NQSVQSGGLLHFATPVDPLFLLLHYLIKADKEGKFQPLDQVVVDNVFPNCILLLKLPGLEKLLHHVTEEKGNPEI
DNKKYYKYSKEKTLKWLEKKVNQTVAALKTNNVNVSSRVQSTAFFSGDQASTDKEEDYIRYAHGLISDYIPKELS
DDLSKYLKLPEPSASLPNPPSKKIKLSDEPVEAKEDYTKFNTKDLKTEKKNSKMTAAQKALAKVDKSGMKSIDTF
FGVKNKKKIGKV

FIGURE 521

CGGACCTGCAGCCCTGGCCTTCCGCCACC**ATG**GAGTACCTCATCGGTATCCAAGGCCCCGACTATGTTCTTGTCG
CCTCCGACCGGGTGGCCGCCAGCAATATTGTCCAGATGAAGGACGATCATGACAAGATGTTTAAGATGAGTGAAA
AGATATTACTCCTGTGTGTTGGAGAGGCTGGAGACACTGTACAGTTTGCAGAATATATTCAGAAAAACGTGCAAC
TTTATAAGATGCGAAATGGATATGAATTGTCTCCCACGGCAGCAGCTAACTTCACACGCCGAAACCTGGCTGACT
GTCTTCGGAGTCGGACCCCATATCATGTGAACCTCCTCCTGGCTGGCTATGATGAGCATGAAGGGCCAGCGCTGT
ATTACATGGACTACCTGGCAGCCTTGGCCAAGGCCCCTTTTGCAGCCCACGGCTATGGTGCCTTCCTGACTCTCA
GTATCCTCGACCGATACTACACACCGACTATCTCACGTGAGAGGGCAGTGGAACTCCTTAGGAAATGTCTGGAGG
AGCTCCAGAAACGCTTCATCCTGAATCTGCCAACCTTCAGTGTTCGAATCATTGACAAAAATGGCATCCATGACC
TGGATAACATTTCCTTCCCCAAACAGGGCTCC**TAA**CATCATGTCCTCCCTCCCACTTGCCAGGGAACTTTTTTTT
GATGGGCTCCTTTATTTTTTTCTACTCTTTTCAGGCGCACTCTTGATAAATGGTTAATTCAGAATAAAGGTGACT
ATGGATATAATT

FIGURE 522

MEYLIGIQGPDYVLVASDRVAASNIVQMKDDHDKMFKMSEKILLLCVGEAGDTVQFAEYIQKNVQLYKMRNGYEL
SPTAAANFTRRNLADCLRSRTPYHVNLLLAGYDEHEGPALYYMDYLAALAKAPFAAHGYGAFLTLSILDRYYTPT
ISRERAVELLRKCLEELQKRFILNLPTFSVRIIDKNGIHDLDNISFPKQGS

FIGURE 523

CCAGATCTGGAGGTGTGTCCATGGCGGCGCTTGACCTGCGAGCGGAGCTGGATTCGCTGGTCCTGCAGCTGCTTG
GGGACCTGGAGGAGCTGGAGGGGAAACGAACGGTGTTGAACGCCCGGGTGGAGGAGGGCTGGCTCTCGCTCGCCA
AGGCTCGCTACGCG**ATG**GGCGCCAAGTCGGTAGGGCCCCTGCAGTATGCTTCCCACATGGAGCCCCAGGTCTGCC
TCCACGCCAGCGAGGCCCAGGAGGGACTCCAGAAGTTCAAGGTGGTGAGAGCTGGTGTCCACGCCCCAGAGGAGG
TGGGGCCTCGCGAAGCAGGTCTGCGGAGGCGCAAGGGCCCCACTAAGACCCCAGAACCGGAGTCCTCTGAGGCCC
CTCAGGACCCCCTGAACTGGTTTGGAATCCTAGTTCCTCACAGTCTACGTCAGGCTCAAGCAAGCTTCCGGGATG
GCCTGCAGCTGGCCGCAGACATAGCCAGCCTCCAGAACCGCATTGACTGGGGTCGAAGCCAGCTCCGGGGACTCC
AAGAGAAACTCAAGCAGCTGGAGCCTGGGGCTGCC**TGA**CATGCGCGCAAAGAGGCAGGGCAGCGAGCACAGCTGT
TCTCCGACATGGCTACGTGATCTCAGGCCTTCTTCCTTCACAATTAGCTCTTGCCCCTACCCCACGCCAGCTAAT
GCCCCTTCTGTGTCCCTGCTCTGCATGTTTCCATTTTCCTTAGGTGTGAAGTTTGAAGAGGCAAACAGTAATTTT
GAAAGCCACTACTTTGAAACCATTCTAAGGCCTGAGTTCCCATAGGACACACTCACATAGGCAGGTACACGTTAG
TCAACAATTGGAACTGCCTCTTGGATCACTCAGCTGTGCTTTCATGGCTGGATGATGGAACACTGTGCGAAGAGA
GATGGGGGCCAGGAAGTAGCGCTTCATGCTTAGTACATCCTCCAAATTGTCTTTGCTGGAGGAGAAAACCGTACT
CAGCCAAAAGATCAGGACAATATGACTTGAGTCCACAAGGACACAAACACCTGAGTAGCTGGGCAGCCCTTGGCA
GGGTCTAAGCCAGGAAGTAAAAATGATCTGGCCTAGATATTTAAGGGAACTCTAGGAAGAGGCCTAGGTTTTTAA
AATCCTGTCTCTTTGTCTTACCATAAGAGGCTGAGCCTCTCTTCATTTTTTTGAAGGGCCACTTGTGTTTTCTGT
TCTGGGAACTTCATTCATTTTTCTACTGGGTTGTTGATCTTTGCAGTAATTTCTAGGAGCTGTTTATGTTTGGAG
GTAATTGGTCCTTTGTCCATATATATGAGATGTAAGTCTTATTTTCCAGTTTATCTTTTTGCTTATTTTTTTTGA
CTTTTTATTGTAAAATAAAACATCAAACTGCACAGAACAGTTGAATAGCTTAATGAATAACTACAGTAAAAGCTA
TGGTAACCACTACCCAAAAAAAAAAAAAAAAAAAA

FIGURE 524

MGAKSVGPLQYASHMEPQVCLHASEAQEGLQKFKVVRAGVHAPEEVGPREAGLRRRKGPTKTPEPESSEAPQDPL
NWFGILVPHSLRQAQASFRDGLQLAADIASLQNRIDWGRSQLRGLQEKLKQLEPGAA

FIGURE 525

TGGAGGTGAGAAAACAGAGCAGCGTATGGCAAAATAGTCTAAGAACAAGTAGTAAAAGCATCAGCATCAAAAACT
CCAGGCTATAAAAGACTAGGCTCAGAAAGTGCAGTTTTCCACCCACAGCTGGGGTGCTTCCAATAGCATCCTTGA
GACAGACTCCGCTCTAGTACCTCCAGCGAGGAGTTCACTACTGCAACAAGCAGCCCATTCTTGGATTTTTATTTT
TTTTAACTTCCATTTTTTCTTATACATCAAGTTCTCACTCCTTTATATTTG**ATG**ACATGCACGTTCAGAACTGCT
GAATATTTCCCCTTTTATCCATGCCTTCACTGCTCAATCACCTTTATACAGTTTCTTTACGGCAGCAGTGAAAGA
AGTGACTCAGAAGACCCGTCTTTGAAAAAAACAAACTATAAAATGTATCCACTCTGACCAAAGCAAAAAAAGACAT
ATTCCTTCCCCTCTCCACACAGAAAAATTCGGGATATTGAGATCTCCC**TAA**AGGAGGTCCTAAAAAGTCAGTATA
TGTTGGGGTAAGAAGAGAAGATGCACGCCCTAAGTAGAGATAAAAAGAGCCAGATTTTAAAACTCTTTGTTCCCT
AACTCCTTGTATGTAATGCTCTTATTGAAAATGTTAACCGATTATTTTGAATGATTATTTTTTTGG

FIGURE 526

MTCTFRTAEYFPFYPCLHCSITFIQFLYGSSERSDSEDPSLKKQTIKCIHSDQSKKRHIPSPLHTEKFGILRSP

FIGURE 527

ATGGCGTCCTATTTCGATGAACACGACTGCGAGCCGTCGGACCCTGAGCAGGAGACGCGAACCAACATGCTGCTG
GAGCTCGCAAGGTCACTTTTCAATAGGATGGACTTTGAAGACTTGGGGTTGGTAGTAGATTGGGACCACCACCTG
CCTCCACCAGCTGCCAAGACTGTGGTTGAGAACCTCCCCAGGACAGTCATCAGAGGCTCTCAGGCTGAGCTCAAG
TGCCCCGTGTGTCTTTTGGAATTTGAGGAGGAGGAGACTGCCATTGAGATGCCTTGCCATCACCTTTTCCATTCC
AGCTGCATTCTGCCCTGGCTAAGCAAGACAAATTCCTGTCCCTTGTGCCGCTATGAGCTGCCCACTGATGACGAC
ACTTATGAGGAGCACAGACGAGATAAGGCTCGAAAACAGCAGCAGCAACACCGACTGGAGAACCTCCATGGAGCC
ATGTACACG**TGA**

FIGURE 528

MASYFDEHDCEPSDPEQETRTNMLLELARSLFNRMDFEDLGLVVDWDHHLPPPAAKTVVENLPRTVIRGSQAELK
CPVCLLEFEEEETAIEMPCHHLFHSSCILPWLSKTNSCPLCRYELPTDDDTYEEHRRDKARKQQQQHRLENLHGA
MYT

FIGURE 529

GTATTCAATATGCTTATGTTTTATTTATGTAGGTGGCATTTAAAATACATGATGTGTTTAGGGTTACATTGTCCA
CAGAAAGCATCAAATACCACTCCTCTCCCCGCCAAAACCAAATAAACAAAGCCAACTCTTTGGCAACAGTTGTGT
TAAATAAAATCCCAGGTCACACTTGTTTCTGGCTCCCAAGCCTGGGTCACTGCTACATGGATTGCGCCAAAAAAT
TCCCAGCTTCAACACTGCTAGATTAAAATTGCTGGCATTTTTAAATCACAGCAAAGCTTTTCACAATGCCCTCAA
GTCCAAGAGGACAAAGGAGAAAGCAACATGAACGGCAGATCCTCATGTGAAAGGGAAGGAAAGTCACTGGGAGGG
AGCATGCAGGGAAGAAGTCAAGGCAGCCCTGGAATTCTACTCCGTGCTCAATAAAAAAAAAACGTGAAGAAGCAA
TACATCATGCAAACGAAATAATGACCGGAAGTGGGCGCATCTAGTTAGAATGAAGTGACTTTCGTAAGGAGTCAA
TGTTCGCGAACTGAAACATGAGTTCAACCTCCTTGTGCCGTCTCTGGGTGTTTTGCACGTGTGTAAATACCGGCC
CGTTTTCCCCAGCATGGCCCTAACCCATGGACACTAGGGAGGGTGCCACTGAGCAAAAATTTTTTGCTAAAAATA
ATTAGCAAAAATCCAAGAAAAAAATATGGAATCTAGCAAAACCTACACCATATTTGAAGTTGAATTTGCACTACC
TGCAAAGCAAATAATTTAAAAGAATAAACATTGTGAACATCAATTCCCATCACAGCAAGCCCTGGATGAAAACAT
GGACCTCTTGGAAGGTATAACTGGCTTTGAAGACTCTGTCCGAAAGTGTAAGTCCCTCTCTGAGGCTGGCTCCC
CAAGGGGAAGGGGTAGGGAGTGGCAGCCAGGTCCGGGGGGACAGCTGCTCACCGGTTTTGTCTCTGACCTCCACA
GTTATCTGCC**ATG**TTGTGGGTATCACTTACCAGCACATTGACCGCTGGCTGCTGGCCGAGATGCTCGGGGATCTG
TCGGGTAACGCCCTCTGGGTCCTGGTGCACATCTGGGAGGTTGGGGGTGGCTAGGGCAGTGGACCTCAGTCAGCT
CCTCCAACAGGCCTGTCTGGGTCTCATCAGGTCAGCATGGAAGGCCCAGCCCAAGGAGGAAATAAGAACTTGGTA
TAAGACAGTCTCTGCCTTGAGGGAGATCCTATGCCATTTGCTCATTTATTTTGCATTAATTGAGTGCCTACCGTG
TGTCAGTGTGCTAAACTGGGCGTGCAGCAGTAAACAAAGTGGGATGGCTCCAATTCATTCTCATGGAGGTAGCAA
AGCACATGGCGACATGGAGGTGTCCAGTGGTGATTCCTGTCATGAAGGAAAGCAAGACAGCTCACAGACCAGCGG
CATC**TGA**GCCCTTACCTCCGTAGAGAGAGGCCCGTGGCCTGAGGTAGTGCAGAGGAGGATAGTAGAGCAGGGCCC
TGACTTGTAACGTTCATGGGTAGCCAGGGTGTATGTGGCCAGAGCAGAGTAAGCATGGGCGAAAGTAGAGAGCTG
GGGGTTGGAGGGGCATTTCCAGGTCATGTGGGGCCTCGGGAGGACCTTGTCCTTTCCCCTGACTGAGAAGGAGCC
ACCGGAGGGCTCTGAGCAGGGTAGGGCTCTGATCAGATGGATATTTTTTAAAGATCCCCCCAAGAACAAAAAAAG
AAAAAATAACTTATTTGCTTACTTTTGTAAAAAGAAACGTAGAAAAGGAAGTCAAGAAACTAAGGAAGGCCGGGT
GCGGTGGCTCCCGCCTGTAATCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCATCTGTGGTCAGGAGTTCGAGA
CCAGCCTGCCCAACGTGGTAAAACCCCCTCTCTACTAAAAATACAAAAAATTGCTGGGTGTGGTGGCGTGCACCT
GTAGTCCCGGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTCAACGCAGGAGGCGGAGGTTGCAGTGAGCTGAG
ATCGCACCATTGCACTAGTGATAAGATCGAAACTCCATCTAAAAAAAAAAAAAAA

FIGURE 530

MLWVSLTSTLTAGCWPRCSGICRVTPSGSWCTSGRLGVARAVDLSQLLQQACLGLIRSAWKAQPKEEIRTWYKTV
SALREILCHLLIYFALIECLPCVSVLNWACSSKQSGMAPIHSHGGSKAHGDMEVSSGDSCHEGKQDSSQTSGI

FIGURE 531

AGTACCGGGTACGCAGGGGTGCCTCAACCACACTCCGTCCACGGACTCTCCGTTATTTAGGAGGTCCCTGGCCA
AAGATTTATTTCTCTTGACAACCAAGGGCCTCCGTCTGGATTTCCAAGGAAGAATTTCCTCTGAAGCACCGGAAC
TTGCTACTACCAGCACC**ATG**CCCTACCAATATCCAGCACTGACCCCGGAGCAGAAGAAGGAGCTGTCTGACATCG
CTCACCGCATCGTGGCACCTGGCAAGGGCATCCTGGCTGCAGATGAGTCCACTGGGAGCATTGCCAAGCGGCTGC
AGTCCATTGGCACCGAGAACACCGAGGAGAACCGGCGCTTCTACCGCCAGCTGCTGCTGACAGCTGACGACCGCG
TGAACCCCTGCATTGGGGGTGTCATCCTCTTCCATGAGACACTCTACCAGAAGGCGGATGATGGGCGTCCCTTCC
CCCAAGTTATCAAATCCAAGGGCGGTGTTGTGGGCATCAAGGTAGACAAGGGCGTGGTCCCCCTGGCAGGGACAA
ATGGCGAGACTACCACCCAAGGGTTGGATGGGCTGTCTGAGCGCTGTGCCCAGTACAAGAAGGACGGAGCTGACT
TCGCCAAGTGGCGTTGTGTGCTGAAGATTGGGGAACACACCCCCTCAGCCCTCGCCATCATGGAAAATGCCAATG
TTCTGGCCCGTTATGCCAGTATCTGCCAGCAGAATGGCATTGTGCCCATCGTGGAGCCTGAGATCCTCCCTGATG
GGGACCATGACTTGAAGCGCTGCCAGTATGTGACCGAGAAGGTGCTGGCTGCTGTCTACAAGGCTCTGAGTGACC
ACCACATCTACCTGGAAGGCACCTTGCTGAAGCCCAACATGGTCACCCCAGGCCATGCTTGCACTCAGAAGTTTT
CTCATGAGGAGATTGCCATGGCGACCGTCACAGCGCTGCGCCGCACAGTGCCCCCCGCTGTCACTGGGATCACCT
TCCTGTCTGGAGGCCAGAGTGAGGAGGAGGCGTCCATCAACCTCAATGCCATTAACAAGTGCCCCCTGCTGAAGC
CCTGGGCCCTGACCTTCTCCTACGGCCGAGCCCTGCAGGCCTCTGCCCTGAAGGCCTGGGGCGGGAAGAAGGAGA
ACCTGAAGGCTGCGCAGGAGGAGTATGTCAAGCGAGCCCTGGCCAACAGCCTTGCCTGTCAAGGAAAGTACACTC
CGAGCGGTCAGGCTGGGGCTGCTGCCAGCGAGTCCCTCTTCGTCTCTAACCACGCCTAT**TAA**GCGGAGGTGTTCC
CAGGCTGCCCCCAACAACTCCAGGCCCTGCCCCCTCCCACTCTTGAAGAGGAGGCCGCCTCCTCGGGGCTCCAGG
CTGGCTTGCCCGCGCTCTTTCTTCCCTCGTGACAGTGGTGTGTGGTGTCGTCTGTGAATGCTAAGTCCATCACCC
TTTCCGGCACACTGCCAAATAAACAGCTATTTAAGGGGG

FIGURE 532

MPYQYPALTPEQKKELSDIAHRIVAPGKGILAADESTGSIAKRLQSIGTENTEENRRFYRQLLLTADDRVNPCIG
GVILFHETLYQKADDGRPFPQVIKSKGGVVGIKVDKGVVPLAGTNGETTTQGLDGLSERCAQYKKDGADFAKWRC
VLKIGEHTPSALAIMENANVLARYASICQQNGIVPIVEPEILPDGDHDLKRCQYVTEKVLAAVYKALSDHHIYLE
GTLLKPNMVTPGHACTQKFSHEEIAMATVTALRRTVPPAVTGITFLSGGQSEEEASINLNAINKCPLLKPWALTF
SYGRALQASALKAWGGKKENLKAAQEEYVKRALANSLACQGKYTPSGQAGAAASESLFVSNHAY

FIGURE 533

ATTCAAGCCTGGGCCCTGGAAGGAGGGGTGGACAGTCCCCTCCCTTCCAGTCCAGCATGGGTCTGGGGAAGAGGA
GCAGCTTTGCCTGGAAGGGGCCTCCTAGGAGGGGGAGCGGTGGTTTCTAGCTCAGGCTTTAGGATCAGAGAGCAG
CAGATTCAAATCCTGACGGTTTTGGTAAAGTCAATTCAATCTCTCCAAGACTCCGTTTACTTGATCTGCGAAGTG
GGGATAATGGTATCACGTCGCAGGGTTGTCAGGCGGAGCTGGTAGGGGAGCTGCCCCCCAGAGCAGC**ATG**GATGC
CCCGCGAAGGGACATGGAGTTGCTCAGCAACAGCCTGGCTGCCTACGCGCACATCCGCGCCAACCCCGAGAGCTT
TGGCCTCTACTTCGTGCTGGGCGTCTGCTTCGGCCTGCTGCTCACCCTCTGCCTGCTCGTCATCAGCATCTCGTG
GGCGCCCCGCCCGCGGCCCCGGGGCCCGGCTCAGCGCCGGGACCCCCGCAGCAGCACCCTGGAGCCCGAGGACGA
CGACGAGGACGAGGAGGACACGGTGACTCGGCTGGGCCCCGACGACACGCTGCCGGGCCCCGAGCTGTCCGCAGA
GCCGGACGGGCCCCTCAACGTCAACGTCTTCACGTCGGCGGAGGAGCTGGAGCGGGCGCAGCGGCTGGAGGAGCG
CGAACGGATCCTGCGGGAGATCTGGCGCACCGGGCAGCCGGACCTGCTGGGCACAGGCACGCTGGGGCCCAGCCC
CACGGCCACGGGCACCCTGGGCCGCATGCACTATTAC**TGA**TGGGCCCTGGCTCCCGCCGCAAGGCGCTCGGGGTA
CCGGACCTGTACATGAGCTCAGAGCTACCCCACACCTTCGGACTGCCTCGGCCCCCACAGCTCCCAGGTGCTACT
GGGCGTGGACCGCCACCCCCTGAGAGGCTCCCTTCCCCAGTCCTGCCAGAAGACCCCGGGGGCGGGGAGGGGGCA
GCATGCAGGGTCCCCACTCCCTCTCTGGGGTCGATGAAGAGGTGAAGTGACCAAATGAAAGAAAGCTGCATTCTC
AGTG

FIGURE 534

MDAPRRDMELLSNSLAAYAHIRANPESFGLYFVLGVCFGLLLTLCLLVISISWAPRPRPRGPAQRRDPRSSTLEP
EDDDEDEEDTVTRLGPDDTLPGPELSAEPDGPLNVNVFTSAEELERAQRLEERERILREIWRTGQPDLLGTGTLG
PSPTATGTLGRMHYY

FIGURE 535

GGACTGTTGAAGACAGGTCTCCACACACAGCTCCAGCAGCCACATTTGCAACCTTGGCCATCTGTCCAGAACCTG
CTCCCACCTCAGGCCCAGGCCAACCGTGCACTGCTGCA**ATG**GGCTCTGAGCTGGAGACGGCGATGGAGACCCTCA
TCAACGTGTTCCACGCCCACTCGGGCAAAGAGGGGGACAAGTACAAGCTGAGCAAGAAGGAGCTGAAAGAGCTGC
TGCAGACGGAGCTCTCTGGCTTCCTGGATGCCCAGAAGGATGTGGATGCTGTGGACAAGGTGATGAAGGAGCTAG
ACGAGAATGGAGACGGGGAGGTGGACTTCCAGGAGTATGTGGTGCTTGTGGCTGCTCTCACAGTGGCCTGTAACA
ATTTCTTCTGGGAGAACAGT**TGA**GCAGACAGCCACATTGGGCAGCGCCCTTCCTCTCCACCCTCCCAGACCTGCC
TCTTCCCCCTGCTTCCACCTCACCCCACTTATCCCTCTCCATAACCCCACCCTTGCCCACCCCACCCCCACCCCC
ACCAAGGGCGCAAGAGTAGCGGTCCAAGCCTGCAACTCATCTTTCATTAAAGGCTTCTCTCTCACCAGCAAAAAA
AAAAAAA

FIGURE 536

MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKDVDAVDKVMKELDENGDGEVDFQEY
VVLVAALTVACNNFFWENS

FIGURE 537

GTCCTCCGGGGATTAGAGCCGGTGGGCTCGTTGTGGGCGCCATTTCTCGGCGTCTCCCGAGGAGCCGCCCCTTTC
TCAGCCTTGCTCGGCTCTTCCCCGCTCTGGTCGCCGGGGCTGCGCCGTCCCCAGCTCAGTGACAAAA**ATG**CTGAG
TTTCTTCCGTAGAACACTAGGGCGTCGGTCTATGCGTAAACATGCAGAGAAGGAACGACTCCGAGAAGCACAACG
CGCCGCCACACATATTCCTGCAGCTGGAGATTCTAAGTCCATCATCACGTGTCGGGTGTCCCTTCTGGATGGTAC
TGATGTTAGTGTGGACTTGCCAAAAAAAGCCAAAGGACAAGAGTTGTTTGATCAGATTATGTACCACCTGGACCT
GATTGAAAGCGACTATTTTGGTCTGAGATTTATGGATTCAGCACAAGTAGCACATTGGTTGGATGGTACAAAAAG
CATCAAAAAGCAAGTAAAAATTGGTTCACCCTATTGTCTGCATCTTCGAGTTAAGTTTTATTCCTCAGAACCAAA
TAACCTTCGTGAGGAGCTAACCCGGTATTTATTTGTTCTTCAGTTAAAACAAGATATTCTCAGTGGAAAATTAGA
CTGTCCCTTTGATACAGCAGTGCAATTGGCAGCTTATAATCTGCAAGCTGAACTTGGTGACTATGATCTTGCTGA
GCATAGTCCTGAACTTGTCTCAGAGTTCAGATTCGTGCCTATTCAGACTGAAGAGATGGAACTGGCTATTTTTGA
GAAATGGAAGGAATACAGAGGTCAAACACCAGCACAGGCTGAAACCAATTATCTGAATAAAGCCAAATGGCTAGA
AATGTATGGGGTTGATATGCATGTGGTCAAGGCTAGAGATGGGAATGACTATAGTTTGGGACTAACACCAACAGG
AGTCCTTGTTTTTGAAGGAGATACCAAAATTGGCTTATTTTTTTGGCCGAAGATAACCAGATTGGATTTTAAGAA
GAATAAATTAACCTTGGTGGTTGTAGAAGATGATGATCAGGGCAAAGAACAGGAACATACATTTGTCTTTAGACT
GGATCATCCAAAAGCATGCAAACATTTATGGAAATGTGCTGTGGAGCATCATGCTTTCTTCCGCCTTCGAGGCCC
CGTCCAAAAGAGTTCTCATCGATCAGGATTTATTCGACTAGGATCACGATTTAGATATAGTGGGAAAACAGAGTA
TCAGACCACAAAAACCAATAAAGCAAGAAGATCAACATCCTTTGAAAGAAGGCCCAGCAAACGATATTCTAGACG
AACTCTACAAATGAAAGCATGTGCTACAAAACCTGAAGAACTTAGTGTTCACAATAATGTTTCGACCCAAAGTAA
TGGCTCCCAACAGGCTTGGGGGATGAGATCTGCTCTGCCTGTGAGTCCTTCCATTTCCTCTGCTCCTGTGCCAGT
GGAGATAGAGAATCTTCCACAGAGTCCTGGAACAGACCAGCATGACAGGAAATGCATTCCTCTGAATATTGATTT
GCTGAATAGCCCAGACTTATTGGAAACAACGATTGGTGATGTAATTGGGGCATCTGACACTATGGAAACATCCCA
AGCACTGAATGACGTTAATGTAGCCACCAGGCTTCCGGGATTAGGGGAACCTGAAGTTGAATATGAGACATTAAA
AGACACCTCAGAGAAGCTCAAACAGCTTGAGATGGAGAACAGTCCTTTGCTGTCCCCTCGATCCAACATCGATGT
TAACATAAACAGCCAGGAGGAAGTGGTGAAGTTGACTGAGAAATGCCTTAATAATGTCATTGAGAGCCCAGGATT
GAATGTCATGAGAGTTCCTCCTGACTTCAAGAGTAACATTTTGAAGGCTCAAGTAGAAGCAGTGCATAAGGTTAC
AAAAGAAGATAGCTTATTAAGTCATAAAAATGCCAATGTTCAGGATGCTGCCACAAACAGTGCTGTGTTAAATGA
GAATAATGTGCCCCTCCCCAAAGAGTCTCTTGAGACTCTGATGCTTATCACACCTGCCGACAGTGGTTCTGTTCT
AAAGGAAGCTACAGATGAATTGGATGCCTTGCTTGCATCTCTAACTGAGAATCTAATTGATCACACAGTTGCACC
TCAGGTGTCTTCCACATCCATGATCACACCCCGGTGGATTGTTCCGCTCTGGTCCCATTTTGGCAGAAGAAGCTG
TCCTGAAGCAGAAGTGTTTACTGACCAC**TGA**GCTCTGAGGGCCTGTAGCTGGAATACGCATCTCTCCAGCATTCC
GTCCTGGGATCCGTTTCAGCTAGAATATGTTGGATTCAGGAGCTTGTCCATTATTTGTAGGTAAAAAAAGCTGCA
CGTAGATTTGACTTCAACTCCGTAAAAAAGACAGCTGTATTTTCCGTCCAACTGGAATTGTTGAATCACACTGCA
TAGCTGCCCAAAAGAGAGTGTTTGGTCTTGAACTTTCTATACTTTTATAAATGTTACAAATTCCCGAAAGAAGGG
AATTTCTTTTTCTGGGGTTTCCTTCAAACTCTTGGCTCCACCTAGCGGTTCTATTTGTTCATAACAACTTCATAA
CAAGCCTGCCTCTGGTAGTCAACAGCCTTTTGAAAGCTATTTCCATCTAGTATCAGGGTGAGAGCATCCTTGATC
TGGCTGCCTGTTAGAGAAATTGCACTTTTCCTGACTTACCTAGAAATCAAGAATTTAGGAAATTAATGTGGACAC
TATAAAGGCAGACTTAGGGCCAACTTTTTTTTTTTTACAATTATTACAACACTAAAGAGAAGTTTAGAATATAG
AGAGTTTTTAAATGTCTCCCATTCTTTTGATTTCTTACTGTACTGGCTATCTTAATATTTCAAGTTTACATCAAG
ATAAACCCTGAGAAGAACTACGGAGAAATCAAATAAAATCCTGTCATATTTTTTTCACCCTGCCTTTCCACAGGA
AGCACTCACAGGCACCACACACGTATCATGTAACTTATCAGTGGGGTGGGTTACTGTTGAAGAGACCCTGGGGCA
TTTACCTCAGGCATCTGCACTCCTCCGAGCCCGGTGGAGAATGCAGGCTGCTGTAGTCTCAGGTAATGAAGGCAC
AGCACAGCAGTACTCCACATTGTTTCCTATTTGGACATAGACTTCATTTCCTTTCAGTATAAGCTGAGTAAATTT
AGAGCTTTCAAACTGG

FIGURE 538

MLSFFRRTLGRRSMRKHAEKERLREAQRAATHIPAAGDSKSIITCRVSLLDGTDVSVDLPKKAKGQELFDQIMYH
LDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSPYCLHLRVKFYSSEPNNLREELTRYLFVLQLKQDILSG
KLDCPFDTAVQLAAYNLQAELGDYDLAEHSPELVSEFRFVPIQTEEMELAIFEKWKEYRGQTPAQAETNYLNKAK
WLEMYGVDMHVVKARDGNDYSLGLTPTGVLVFEGDTKIGLFFWPKITRLDFKKNKLTLVVVEDDDQGKEQEHTFV
FRLDHPKACKHLWKCAVEHHAFFRLRGPVQKSSHRSGFIRLGSRFRYSGKTEYQTTKTNKARRSTSFERRPSKRY
SRRTLQMKACATKPEELSVHNNVSTQSNGSQQAWGMRSALPVSPSISSAPVPVEIENLPQSPGTDQHDRKCIPLN
IDLLNSPDLLETTIGDVIGASDTMETSQALNDVNVATRLPGLGEPEVEYETLKDTSEKLKQLEMENSPLLSPRSN
IDVNINSQEEVVKLTEKCLNNVIESPGLNVMRVPPDFKSNILKAQVEAVHKVTKEDSLLSHKNANVQDAATNSAV
LNENNVPLPKESLETLMLITPADSGSVLKEATDELDALLASLTENLIDHTVAPQVSSTSMITPRWIVPLWSHFGR
RSCPEAEVFTDH

FIGURE 539

CCACCCGCCTCGCCTCCCACGTGATGGACTATAGACATGAGCCATCGTGCTTGGCCTTCTTGATTCTTGAATACG
GGGTTTTGAGGTGAAAGCATTTCATGAAAACTTAAGTTCATACACAAGAGCATCATGAATATTCTAAAAGAGGTA
TCTGTGCTTTTTTTGTGACCACAAAATATTACTTCTTATGAAATGTTTACACTAGGTGAGGAAAAGTTCATTAAT
TACCTTTAAACCGTTCCTTATTTTTTTTAAGATTTTAAATTGTATTTTGGCTTTTGCCTCCAGTATCCTTTCTGG
TTGCTCTGGTTTGAATTAAGTTCCTATTATGCTGCAGCACATATCAACCTTCCCTAAGTAACCATTTCCTGGAAT
GTGAAGCATCGGTGCCATTAGCAGACCATATGCAGAAATGTCGTGTACTTGCATTTCTTTTTTGTGCACTCTATA
AGGCTGGTTGTGACTCAGATCAGCTTAACTTTTTATATTATGTTATTTCACTAACTGCTACAGTCAAAATGATCA
AATCTTTGTACAATAGAAAATTATTTAAATTTTATTTTTCTACTGACATTTCTAATTCTAGTGTAAATGTTTATC
AATAAAAAATTACTTTCAATTCTGAGTTGGAATTATATTTCTTTTTGGTGGCTAATGAGTTTAATCTTTTGTAAT
AAAATTGACTTCAGTTTTCATTTTTTAAATAACTTAATATCTAGCATGTGTAACTTTTTTTATGTTCTACTTCTT
ACTAATTT**ATG**ATAAAATTCTTGTTCAAAGTTGTGATTAAACCGTACTTAACATGTA

FIGURE 540

MIKFLFKVVIKPYLTC

FIGURE 541

GCATGTCATGGCCGCCTCCATGGCCCGGGGAGGCGTGAGTGCCAGGGTTCTGCTGCAGGCTGCCAGGGGCACCTG
GTGGAACAGACCTGGGGGCACTTCCGGGTCGGGGGAGGGGGTGGCGCTGGGGACAACCAGAAAGTTTCAAGCGAC
AGGCTCGCGCCCGGCGGGAGAGGAGGACGCGGGCGGCCCGGAGCGGCCCGGGGACGTGGTGAACGTGGTGTTCGT
AGACCGCTCAGGCCAGCGGATCCCAGTGAGTGGCAGAGTCGGGGACAATGTTCTTCACCTGGCCCAGCGCCACGG
GGTGGACCTGGAAGGGGCCTGTGAAGCCTCCCTGGCCTGCTCCACCTGCCATGTGTATGTGAGTGAAGACCACCT
GGATCTCCTGCCTCCTCCCGAGGAGAGGAGAACTCGCGGCTGGGCTGCCAGATTGTGC**TGA**CACCGGAGCTGGAA
GGAGCGGAATTCACCCTGCCCAAGATCACCAGGAACTTCTACGTGGATGGCCATGTCCCCAAGCCCCACTGACAT
GAACACCTGGACCATTCCACATTGCCATGGCCCCAGGGCCCAGATTGAGGGAATAGCCAGGTGCCAGCCCTGCCC
AGAGTGCGGACAGGCCCGGGAGAGACGTGGAAGCCCCTGTGAAGGACAACACCCCTGCTTGGGAGAGAGTCCCAT
GTCCAGGCTCTGGTGGGGACAGGGCCCCTAGTGGGGTGGCCTTCCCCAGGCCCCTGAGAATCAGGGTTTGAGTAG
GAGTGGACTCATATTGGAGCTGCAATAAATCAATAACACAG

FIGURE 542

HVMAASMARGGVSARVLLQAARGTWWNRPGGTSGSGEGVALGTTRKFQATGSRPAGEEDAGGPERPGDVVNVVFV
DRSGQRIPVSGRVGDNVLHLAQRHGVDLEGACEASLACSTCHVYVSEDHLDLLPPPEERRTRGWAARLC

FIGURE 543A

CGCCGGCGGGCCGTGTGTGAGGAGCAGTAGAGAACTGTGGACTATTCTGCTTGGAAGGTCAGCTCTGAGAGAGCT
GAGTCAGATTGAGGCAGAACTGAATAAACATTGGCGGCGATTGTTAGAGGGGCTTTCTTACTACAAACCTCCCAG
TCCAAGTTCAGCTGAAAAAGTGAAAGCTAATAAAGATGTAGCTTCACCATTGAAGGAACTGGGTTTAAGAATCAG
CAAGTTTTTGGGTCTTGATGAAGAACAGAGTGTGCAGTTACTCCAGTGTTACCTGCAAGAGGACTACAGGGGTAC
TCGGGACTCAGTAAAGACAGTACTGCAAGATGAGAGGCAGAGCCAGGCCTTAATCCTGAAGATTGCAGATTATTA
TTATGAAGAAAGAACCTGTATTCTTCGTTGTGTCTTACACCTTCTCACTTACTTCCAAGATGAAAGACACCCCTA
TAGGGTTGAATATGCAGACTGTGTTGATAAATTGGAGAAGGAACTAGTTTCAAAATACAGACAGCAGTTCGAAGA
GCTTTATAAAACTGAAGCACCAACTTGGGAGACACATGGAAATCTCATGACAGAGCGCCAAGTGTCTCGCTGGTT
TGTTCAGTGCCTTCGGGAACAGTCCATGCTGCTAGAAATTATTTTCCTTTATTATGCATACTTTGAGATGGCACC
CAGTGACTTACTTGTATTAACCAAGATGTTTAAAGAGCAAGGATTTGGTAGTAGGCAGACCAATAGGCACCTGGT
GGATGAGACTATGGATCCTTTTGTAGATCGGATTGGCTACTTCAGTGCCCTCATCCTGGTGGAGGGCATGGATAT
CGAGTCCTTGCATAAGTGTGCTTTGGATGACAGAAGAGAACTGCATCAGTTTGCGCAGGATGGGCTTATTTGTCA
GGATATGGACTGTTTAATGTTGACCTTTGGGGACATTCCACATCATGCCCCAGTGCTTTTGGCCTGGGCTCTCCT
CCGTCACACTCTGAACCCAGAAGAGACAAGCAGTGTGGTCCGGAAGATAGGTGGCACAGCCATCCAGCTGAATGT
GTTTCAGTACTTGACCCGATTGCTCCAGTCCCTTGCCAGTGGGGGAAATGATTGCACCACCAGCACTGCATGCAT
GTGTGTCTATGGACTGCTCTCTTTCGTTCTGACCTCGTTGGAGCTGCACACCCTGGGCAATCAGCAGGATATAAT
TGATACAGCATGTGAAGTATTGGCCGACCCTTCTCTTCCGGAACTGTTCTGGGGAACAGAGCCAACTTCTGGCCT
TGGGATCATTCTGGACAGTGTGTGTGGAATGTTTCCCCACCTTCTCTCCCCACTCCTGCAACTGCTCCGAGCCCT
GGTATCAGGGAAGTCCACAGCCAAAAAGGTGTATAGCTTCTTGGATAAGATGTCTTTCTACAATGAACTTTATAA
ACACAAGCCTCATGATGTGATCTCCCATGAAGATGGAACTCTTTGGCGGAGACAAACACCCAAACTCCTTTATCC
CCTTGGGGGTCAAACCAACCTTCGCATACCTCAAGGCACTGTGGGCCAAGTAATGTTGGATGATAGGGCATACCT
GGTACGCTGGGAATACTCCTATAGCAGCTGGACCCTCTTTACCTGCGAGATTGAAATGTTGCTTCATGTTGTTTC
AACTGCAGATGTGATTCAGCACTGCCAGCGAGTCAAACCCATCATTGATCTCGTCCATAAGGTCATCAGTACAGA
CCTGTCGATAGCAGACTGTCTCCTGCCCATCACATCTCGCATCTACATGCTGCTGCAGCGGTTAACGACAGTGAT
CTCCCCACCTGTGGATGTCATTGCTTCTTGTGTCAACTGCTTAACTGTTTTGGCTGCCCGCAATCCAGCAAAGGT
CTGGACTGATCTTCGTCACACAGGTTTTTTACCATTTGTGGCCCATCCTGTCTCCAGCCTGAGTCAGATGATTAG
TGCGGAAGGGATGAATGCTGGAGGGTACGGAAACCTCTTGATGAACAGTGAACAGCCTCAGGGCGAGTATGGGGT
TACTATTGCCTTTCTGCGCTTGATCACCACCCTTGTCAAGGGGCAACTTGGTAGTACCCAGAGCCAAGGACTTGT
ACCCTGTGTAATGTTTGTGCTGAAGGAGATGCTTCCCAGCTACCATAAGTGGCGCTACAACTCTCATGGAGTGAG
GGAACAGATTGGTTGCCTGATCTTGGAGCTGATTCATGCGATACTGAACCTGTGCCACGAGACAGACCTGCACAG
CAGTCATACTCCCAGCCTGCAGTTTCTCTGCATCTGCAGCCTGGCATACACAGAAGCAGGACAGACAGTTATCAA
TATCATGGGCATTGGCGTGGACACCATTGACATGGTGATGGCTGCTCAGCCTCGAAGTGATGGGGCAGAGGGCCA
GGGGCAGGGCCAGCTGCTGATCAAGACAGTGAAACTGGCATTCTCCGTCACCAACAATGTTATTCGGCTGAAACC
TCCTTCTAATGTGGTGTCCCCCCTGGAACAGGCTCTCTCACAACATGGTGCTCATGGAAACAACCTCATTGCTGT
TCTAGCCAAATACATCTACCACAAACATGACCCTGCTTTGCCACGTCTTGCCATTCAGCTGCTGAAACGTCTGGC
CACGGTGGCCCCAATGTCAGTGTATGCTTGTCTGGGCAATGATGCGGCTGCCATTCGTGATGCCTTCCTGACCCG
ATTGCAGAGCAAAATTGAGGACATGCGCATCAAAGTCATGATTCTAGAGTTCCTCACTGTTGCAGTAGAGACCCA
GCCAGGCCTCATCGAACTGTTTCTGAACCTGGAAGTTAAGGATGGCAGTGATGGCTCAAAGGAATTCAGCCTTGG
GATGTGGAGCTGTCTCCATGCAGTGCTGGAGCTGATTGATTCCCAACAGCAAGATCGATACTGGTGCCCACCCCT
GCTGCATCGTGCCGCCATTGCCTTTTTGCATGCTCTGTGGCAGGATCGGAGGGACAGTGCCATGCTGGTCCTCCG
AACCAAACCCAAGTTTTGGGAAAATTTAACCAGTCCGCTGTTTGGAACCCTTTCTCCTCCCTCTGAAACATCAGA
GCCCAGCATCCTGGAAACCTGTGCCCTAATCATGAAGATAATTTGCTTGGAGATATACTATGTAGTAAAGGGTTC
ATTAGACCAGTCATTAAAGGATACACTGAAGAAATTTTCCATCGAGAAACGCTTTGCCTACTGGTCAGGGTATGT
CAAGTCATTGGCAGTTCACGTGGCCGAAACAGAAGGCAGCAGCTGCACCTCCTTGTTAGAGTACCAGATGCTGGT
GTCCGCCTGGAGGATGCTTCTCATCATTGCCACCACTCATGCAGATATAATGCACCTGACTGACTCTGTGGTGCG
TCGCCAGCTCTTTCTTGACGTGCTTGATGGAACCAAAGCATTACTCCTAGTTCCAGCCTCAGTGAACTGCCTTCG
CCTTGGCTCCATGAAGTGCACTCTGCTGCTTATCCTCCTCCGGCAGTGGAAGAGAGAGTTAGGTTCTGTGGATGA
AATCCTTGGACCCTTGACGGAGATCCTGGAGGGAGTGCTGCAGGCCGACCAGCAACTCATGGAGAAGACCAAGGC

FIGURE 543B

CAAGGTGTTCTCAGCATTCATCACAGTGTTGCAAATGAAGGAGATGAAAGTAAGTGACATCCCCCAGTACTCCCA
GCTGGTGCTGAATGTCTGTGAGACCCTCCAAGAGGAAGTGATTGCACTCTTCGACCAGACCCGCCACAGTCTGGC
ATTAGGCAGTGCCACAGAGGACAAGGACAGCATGGAGACTGACGACTGTTCTCGGTCCCGGCACAGGGACCAGCG
TGATGGGGTGTGTGTCCTGGGCCTGCACCTGGCCAAGGAGCTGTGTGAGGTAGACGAGGATGGTGACTCCTGGCT
GCAGGTAACCCGCAGGCTCCCCATCCTACCCACCCTCCTCACCACTCTAGAGGTGAGCCTTCGCATGAAGCAGAA
CCTGCATTTCACTGAGGCCACATTGCATCTGCTCCTCACCCTGGCTCGCACTCAGCAGGGAGCCACAGCAGTGGC
TGGAGCTGGCATCACCCAGAGCATTTGTTTGCCCCTTCTGAGTGTGTACCAGCTGAGCACCAACGGCACAGCACA
GACACCTAGTGCCTCTCGGAAGTCCCTGGATGCCCCCTCTTGGCCAGGAGTCTACCGCCTGTCCATGTCCCTGAT
GGAGCAGCTGCTCAAAACTCTGCGCTACAACTTCCTGCCTGAGGCCCTGGACTTCGTGGGTGTCCACCAGGAGCG
GACCTTACAGTGCCTCAACGCAGTGAGGACAGTGCAGAGTCTGGCCTGCCTGGAGGAGGCGGACCACACCGTGGG
TTTTATTCTGCAGCTCTCTAACTTCATGAAGGAGTGGCACTTCCACCTGCCTCAGCTCATGCGTGATATCCAGGT
CAACCTGGGTTACTTGTGCCAGGCATGTACCTCTCTCCTGCACAGTCGAAAGATGCTGCAGCATTACTTACAGAA
CAAAAATGGGGATGGCCTCCCCTCAGCTGTTGCCCAGCGAGTCCAGAGGCCACCGTCTGCTGCTTCTGCTGCCCC
CTCCTCCTCAAAGCAGCCCGCTGCTGACACAGAGGCATCAGAGCAGCAGGCCTTGCACACAGTCCAGTATGGCCT
TCTCAAGATCCTCAGCAAGACGCTGGCAGCCCTGCGCCACTTCACCCCAGATGTCTGCCAGATTCTGCTGGATCA
GTCCCTGGACCTTGCTGAATACAACTTCCTGTTTGCCCTGAGCTTTACCACTCCCACCTTTGACTCCGAAGTGGC
CCCCTCCTTCGGGACCCTTCTGGCCACAGTGAATGTGGCCCTCAACATGCTTGGAGAGCTGGACAAGAAAAAGGA
GCCCCTCACCCAGGCAGTGGGGCTCAGCACACAGGCAGAAGGGACCAGGACGTTAAAGTCCCTCCTGATGTTTAC
CATGGAAAACTGCTTCTACCTGCTCATCTCTCAGGCGATGCGGTACCTTAGGGACCCGGCTGTGCACCCCCGGGA
CAAACAGCGGATGAAGCAGGAGCTCAGCTCTGAGTTGAGCACGCTGCTGTCCAGCCTCTCGCGCTACTTCCGCCG
GGGAGCCCCCAGCTCCCCTGCCACTGGTGTCCTCCCCTCGCCGCAGGGCAAGTCCACCTCTCTCTCCAAAGCCAG
CCCTGAGAGTCAGGAGCCTCTGATCCAGTTGGTGCAGGCGTTTGTCCGGCATATGCAAAGA**TAG**GGCAGTGCTGT
TCTGCCCACCTACCCCTCTCCACCAGCCTACACTGCACCCTGGCTGGCAGGGGTGCTGCTGGCTGCTAGGGCCTA
TACAATGGAGGGCACCTCCTGTCACCCCCCTCCCGGAGTAGCCACGACTCCAGCCACCACCCACTGACGTTATTT
TTATACTAGATGAAGAGGTCAACAGCAGGCATGGGGAGCCGAGTCTTCTGTGCTCAGGTCCTCACGCTGCAGACG
CCCCCTAGAGGAACTTTCCTTCCTTTCCAGCATTCCCCACAGCACTGCCGGCCAGGGGAGAGGCGGCAGCCCAGC
AGAGGGCTCTATGCACGGGTTTCAAACCTGTTTTCCACACTCTGTCTTTGCAGTTTTGGTAATTCTGTGGTCTAT
TTATACAGATATTAAAATCTTGTTTATAGAC

FIGURE 544

AGGPCVRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSPSSAEKVKANKDVASPLKELGLRIS
KFLGLDEEQSVQLLQCYLQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTYFQDERHPY
RVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAP
SDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQFAQDGLICQ
DMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQSLASGGNDCTTSTACM
CVYGLLSFVLTSLELHTLGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLLRAL
VSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYL
VRWEYSYSSWTLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQRLTTVI
SPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGV
TIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHS
SHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKP
PSNVVSPLEQALSQHGAHGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAAIRDAFLTR
LQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPL
LHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGS
LDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRMLLIIATTHADIMHLTDSVVR
RQLFLDVLDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQQLMEKTKA
KVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQR
DGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLARTQQGATAVA
GAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKTLRYNFLPEALDFVGVHQER
TLQCLNAVRTVQSLACLEEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRKMLQHYLQN
KNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQ
SLDLAEYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRTLKSLLMFT
MENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLPSPQGKSTSLSKAS
PESQEPLIQLVQAFVRHMQR

FIGURE 545

CTATTTTAGTACAAGTGAAACAGCCTCGAAAAAAGGTC**ATG**GCTTGCAAAACCGCTTTTAATAAAACCGGGTTCC
AAGAAGTGTTTGATCCTCCTCATTATGAACTGTTTTCACTAAGGGACAAAGAGATTTCTGCAGACCTGGCAGACT
TGTCGGAAGAATTGGACAACTACCAGAAGATGCGGCGCTCCTCCACCGCCTCCCGCTGCATCCACGACCACCACT
GTGGGTCGCAGGCCTCCAGCGTCAAACAAAGCAGGACCAACCTCAGTTCCATGGAACTTCCTTTCCGAAATGACT
TTGCACAACCACAGCCAATGAAAACATTTAATAGCACCTTCAAGAAAAGTAGTTACACTTTCAAACAGGGACATG
AGTGCCCTGAGCAGGCCCTGGAAGACCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTCAGGGGGCGAGAAG
ATTCTGCACAAGCATCCATATCCATTGACTTC**TAA**TCTTCTGCTAATGGTGATGTGAATTCTTAGGGTGTGTACG
TACGCAGCCTCCAGGGCACCATACTGTTTCCAGCAGCCAACCCTTTTCTCCCATCACAACTACGAAGACCTTGAT
TTACCGTTAACCTATTGTATGGTGATGTTTTTATTCTCTCAGGCAGTCTATATATGTTAAACCAATCAAGGAACT
TACTCTATTCAGTGGAAACAATAATCATCTCTATTGCTTGGTGTCATTTATAGGAAGCACTGCCAGTTAAAGAGC
ATTAGAAGAGGTGGTTGGATGGAGCCAGGCTCAGGCTGCCTCTTCGTTTTAGCAACAAGAAGACTGCTCTTGACT
GATAACAGCTCTGTCAATATTTTGATGCCACAATAAACTTGATTTTTCTTTACATTCCTTTTATTTTTCCTTTCT
CTAAATTTAATTTGTTTTATAAGCCTATCGTTTTACCATTTCATTTTCTTACATAAGTACAAGTGGTTAATGTAC
CACATACTTCAGTATAGGCATTTGTTCTTGAGTGTGTCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGT
TGTATTTCACCCATCTGTTTCTTCTTGGCTAATCTCTGTACTTCTGCCTTTTAATTACTGGGCCCTTATTCCTTA
TTTTCTGTGAGAAATAATAGATGATATGATTTATTACCTTTCAATTATATTTTTCTCAGTTATACTAGAAAATTT
CATAATCCTGGGATATATGTACCATTGTCAGCTATGACTAAAAATTTGAAAAAGATAAAAATTTCTAGCAAGCCT
TTGAAGTTTACCAAGTATAGTCACATTCAGTGACAGCCCATTCATTCCAGTAAAGAATCATTTCATTCACTTTGG
GAGAGGCCTATAATTACATTTATTTGCAATGTTTCTCTTCGCTAGATTGTTACATAGCTCCCATTCTGTTGGTTT
TGCTTACAGCATATGGTAACCAAGGTTAGATGCCAGTTAAAATTCCTTAGAAATTGGATGAGCCTTGAGATTGCT
TCTTAACTGGGACATGACATTTTTCTAGCTCTTATCAAGAATAACAACTTCCACTTTTTTTAAACTGCACTTTT
GACTTTTTTTATGGTATAAAAACAATAATTTATAAACATAAAAGCTCATTGTGTTTTTTAGACTTTTGATATTAT
TTGATACTGTACAAACTTTATTAAATCAAGATGAAAGACCTACAGGACAGATTCCTTTCAGTGTTCACATCAGTG
GCTTTGTATGCAAATATGCTGTGTTGGACCTGGACGCTATAACTTATTGTAAAGACCTTGGAAATGTGGACATAA
GCTCTTTCTTTCCTTTTGTTACTGTATTTAGTTTGTGATAAATTTTTCACTGTGTGATATTTATGCTCTAAATCA
CTACACAAATCCCATATTAAAATATACATTGTACCTG

FIGURE 546

MACKTAFNKTGFQEVFDPPHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHCGSQASSVKQSRT
NLSSMELPFRNDFAQPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEIPCEIYVRGREDSAQASISIDF

FIGURE 547

TGGTCCATCAGCTGCTGGTTCATTATAGCCTTCTCTTAAGTACTGAATAAGACAAAATATAAATCTTGGAAGAAC
AAATTCAGACATCATCAGTAAGTCTTTAGGGACACAGGGAATATTTGAACTTGATTTAATTTG**ATG**CCTTTTGCA
AAACCCGCTCTCCCGCATCACGTTGCTGTCCCCGCAGTCGCAGGCGCCCCCGGCCTGGCTGCGGAACATGTTGAA
GTCGTGTCCGGTGTGGTCGCCCTGGTGGAAGCACTCGGCGCACAGCGACATGCAGGGCGAGATGCCGCACGTCCG
GCAGCGGTAGGCCACGAAGTTGGCTGTCCAGACCAGGCCGCAGAGCGCCGCGGGATCGTAGGCCCGCACCGCCGC
GCAGAACTCGTCGTAGCCGCCGCCGCCCGCCAGAAGGCACTTACACCACTCCAGGGCCTCCTCCTCGGCCGCCCC
CGGACCGCCCCCGCCTCCGGCCGCCGCCGCGTCCTCGCCGCCAGCAGCCGCGGCCAGCGGCCGC

FIGURE 548

MPFAKPALPHHVAVPAVAGAPGLAAEHVEVVSGVVALVEALGAQRHAGRDAARPAAVGHEVGCPDQAAERRGIVG
PHRRAELVVAAAARQKALTPLQGLLLGRPRTAPASGRRRVLAASSRGQR

FIGURE 549

CTCCTTGGGCGATCGCCTGGGTAGAGGAGAGGAGTTTCCGGGGCTCGGGTCCGGGTCGCCTTCCAGGGGAACGAG
CGCGGAAGCAAGTGGGCGGCGAGAGGCGGAGCAAGAGACGCTGGAGGGCGTGGACGCAGCGGGCTTTGGAAAGGC
CCCAAGTTA**ATG**AGGCGTGCGCCGGCTGCCGAGCGCCTCTTGGAGCTGGGCTTTCCCCCGCGGTGCGGGCGCCAG
GAGCCGCCTTTTCCGCTGGGTGTCACTCGGGGGTGGGAAGATGGCCCATTCAAAAGCGCCGCGAGGGGGCCCGG
CCAGTGCCCTTCAGTGAGCGCTCGCAAGAGGACGGCAGAGGCCCGGCAGCTCGGAGCTCCGGGACCTTGTGGCGC
ATCAGGACGCGGCTGTCCCTCTGCCGGGACCCAGAGCCGCCGCCGCCGCTCTGCCTCCTGCGTGTTAGCCTCCTC
TGCGCGCTCCGGGCAGGCGGCCGTGGGAGCCGCTGGGGCGAGGACGGCGCGAGGCTGCTGCTGCTGCCCCCGGCC
CGCGCGGCTGGAAACGGAGAGGCCGAGCCAAGCGGCGGCCCCTCTTATGCTGGGAGGATGCTGGAGAGTAGCGGC
TGCAAAGCGCTGAAGGAGGGCGTGCTGGAGAAGCGCAGCGACGGGTTGTTGCAGCTCTGGAAGAAAAAGTGTTGC
ATCCTCACCGAGGAAGGGCTGCTGCTTATCCCGCCCAAGCAGCTGCAACACCAGCAGCAGCAGCAACAGCAGCAG
CAGCAGCAGCAACAACAGCCCGGGCAGGGGCCGGCCGAGCCGTCCCAACCCAGTGGCCCCGCTGTCGCCAGCCTC
GAGCCGCCGGTCAAGCTCAAGGAACTGCACTTCTCCAACATGAAGACCGTGGACTGTGTGGAGCGCAAGGGCAAG
TACATGTACTTCACTGTGGTGATGGCAGAGGGCAAGGAGATCGACTTTCGGTGCCCGCAAGACCAGGGCTGGAAC
GCCGAGATCACGCTGCAGATGGTGCAGTACAAGAATCGTCAGGCCATCCTGGCGGTCAAATCCACGCGGCAGAAG
CAGCAGCACCTGGTCCAGCAGCAGCCCCCCTCGCAGCCGCAGCCGCAGCCGCAGCTCCAGCCCCAACCCCAGCCT
CAGCCTCAGCCGCAACCCCAGCCCCAATCACAACCCCAGCCTCAGCCCCAACCCAAGCCTCAGCCCCAGCAGCTC
CACCCGTATCCGCATCCACATCCACATCCACACTCTCATCCTCACTCGCACCCACACCCTCACCCGCACCCGCAT
CCGCACCAAATACCGCACCCACACCCACAGCCGCACTCGCAGCCGCACGGGCACCGGCTTCTCCGCAGCACCTCC
AACTCTGCC**TGA**AAGGGGCAGCTCCCGGGCAAGACAAGGTTTTGAGGACTTGAGGAAGTGGG

FIGURE 550

MRRAPAAERLLELGFPPRCGRQEPPFPLGVTRGWGRWPIQKRREGARPVPFSERSQEDGRGPAARSSGTLWRIRT
RLSLCRDPEPPPPLCLLRVSLLCALRAGGRGSRWGEDGARLLLLPPARAAGNGEAEPSGGPSYAGRMLESSGCKA
LKEGVLEKRSDGLLQLWKKKCCILTEEGLLLIPPKQLQHQQQQQQQQQQQQQQPGQGPAEPSQPSGPAVASLEPP
VKLKELHFSNMKTVDCVERKGKYMYFTVVMAEGKEIDFRCPQDQGWNAEITLQMVQYKNRQAILAVKSTRQKQQH
LVQQQPPSQPQPQPQLQPQPQPQPQPQPQSQPQPQPQPKPQPQQLHPYPHPHPHSHPHSHPHPHPHPHQ
IPHPHPQPHSQPHGHRLLRSTSNSA

FIGURE 551

GGAGTCCTCATGGGAATAAGGATATTACAAATGTAAACAGGTACCTAAGCACTCCTTGATCACGTGACGTTGTTG
AATATTTTAGGCACACTTTCTTTTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGACTTTCAACAAATTGATAGTGAGCATTAAGGGTTTCCAAGTTGG
ATTTGTAACTCCTCATCATTCCTTGTATGACAACTTTCTGAATATATGTCACTATGTAGTAAAATTAAACACTCC
AAACTCATCTTTCTGTTGTTAGAAGTTTTCAGCGGTACTTCCATGCAACTTTAAATCTCACTGCTCTCTATGGTT
GATGTCAAATGACCTTCAGTAATGACTGAGAATTGAATACAAATAGATTACAAAGCCAAAATTTGATGTTAA**ATG**

ACTCAGGAAATTTTAGTTGTATTTTCAATTCAAGTACTTAGTAGCCTACGTTTGCTTGGCCTCTGGTTCTTTATG
GAAAATAGGCTTTGTAGTGGCATTGTGGAGCAAAGGAGACTGTTACACCTTAAT**TAA**CTTTTTTTACTGATGCAA
ATAATTTGAGGATAGAGAGGAGGGAAGTAGTGAAAGCTATGACCTAAAACATTGGGACCAAATAGAGGCTCACAG
ATATTTGGATTATTTTATGTGCTTATTATTAAATAAGGAAAGCATTTTGTGATATGTGGAAGACGCTATGTGAAG
TTTTACCTATCTTCTCAAAGACCTTTTCTTTTGTATTTTCTTTTGGTGTTTCTTAAAGCCAAACAAAGAAATGTT
CTTAAGGAGACAGGGTGGGTTTTTCTGTGGGCCTTTGTTGGTTTTTCTGTGGGCCATCGCCCTCTAATGGAATTG
ATCTCTGGCTGTTTGATTTTTTTCATATTGTATTTTTAAAATTTGTTGTACAGTGCCCTGTGAGCACCAAGTACC
ACTAGATGAATAAAACGTATTATATCTAAAGTCTTAGTAGACCAATTTTTAATCTTAGTTGACTCTGTATTGTTA
TCACACTGCACTCTTGTGGTTGTGCCATTTTTGCAAAATTGAGCTCTTTCGGTTGTTTTCGAAATAAGGGAACTT
AGTGTTGAAAAACCAGAGAACTTTTTCTTTAATAAGAAACTAAAAAAGTTGCAGCCACATAGGTTCAGTTTGGCT
CTTTGGTTTCCAGTGGCTCTCAAATCCCCTAAGGTTAAAAGAAAACACTACAGCTACCCTAGGGTTTCTCAACCT
TGGCATTATTGACATCTTGAATCAAATAATTCATTATTGTGGGGGTGCTGTCCTGTGCCTTGCAGAATCTTGAGC
AGTGTTCCTGACCTCTACCTATTGAGATGCCAGCAGCACACCCCCATC

FIGURE 552

MTQEILVVFSIQVLSSLRLLGLWFFMENRLCSGIVEQRRLLHLN

FIGURE 553

AAGTTTGTGATAATTTGTTAGGACAGCAATAGAAAACAAATACAATATACAGGTTCACTCATTTAACATAATCTG
CCGTTTTACAAAACTGTGATTTTGAAGTTTCTTGTTGCATTGAATACACTTTTTTGAAGCTGATGTTGACACAGG
AATAAGGCAATTGAGCAAGAACAACAAGGCATGGTGTGTTAATTATGCACTAAATGACCGTGGCCATTTTGTCTA
ATAGTTTCAATAGTTTCCAATAGTTTCAAGTGTATAGGTTGAGGGCAGGGACTATATCTGGTCTTTATATCTTAC
AATGATTTTCTTATATAGTTATTAGCACAGTGCCAGAAATGTTTCCTGAATTAATAAATGCTAAAACATTTCCTC
ATTAAGACTGTAAGCTGTTTGGTGTAGGAAAACTAACTTTTTAAAATTGATCATAACAATTCCAACGTTGAACAT
GGCCTGGAGCTTAACAGATGTTTATTTAAATACTAAGGAGTATGTCTGGGCTTAGGAAGGAGAGGGTGGTTACAT
TTCAGGGTGGTAGAATTCTGCCTGAAATATCTGCTTTATAATAAAAGTAAAATGTCTCACCGATACACTGTTAAA
CTGAGAAAACAAAGATGAGGTAAGGTGGGTCAGATTATTTCTAAGGTCTGTTTACTATTTACATTTCATATAATT
TTCATTAAATGTGGAGAATGCAAGTCTTAGGAGTCACCTGAGGTACATCCAGTTTTTTGTGACTATTTCCTGATG
TTTGACAGACTGTTCTTTCAACTTGGTGTAGAGTTACAGTCTACTCTTTTAGGGAGAATGCTGTTTGTTCACATC
ATGAGGCTGTAAATATTTAAAATGTTCTCACCATTGTGTTAGTTTCCAACTGACACATGGCCTGAGAGATTGGAG
TATCATTAATTCTGCAACTCTTTTAGTGCTCAGGATGTGCATGTTTATTTACTTTCAGGACTAGTTCAGACATAG
TAAAACTGCTAGTGACTTCATGTAATCCTTATTCTGAACTGTATTTGAAAGCAAGGGAAATGAAAC**ATG**ATCCCT
AATAACCTCAAACATCCAAAGATCAAGTCAATTAAGGGCAAAAAA

FIGURE 554

MIPNNLKHPKIKSIKGK

FIGURE 555

CTGAAAAACACTTGAAATAGCTTCTTCAACACATATATTGTATAGCTATTTAAAACCCAAATACAAATGTTATAT
GAAGACTTTCAAAAGGCCGCAGGATAATTCCAATGGATCTATTTGTTCAGTCATTCAGAAGCTATATCGGGAACC
CATCATGGATGAGCTCTGCTCTAGGCATGGGGAGAAAGGATGAGGAAGACAAATATGGCCCTAGTTCTTGTGGAT
CTTATGTTCTAGTGGTGGTGACTATTACTTTTTGAATTGTGTATTTGCCACAGGGGAGATTGGATTACTCTTCAG
AAATTTTATAAGCATCTAGAGATGACCTGCATTATTGCCTTGGGCAGGAAAATAACAGGGTTGAAAAAAATCTGA
ACAAAGAAATCACCATTTG**ATG**GATATACACAGGATAATCTTTTCTGAAGTTACTAAAATGGCGAAGTTCCCAAA
AAATGTAATGCGAATTAAATTTCACTTTGCCTCTGAGAAAAAGTTAAAAGAATTTATTATTACTCTCGCTACATG
TATTATCAAAAATGAAGGGTTGATATTTTTAAGGAATGAAGAGTTGGCCAGTCACTTTAGTGAAGTTTTATTTTT
TCGTAAATATAGTTTGCCTTTGCTTCCA**TGA**AAAAATAGCTCATAAACCTTGACCCTGATGAAAGCACTGGGCCA
GTTTTCCAATTCTCTGTTATGTAAAAAGGCATAAGTCAATTGTTCAAAGT

FIGURE 556

MDIHRIIFSEVTKMAKFPKNVMRIKFHFASEKKLKEFIITLATCIIKNEGLIFLRNEELASHFSEVLFFRKYSLP
LLP

FIGURE 557

GGCACAAGGGGGGATAGGTGGGGGGCCCAAAGAAGGGCATGGTCAGCCTGTCTGGGAGGGAGTTGCATGTGTGCA
TCTGAGGTAGGGACAGGCATGCATCTTACAGGA**TGA**ATATCGAGCAGAGTTACAGAGAGGGGGAAACTCCTTGAG
GTTTCAGGAATCACCTAATCCACTGTGACTCACAAATTCCTGCCTCTTGGCTTTGCCTGCAGCATATCTCCTGGA
AGTGTGCTGGGGCAAAACTCATCCCAGACCACCATCTCCATCCTCCCCCAATACACCCTGGCTCTCCCTGGCTAC
CCTTGAGCACGGTGCACGTGTGCATGGGTGCATGCCTGCATATATAGCTATCCCCCATGTATTTCCCAAAGCCCT
ACATAATGCTTCAGTTTGCTAAGGAAAAAATGTTAATTACTGCAAATGTGTTTAAAACTGTAAAAGTACATTAAA
CAAACTCTGTAAAGTGTGAAAAA

FIGURE 558

GTRGDRWGAQRRAWSACLGGSCMCASEVGTGMHLTG

FIGURE 559

GTACTATCCTCCTTACTTTTGGGTCGGGCCCTCCGGGAAG**ATG**GCGGCCGTGCAGGCGGCCGAGGTGAAAGTGGA
TGGCAGCGAGCCGAAACTGAGCAAGAATGAGCTGAAGAGACGCCTGAAAGCTGAGAAGAAAGTAGCAGAGAAGGA
GGCCAAACAGAAAGAGCTCAGTGAGAAACAGCTAAGCCAAGCCACTGCTGCTGCCACCAACCACACCACTGATAA
TGGTGTGGGTCCTGAGGAAGAGAGCGTGGACCCAAATCAATACTACAAAATCCGCAGTCAAGCAATTCATCAGCT
GAAGGTCAATGGGGAAGACCCATACCCACACAAGTTCCATGTAGACATCTCACTCACTGACTTCATCCAAAAATA
TAGTCACCTGCAGCCTGGGGATCACCTGACTGACATCACCTTAAAGGTGGCAGGTAGGATCCATGCCAAAAGAGC
TTCTGGGGGAAAGCTCATCTTCTATGATCTTCGAGGAGAGGGGGTGAAGTTGCAAGTCATGGCCAATTCCAGAAA
TTATAAATCAGAAGAAGAATTTATTCATATTAATAACAAACTGCGTCGGGGAGACATAATTGGAGTTCAGGGGAA
TCCTGGTAAAACCAAGAAGGGTGAGCTGAGCATCATTCCGTATGAGATCACACTGCTGTCTCCCTGTTTGCATAT
GTTACCTCATCTTCACTTTGGGCTCAAAGACAAGGAAACAAGGTATCGCCAGAGATACTTGGACTTGATCCTGAA
TGACTTTGTGAGGCAGAAATTTATCATCCGCTCTAAGATCATCACATATATAAGAAGTTTCTTAGATGAGCTGGG
ATTCCTAGAGATTGAAACTCCCATGATGAACATCATCCCAGGGGGAGCCGTGGCCAAGCCTTTCATCACTTATCA
CAACGAGCTGGACATGAACTTATATATGAGAATTGCTCCAGAACTCTATCATAAGATGCTTGTGGTTGGTGGCAT
CGACCGGGTTTATGAAATTGGACGCCAGTTCCGGAATGAGGGGATTGATTTGACGCACAATCCTGAGTTCACCAC
CTGTGAGTTCTACATGGCCTATGCAGACTATCACGATCTCATGGAAATCACGGAGAAGATGGTTTCAGGGATGGT
GAAGCATATTACAGGCAGTTACAAGGTCACCTACCACCCAGATGGCCCAGAGGGCCAAGCCTACGATGTTGACTT
CACCCCACCCTTCCGGCGAATCAACATGGTAGAAGAGCTTGAGAAAGCCCTGGGGATGAAGCTGCCAGAAACGAA
CCTCTTTGAAACTGAAGAAACTCGCAAAATTCTTGATGATATCTGTGTGGCAAAAGCTGTTGAATGCCCTCCACC
TCGGACCACAGCCAGGCTCCTTGACAAGCTTGTTGGGGAGTTCCTGGAAGTGACTTGCATCAATCCTACATTCAT
CTGTGATCACCCACAGATAATGAGCCCTTTGGCTAAATGGCACCGCTCTAAAGAGGGTCTGACTGAGCGCTTTGA
GCTGTTTGTCATGAAGAAAGAGATATGCAATGCGTATACTGAGCTGAATGATCCCATGCGGCAGCGGCAGCTTTT
TGAAGAACAGGCCAAGGCCAAGGCTGCAGGTGATGATGAGGCCATGTTCATAGATGAAAACTTCTGTACTGCCCT
GGAATATGGGCTGCCCCCCACAGCTGGCTGGGGCATGGGCATTGATCGAGTCGCCATGTTTCTCACGGACTCCAA
CAACATCAAGGAAGTACTTCTGTTTCCTGCCATGAAACCCGAAGACAAGAAGGAGAATGTAGCAACCACTGATAC
ACTGGAAAGCACAACAGTTGGCACTTCTGTC**TAG**AAAATAATAATTGCAAGTTGTATAACTCAGGCGTCTTTGCA
TTTCTGCGAAAGATCAAGGTCTGCAAGGGAATTCTTGTGTGCTGCTTTCCATTTGACACCGCAGTTCTGTTCAGC
CATCAGAAGAGAGACAAGGAATTAAAAATTTCTTTTTAATCCTGTTA

FIGURE 560

MAAVQAAEVKVDGSEPKLSKNELKRRLKAEKKVAEKEAKQKELSEKQLSQATAAATNHTTDNGVGPEEESVDPNQ
YYKIRSQAIHQLKVNGEDPYPHKFHVDISLTDFIQKYSHLQPGDHLTDITLKVAGRIHAKRASGGKLIFYDLRGE
GVKLQVMANSRNYKSEEEFIHINNKLRRGDIIGVQGNPGKTKKGELSIIPYEITLLSPCLHMLPHLHFGLKDKET
RYRQRYLDLILNDFVRQKFIIRSKIITYIRSFLDELGFLEIETPMMNIIPGGAVAKPFITYHNELDMNLYMRIAP
ELYHKMLVVGGIDRVYEIGRQFRNEGIDLTHNPEFTTCEFYMAYADYHDLMEITEKMVSGMVKHITGSYKVTYHP
DGPEGQAYDVDFTPPFRRINMVEELEKALGMKLPETNLFETEETRKILDDICVAKAVECPPPRTTARLLDKLVGE
FLEVTCINPTFICDHPQIMSPLAKWHRSKEGLTERFELFVMKKEICNAYTELNDPMRQRQLFEEQAKAKAAGDDE
AMFIDENFCTALEYGLPPTAGWGMGIDRVAMFLTDSNNIKEVLLFPAMKPEDKKENVATTDTLESTTVGTSV

FIGURE 561A

CCAGAC**ATG**GCGGAAGAGGAGGTGGCCAAGTTGGAGAAGCACTTGATGCTTCTGCGGCAGGAGTATGTCAAGCTG
CAGAAGAAGCTGGCGGAGACAGAGAAGCGCTGCGCTCTCTTGGCTGCGCAGGCAAACAAGGAGAGCAGCAGCAAG
TCCTTCATCAGCCGTCTGCTGGCCATCGTGGCAGACCTCTACGAGCAGGAGCAGTACAGCGATCTGAAGATAAAG
GTTGGGGACAGGCACATCAGTGCTCACAAGTTTGTCCTGGCAGCCCGCAGTGACAGCTGGAGTCTGGCTAACTTG
TCTTCCACTAAAGAGTTGGACCTGTCAGATGCTAATCCTGAGGTGACGGTGACAATGCTTCGCTGGATCTATACA
GATGAGCTGGAGTTCAGAGAGGATGATGTGTTCCTGACTGAACTGATGAAACTAGCAAATCGGTTTCAGCTACAG
CTCCTCAGGGAGAGATGTGAGAAGGGTGTTATGTCTCTAGTGAATGTCAGGAACTGTATTCGCTTCTACCAGACG
GCAGAGGAGCTGAATGCCAGCACACTGATGAACTACTGTGCAGAAATTATTGCAAGTCATTGGGACGACCTGAGG
AAGGAGGATTTCAGCAGCATGAGCCCTCAGTTGTTATACAAAATGATCAAATCCAAGACAGAGTACCCGCTACAT
AAAGCCATCAAAGTGGAGAGAGAAGACGTGGTCTCCCTGTATCTGATTGAAATGGATTCCCAGCTCCCTGGGAAG
CTGAATGAAGCGGACCATAACGGGGACCTGGCATTAGACCTAGCCCTCTCACGACGACTGGAGAATATTGCCACC
ACGCTGGTTAGTCACAAAGCTGATGTGGCATGGTGGCCAAGAGTGCTGGAGCTGTTACACAAAGGGATCCAAGAG
GATCTCTTTGCTGCCACTTTCCTCATTAAGAATGGGGCCTTTGTCAACGCTGCTACACTAGGGTGCCAGGAGACA
CCACTGCACCTTGTGGCCTTGTACAGTTCAAGGAACCACTCAGCAGATGTGATGTCTGAGATGGCGCAGATTGCA
GAGGCCCTTCTGCAGGCTGGTGCCAACCCCAACATGCAGGACAGCAAGGGAAGGACCCCTTTACATGTGTCCATC
ATGGCCGGGGATGAATATGTGTTCAGTCACCTGCTGCAGTGCAAACAACTAGATTTAGAACTCAAAGACCACGAG
GGCAGCACGGCTCTGTGGCTGGCAGTGCAGCATATCACAGTGTCTTCTGACCAGTCTGTGAACCCCTTCGAAGAT
GTCCCCGTGGTAAATGGGACTTCATTTGATGAGAACAGCTTTGCAGCCAGACTCATCCAGCGCGGCAGCCACACA
GACGCACCTGACACGGCGACAGGAAACTGTTTACTACAGCGGGCAGCTGGAGCAGGAAACGAGGCAGCAGCTCTT
TTCCTGGCAACCAACGGTGCCCATGTCAACCACAGAAACAAGTGGGGAGAAACCCCGTTGCACACAGCGTGTCGG
CATGGCCTGGCCAACCTCACAGCAGAGCTCCTGCAGCAAGGCGCCAACCCAAACCTGCAGACGGAGGAAGCTCTG
CCTCTGCCAAAGGAGGCCGCATCCCTGACCAGCTTGGCGGACAGCGTCCATCTGCAGACGCCACTGCACATGGCG
ATCGCCTATAACCATCCGGATGTGGTGTCTGTCATCCTGGAGCAGAAAGCCAATGCTCTTCATGCCACCAACAAC
TTGCAGATCATTCCGGACTTCAGCCTCAAAGATTCCCGAGACCAGACTGTGCTGGGCCTGGCATTATGGACTGGC
ATGCACACGATCGCAGCCCAGCTGCTGGGCTCTGGAGCCGCCATCAATGACACCATGTCGGATGGGCAGACGCTA
CTACACATGGCCATACAGCGGCAGGACAGCAAGAGCGCACTCTTCCTGCTGGAGCACCGGGCAGATATAAATGTC
AGGCCTCAGGCCGGGGAGACAGCCCTCCAGCTGGCCATCAGAAACCAGCTTCCACTCGTAGTTGATGCAATATGC
ACCCGAGGGGCTGACATGTCTGTGCCAGATGAGGAGGGGAACCCCCCGCTGTGGCTTGCATTGGCAAACAATCTG
GAGGACATCGCATCCACTCTGGTCAGACATGGCTGTGGTGCCACATGCTGGGGTCCGGGACCTGGTGGGTGCCTT
CAGACGCTCCTGCACAGAGCCATTGATGAGAACAACGAGCCCACCGCCTGCTTTCTTATTCGCAGTGGCTGTGAC
GTGAACAGTCCCAGACAACCAGGCGCCAATGGAGAAGGAGAGGAAGAGGCTAGAGATGGGCAGACCCCTTTGCAT
TTGGCAGCCTCTTGGGGGCTGGAGACAGTACAGTGTCTTCTGGAGTTTGGTGCCGACGTGAACCCACAGGATGCA
GAAGGAAGAACCCCATGCCACGTGGCCATCAGCAGCCAACACGGTGTCATCATTCAGCTGTTGGTTTCTCACCCG
ATATCCAGTTTGAATGTACGGGACAAACAAGGGCTGACCCCGTTTGCCTGTGCCATGACTTTCAAGGACAACAAG
TCAGCCGAGGCCATTCTCAAACGGGGGTCCGGGGCTGCTGAGCAGGTGGATAACAAGGGCCGGAATTCCCTTCAT
GTGGCAGTTCAGAACTCTGATATTGAAAGTGTGCTGTCCCTGATCAGTGTCCACGCTAATGTGAATTCAAGAGCC
CAGGATGCCCCCAAGTTGACCCCCCTGCACCTGGTTGTCCAAGAAGGCTCAGAAATTATTGTCCGCAATTTGCTT
CTTGCGGGAGCCAAAGTGACCGAATTAACCAAGCATCGCAAGACTGCCCTCCATCTTGCTGCCCAGGAGGACCTG
CCCACCATCTGCTCAGTCCTCCTAGAGAATGCCGTGGACTTTGCTGCCGTGGATGAGAATGGAAACAATGCTCTT
CATCTTGCTGTAATGCACGGCCGGCTCAACAACATCCGGGTTCTCCTGACAGAGTGCACAGTGGACGCCGAAGCC
TTTAATCTCAGAGGCCAGTCACCACTGCACATTTTGGGACAATATGGCAAGGAGAATGCAGCGGCCATCTTTGAT
CTCTTCCTAGAATGCATGCCGGGGTATCCTCTGGACAAGCCGGATGCAGACGGCAGCACGGTGCTGCTCCTGGCA
TACATGAAAGGGAACGCCAACTTGTGCCGCGCCATCGTCCGGTCGGGGGCTCGCCTCGGGGTGAATAACAACCAG
GGAGTCAACATCTTCAACTACCAGGTCGCCACCAAGCAGCTCCTGTTCCGACTGCTGGATATGCTGTCCAAGGAG
CCCCCGTGGTGTGACGGCTCCTACTGCTATGAGTGCACTGCCAGGTTCGGAGTCGCCACTCGCAAACACCACTGT
CGTCACTGCGGACGTCTTCTTTGCCATAAATGCTCGACCAAGGAGATTCCTATTATAAAGTTTGATCTGAACAAG
CCTGTGCGGGTTTGCACAATTTGTTTTGATGTACTGACTCTGGGTGGGGTTTCT**TAG**TGAGCCCCCGGAGGTCCA
GGCACGTCCTTGGTCACCTCCCAGCAGCTTCTCTCTCACCAGCCTGACCCACCCAGAGCAGGAGCTGGCGGGTGT

FIGURE 561B

CTTCCTGCGGCAATAGACTTGGACGATTAAGGACCATGGTGTGATAGATCCATGTCAAATGATCCCATATGATTG
TCAGTGTGTGTGTCAGACTGTGATCGATTTCACTAGATGTCTAACTCATCAGCCCAGCCATTGGCCTAAGTGGTA
AATGTGATTAGGAATTAGACCTCTCCCCATTCTGCTAGCAACATACAGGACACTTGGAAAACCATTTCCCCTTCC
AGTAGCTTGGTGTCCATCCCAGAGCATTCATGAAGTCTTCCCGCCTGGCTGACTGATGAGCAGAGCCTCTCAGCG
TAGGAAGCTGGCTGCTTAATGAGCTGGCTTTACTCTAGGGTAAGTGGCTGTGGACTTTTCTGCACAGTGTTTTCA
TAAAGATAATAGGATCCTCTTGCCCTGAAGTCTTTTTTCTTTTTACGCTAAGCTGTATTTTTAGTGAGCTACCCC
TTTTAAAAAGGTGAAATCTTTCTTAACAGGGTTCAAAGATGAGAGCTGAAAAATCGTGGCCTTAACAACTGAAAG
CTTTACAGTGTTCATGCTACTGAGGTGTCAGGAGTGCAGCTGGGCCGCTTGACACCTCGTAGCAGCCGTCTCATT
CTCTCGTCTTGCTGCGTCCTGTCTGTGGAGTCCTCAGTCACTCTGCTGTTGGAGAGTGCTGGAGGAAATGCACTT
TTACTGTGCTGCACTTTTTATAGAGCTGCATTGTCGGTGATTCCAGTTTAAAATCCATATTCAAAATACCTAACA
CATCCCTGCATCAGTGATTCTAATGATCAGCTTTGACTGGACCTCAGCTCACACGATCTCCAAGGAAAACTCTAC
AGGGCATCTTTTAGAGCAGAGATCATACAGGCCAGTGATGAGAGGGGAGTCACCAAGGCTTCAGCCCAAGGGCAT
CTCCAGCCTCAGGCCGGCAGGTCCTATGTCCTTGACACAAACGTTCTTGCTGAAATCCTCCCTAGTGATGCTGCG
AGTGCTGTTGGTCCCAGTTCTGTGTAGCTTGCCCTGCCCCATGAAGGGCCACCAGCCAAGGGCCCTGGCCACGTG
TGCGCCACCTTACTTTGGGAAGTCTCTGGCTTGTGTGCTGGATGAGGCTGCCAGAACTTGTTGGGCGTTCATCGC
TGTTAGTACATATATTAACCGTGAGTGTTAAACTTTTCTTTTGAAGGTTTGGCAGTTTCTAAAAAATGCACATTT
AAAGAGAAGCATCTACCACGGCTTTAAAACAAAACAACTCTGAGATGAACAATATGTGTTATACTCAGAGATTAA
CAATCTCAATCATACATACTGATTCTTTCAGACATTTAATAACCACTACATTTTTTTGCATTAATGAAGTTTGAC
TATATGTGTAAAGGGCCTAAATATTTTCGCACAGCCTGTTCTTTGTTCATTCTTTCTGGATAGTGTGTCCTCTGT
ATTGCGGTAGATTATACATCTGTTGCCTAAATATGTGTGTAATGAGCTGATAAACTGGAGTACTACTTAAAAAAA
GTCTGTGATTTATAAGATGTATATGCTTCTATGTGATATAAGCTTGTCACAATGTTTAAAGGAAACAATGAATTA
GAAGGGATCCCCCGTCCCAGTCTGACATATTCATACAGATGTTTAAAGAAAACTCTGCTAGTCTTGCAAACATTG
GCCATGTGAGCATGTGGCAGTTCCATTTCTATTACCTGGAAAGGCCATAAGGAAGCAGGCAGGGCTTAGGTAGCT
TGGTTACCTAAGTTAGAAAGTAAGAGAATCATGGTTCGGATATGAATTGAAGTGGGTGGTACATGGATACCTGTT
CTTTAAAAGGAATGTGGAGATGAGTCAAGGGTGAGGCCGATTGTTCTGCCCATGCCCTACCATACCAATTTCAAT
AACAATCTTGCCTGTCATTGCACTCAGAATCTTAAGATCATGTTTCAAATATGTTGATTCAAACTTGCTTCTAAG
CCTGAGTCCAGGGATAGCAATGGTACTGACCAGCTATGGACTGGAGAACATTGAGTCCTGTTTTCCATTGGCTTC
AGGGCGCATCCATGTGGATATAGGAAAAGCCTCTTTCCACAGACTTAGGAAGCCCCCCGACCCACGCGGACGCTC
GCTGGGCTGCACTCAGCAGGCTGCTTGAGTGGGAGCTGACTCCAACATGCCCTGCCCTGGCTGGGACTAGGCATG
CTTCCAGCCCTTCCCGTGCTCTCCCTGCTGTCAACACTTGCGTACAAACCTGCCTAGCTGTTGTAAGTTTTCATC
AGTAGCTTAAGTACTAGTAGCAAAAACTTAAATTCATTCAGAAAGTTGCCACTTCTGAATGAGTAGAGCAG

FIGURE 562

MAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQANKESSSKSFISRLLAIVADLYEQEQYSDLKIKVG
DRHISAHKFVLAARSDSWSLANLSSTKELDLSDANPEVTVTMLRWIYTDELEFREDDVFLTELMKLANRFQLQLL
RERCEKGVMSLVNVRNCIRFYQTAEELNASTLMNYCAEIIASHWDDLRKEDFSSMSPQLLYKMIKSKTEYPLHKA
IKVEREDVVSLYLIEMDSQLPGKLNEADHNGDLALDLALSRRLENIATTLVSHKADVAWWPRVLELLHKGIQEDL
FAATFLIKNGAFVNAATLGCQETPLHLVALYSSRNHSADVMSEMAQIAEALLQAGANPNMQDSKGRTPLHVSIMA
GDEYVFSHLLQCKQLDLELKDHEGSTALWLAVQHITVSSDQSVNPFEDVPVVNGTSFDENSFAARLIQRGSHTDA
PDTATGNCLLQRAAGAGNEAAALFLATNGAHVNHRNKWGETPLHTACRHGLANLTAELLQQGANPNLQTEEALPL
PKEAASLTSLADSVHLQTPLHMAIAYNHPDVVSVILEQKANALHATNNLQIIPDFSLKDSRDQTVLGLALWTGMH
TIAAQLLGSGAAINDTMSDGQTLLHMAIQRQDSKSALFLLEHRADINVRPQAGETALQLAIRNQLPLVVDAICTR
GADMSVPDEEGNPPLWLALANNLEDIASTLVRHGCGATCWGPGPGGCLQTLLHRAIDENNEPTACFLIRSGCDVN
SPRQPGANGEGEEEARDGQTPLHLAASWGLETVQCLLEFGADVNPQDAEGRTPCHVAISSQHGVIIQLLVSHPIS
SLNVRDKQGLTPFACAMTFKDNKSAEAILKRGSGAAEQVDNKGRNSLHVAVQNSDIESVLSLISVHANVNSRAQD
APKLTPLHLVVQEGSEIIVRNLLLAGAKVTELTKHRKTALHLAAQEDLPTICSVLLENAVDFAAVDENGNNALHL
AVMHGRLNNIRVLLTECTVDAEAFNLRGQSPLHILGQYGKENAAAIFDLFLECMPGYPLDKPDADGSTVLLLAYM
KGNANLCRAIVRSGARLGVNNNQGVNIFNYQVATKQLLFRLLDMLSKEPPWCDGSYCYECTARFGVATRKHHCRH
CGRLLCHKCSTKEIPIIKFDLNKPVRVCTICFDVLTLGGVS

FIGURE 563

TTCCGGCCTTGTAATCGCCGAGGGCACGTGCATGCCCCCTGGTTAAGAGTTGCAGGTAGCGGTAGCGATGGACAC
TCTGGATCGAGTAGTAAAGCCCAAAACGAAAAGAGCCAAGAGATTCCTTGAGAAGAGAGAACCGAAACTCAATGA
AAATATTAAAAATGCCATGCTGATTAAAGGGGGAAATGCAAATGCAACAGTGACAAAAGTACTTAAAGATGTGTA
TGCACTGAAAAAACCATACGGTGTACTATATAAAAAGAAAAATATTACAAGACCTTTTGAGGATCAGACATCACT
GGAATTCTTTTCAAAGAAGTCAGATTGTTCTTTATTCATGTTTGGCTCCCATAATAAGAAGCGGCCAAATAATCT
AGTAATAGGTCGTATGTATGACTACCATGTGCTGGATATGATTGAATTAGGTATTGAGAATTTTGTCTCTCTAAA
AGACATTAAGAACAGTAAATGTCCTGAGGGAACAAAACCCATGCTGATATTTGCTGGCGATGATTTCGATGTAAC
AGAAGATTATAGAAGACTAAAAAGTCTTCTTATTGATTTCTTCAGAGGCCCCACAGTATCAAATATCCGCCTGGC
TGGATTAGAGTATGTTCTGCACTTCACTGCACTGAATGGGAAGATTTACTTTCGAAGCTATAAGTTGCTGTTGAA
GAAATCTGGTTGCAGAACACCACGGATTGAATTGGAAGAGATGGGACCCTCATTGGATCTGGTTCTGAGGAGGAC
ACACCTGGCATCGGATGACCTTTATAAATTATCTATGAAAATGCCAAAAGCTCTCAAGCCAAAAAAAAAAAAAAA
A

FIGURE 564

MDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIKGGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQ
TSLEFFSKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFVSLKDIKNSKCPEGTKPMLIFAGDDF
DVTEDYRRLKSLLIDFFRGPTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIELEEMGPSLDLVL
RRTHLASDDLYKLSMKMPKALKPKKKK

FIGURE 565

GATACCATACCTGAACACCTGAACATTCTTCACAAGGTAGTAAATGCACTGCTTTATTCTGGTCTCAGTATTGTG
TGCTTAATAAGGAAATGAGAAAGGGTGGATCAGGGCATAGGATGAACAAGTTACTGCTAGACCTCTCACAATGCC
ACTAATGGATAAGATTGTATTTTCATCATTCTTGTCTCTTCGGAAGCTAACACCATGCTATAATAGGCACTAAAT
AGATGTCTAAAAACACCTTAAGTATTTGTCTAGAAATCTGGTGCATTGTTCAGAAAGAACCAAAATTCAAAATAA
TTTCAAAGGGCCTAAAGCACTAGTTAATCAAAATTCATTAGTTTTTAATGGTACTACCACTCTCAAATTTAAAAT
GTCATCTTACGTTCCTCTTCCTCGCATTGGATTTATTGCTAAAACCTGGTAAACACTTTTAATCCTTTTCAATTC
CATTACCACTGCTCTTGTCCAGAATTACTTCGCAGACTAATAGTCACCTGACTTCTCCCCTGCATCCGATTTGCT
GTCTAATTCTGGTTACAAATAAGTAACTGCCAAACTAATCTTTCTAAAAAGCAAGACTGATCTCGTCACTCCTTT
GCTCAACAATGTAAAAGCTCCCATTGTCTCCCAAATAAAACCAGCTTTCCACTGTGTATACAATACATCC**ATG**AT
CTGTATCCAGCATCATTTTGTATTAGCTCACTTTATACACCACCCCCCATGCCACATCAAATTAAATTATCCTGA
TAAATGCAACTGCATTTACCCTTTCCCTTATTTTGTTCTTTATGTTGTAGGCCTCCTTTGTGCCCATTTCTTCAG
AAGACATCCCCTACAGCCATGGTTCTCATCCAGAGGGTCTTTTGCCCCCGCAGGAGACATC**TGA**CAACGTTTAGA
GACAGTTACCACAACTGGAAGATGGAATAAAAAGATGCTGCTAAACATCCTACAACAATTATCTGGCCAAAAATG
TGCTGAGGTTAAGAAACCCTGTCCTACAGATTATTTCCCTTATTCTGGGTACATAGAAGTAACTCCTTTTTTTCT
ATGAAAATTTCCACAATTTTTTTTTTT

FIGURE 566

MICIQHHFVLAHFIHHPPCHIKLNYPDKCNCIYPFPYFVLYVVGLLCAHFFRRHPLQPWFSSRGSFAPAGDI

FIGURE 567

CCCGGACGTGCGGCTCCCCTCGGCCTCCTCGCC**ATG**GACGCGGACGACTCCCGGGCCCCCAAGGGCTCCTTGCGG
AAGTTCCTGGAGCACCTCTCCGGGGCCGGCAAGGCCATCGGCGTGCTGACCAGCGGCGGGGATGCTCAAGGTATG
AACGCTGCCGTCCGTGCCGTGGTGCGCATGGGTATCTACGTGGGGGCCAAGGTGTACTTCATCTACGAGGGCTAC
CAGGGCATGGTGGACGGAGGCTCAAACATCGCAGAGGCCGACTGGGAGAGTGTCTCCAGCATCCTGCAAGTGGGC
GGGACGATCATTGGCAGTGCGCGGTGCCAGGCCTTCCGCACGCGGGAAGGCCGCCTGAAGGCTGCTTGCAACCTG
CTGCAGCGCGGCATCACCAACCTGTGTGTGATCGGCGGGGACGGGAGCCTCACCGGGGCCAACCTCTTCCGGAAG
GAGTGGAGTGGGCTGCTGGAGGAGCTGGCCAGGAACGGCCAGATCGATAAGGAGGCCGTGCAGAAGTACGCCTAC
CTCAACGTGGTGGGCATGGTGGGCTCCATCGACAATGATTTCTGCGGCACCGACATGACCATCGGCACGGACTCC
GCCCTGCACAGGATCATCGAGGTCGTCGACGCCATCATGACCACGGCCCAGAGCCACCAGAGGACCTTCGTTCTG
GAGGTGATGGGACGACACTGTGGGTACCTGGCCCTGGTGAGTGCCTTGGCCTGCGGTGCGGACTGGGTGTTCCTT
CCAGAATCTCCACCAGAGGAAGGCTGGGAGGAGCAGATGTGTGTCAAACTCTCGGAGAACCGTGCCCGGAAAAAA
AGGCTGAATATTATTATTGTGGCTGAAGGAGCAATTGATACCCAAAATAAACCCATCACCTCTGAGAAAATCAAA
GAGCTTGTCGTCACGCAGCTGGGCTATGACACACGTGTGACCATCCTCGGGCACGTGCAGAGAGGAGGGACCCCT
TCGGCATTCGACAGGATCTTGGCCAGCCGCATGGGAGTGGAGGCAGTCATCGCCTTGCTAGAGGCCACCCCGGAC
ACCCCAGCTTGCGTCGTGTCACTGAACGGGAACCACGCCGTGCGCCTGCCGCTGATGGAGTGCGTGCAGATGACT
CAGGATGTGCAGAAGGCGATGGACGAGAGGAGATTTCAAGATGCGGTTCGACTCCGAGGGAGGAGCTTTGCGGGC
AACCTGAACACCTACAAGCGACTTGCCATCAAGCTGCCGGATGATCAGATCCCAAAGACCAATTGCAACGTAGCT
GTCATCAACGTGGGGGCACCCGCGGCTGGGATGAACGCGGCCGTACGCTCAGCTGTGCGCGTGGGCATTGCCGAC
GGCCACAGGATGCTCGCCATCTATGATGGCTTTGACGGCTTCGCCAAGGGCCAGATCAAAGAAATCGGCTGGACA
GATGTCGGGGGCTGGACCGGCCAAGGAGGCTCCATTCTTGGGACAAAACGCGTTCTCCCGGGGAAGTACTTGGAA
GAGATCGCCACACAGATGCGCACGCACAGCATCAACGCGCTGCTGATCATCGGTGGATTCGAGGCCTACCTGGGA
CTCCTGGAGCTGTCAGCCGCCCGGGAGAAGCACGAGGAGTTCTGTGTCCCCATGGTCATGGTTCCCGCTACTGTG
TCCAACAATGTGCCGGGTTCCGATTTCAGCATCGGGGCAGACACCGCCCTGAACACTATCACCGACACCTGCGAC
CGCATCAAGCAGTCCGCCAGCGGAACCAAGCGGCGCGTGTTCATCATCGAGACCATGGGCGGCTACTGTGGCTAC
CTGGCCAACATGGGGGGGCTCGCGGCCGGAGCTGATGCCGCATACATTTTCGAAGAGCCCTTCGACATCAGGGAT
CTGCAGTCCAACGTGGAGCACCTGACGGAGAAAATGAAGACCACCATCCAGAGAGGCCTTGTGCTCAGAAATGAG
AGCTGCAGTGAAAACTACACCACCGACTTCATTTACCAGCTGTATTCAGAAGAGGGCAAAGGCGTGTTTGACTGC
AGGAAGAACGTGCTGGGTCACATGCAGCAGGGTGGGGCACCCCTCTCCATTTGATAGAAACTTTGGAACCAAAATC
TCTGCCAGAGCTATGGAGTGGATCACTGCAAAACTCAAGGAGGCCCGGGGCAGAGGAAAAAAATTTACCACCGAT
GATTCCATTTGTGTGCTGGGAATAAGCAAAAGAAACGTTATTTTTCAACCTGTGGCAGAGCTGAAGAAGCAAACG
GATTTTGAGCACAGGATTCCCAAAGAACAGTGGTGGCTCAAGCTACGGCCCCTCATGAAAATCCTGGCCAAGTAC
AAGGCCAGCTATGACGTGTCGGACTCAGGCCAGCTGGAACATGTGCAGCCCTGGAGTGTC**TGA**CCCAGTCCCGCC
TGCATGTGCCTGCAGCCACCGTGGACTGTCTGTTTTTGTAACACTTAAGTTATTTTATCAGCACTTTATGCACGT
ATTATTGACATTAATACCTAATCGGCGAGTGCCCATCTGCCCCACCAGCTCCAGTGCGTGCTGTCTGTGGAGTGT
GTCTCATGCTTTCAGATGTGCATATGAGCAGAATTAATTAA

FIGURE 568

MDADDSRAPKGSLRKFLEHLSGAGKAIGVLTSGGDAQGMNAAVRAVVRMGIYVGAKVYFIYEGYQGMVDGGSNIA
EADWESVSSILQVGGTIIGSARCQAFRTREGRLKAACNLLQRGITNLCVIGGDGSLTGANLFRKEWSGLLEELAR
NGQIDKEAVQKYAYLNVVGMVGSIDNDFCGTDMTIGTDSALHRIIEVVDAIMTTAQSHQRTFVLEVMGRHCGYLA
LVSALACGADWVFLPESPPEEGWEEQMCVKLSENRARKKRLNIIIVAEGAIDTQNKPITSEKIKELVVTQLGYDT
RVTILGHVQRGGTPSAFDRILASRMGVEAVIALLEATPDTPACVVSLNGNHAVRLPLMECVQMTQDVQKAMDERR
FQDAVRLRGRSFAGNLNTYKRLAIKLPDDQIPKTNCNVAVINVGAPAAGMNAAVRSAVRVGIADGHRMLAIYDGF
DGFAKGQIKEIGWTDVGGWTGQGGSILGTKRVLPGKYLEEIATQMRTHSINALLIIGGFEAYLGLLELSAAREKH
EEFCVPMVMVPATVSNNVPGSDFSIGADTALNTITDTCDRIKQSASGTKRRVFIIETMGGYCGYLANMGGLAAGA
DAAYIFEEPFDIRDLQSNVEHLTEKMKTTIQRGLVLRNESCSENYTTDFIYQLYSEEGKGVFDCRKNVLGHMQQG
GAPSPFDRNFGTKISARAMEWITAKLKEARGRGKKFTTDDSICVLGISKRNVIFQPVAELKKQTDFEHRIPKEQW
WLKLRPLMKILAKYKASYDVSDSGQLEHVQPWSV

FIGURE 569

AGCCTTAGCAAGACATTTCTACATTAAAGAGAAGGACTTTAACACAGCTCTGGACTGGGCACNTCAGGCCAAAAT
GAAAGCACCTAAAAATTCCTATATTTCAGATACACTAGGTCAAGTCTACAAAAGTGAAATCAAATGGTGGTTGGA
TGGGAACAAAAACTGTAGGAGCATTACTGTTAATGACCTAACACATCTCCTAGAAGCTGCGGAAAAAGCCTCAAG
AGCTTTCAAAGAATCCCAAAGGCAAACTGATAGTAAAAACTATGAAACCGAGAACTGGTCACCACAGAAGTCCCA
GAGACGATATGACATGTATAACACAGCTTGTTTCTTGGGTGAAATAGAAGTTGGTCTTTACACTATCCAGATTCT
TCAGCTCACTCCCTTTTTCCACAAAGAAAATGAATTAGCCAAA**TAA**CATTCATTTCTGGGATCAGGAGGAATGGT
CCACTTTCCTGATAAAAATTGC

FIGURE 570

ALARHFYIKEKDFNTALDWAXQAKMKAPKNSYISDTLGQVYKSEIKWWLDGNKNCRSITVNDLTHLLEAAEKASR
AFKESQRQTDSKNYETENWSPQKSQRRYDMYNTACFLGEIEVGLYTIQILQLTPFFHKENELAK

FIGURE 571

GGCACGAGGGTCCGCAAGCCCGGCTGAGAGCGCGCC**ATG**GGGCAGGCGGGCTGCAAGGGGCTCTGCCTGTCGCTG
TTCGACTACAAGACCGAGAAGTATGTCATCGCCAAGAACAAGAAGGTGGGCCTGCTGTACCGGCTGCTGCAGGCC
TCCATCCTGGCGTACCTGGTCGTATGGGTGTTCCTGATAAAGAAGGGTTACCAAGACGTCGACACCTCCCTGCAG
AGTGCTGTCATCACCAAAGTCAAGGGCGTGGCCTTCACCAACACCTCGGATCTTGGGCAGCGGATCTGGGATGTC
GCCGACTACGTCATTCCAGCCCAGGGAGAGAACGTCTTTTTTGTGGTCACCAACCTGATTGTGACCCCCAACCAG
CGGCAGAACGTCTGTGCTGAGAATGAAGGCATTCCTGATGGCGCGTGCTCCAAGGACAGCGACTGCCACGCTGGG
GAAGCGGTTACAGCTGGAAACGGAGTGAAGACCGGCCGCTGCCTGCGGAGAGGGAACTTGGCCAGGGGCACCTGT
GAGATCTTTGCCTGGTGCCCGTTGGAGACAAGCTCCAGGCCGGAGGAGCCATTCCTGAAGGAGGCCGAAGACTTC
ACCATTTTCATAAAGAACCACATCCGTTTCCCCAAATTCAACTTCTCCAAAAACAATGTGATGGACGTCAAGGAC
AGATCTTTCCTGAAATCATGCCACTTTGGCCCCAAGAACCACTACTGCCCCATCTTCCGACTGGGCTCCATCGTC
CGCTGGGCCGGGAGCGACTTCCAGGATATAGCCCTGCGAGGTGGCGTGATAGGAATTAATATTGAATGGAACTGT
GATCTTGATAAAGCTGCCTCTGAGTGCCACCCTCACTATTCTTTTAGCCGTCTGGACAATAAACTTTCAAAGTCT
GTCTCCTCCGGGTACAACTTCAGATTTGCCAGATATTACCGAGACGCAGCCGGGGTGGAGTTCCGCACCCTGATG
AAAGCCTACGGGATCCGCTTTGACGTGATGGTGAACGGCAAGGGTGCTTTCTTCTGCGACCTGGTACTCATCTAC
CTCATCAAAAAGAGAGAGTTTTACCGTGACAAGAAGTACGAGGAAGTGAGGGGCCTAGAAGACAGTTCCCAGGAG
GCCGAGGACGAGGCATCGGGGCTGGGGCTATCTGAGCAGCTCACATCTGGGCCAGGGCTGCTGGGGATGCCGGAG
CAGCAGGAGCTGCAGGAGCCACCCGAGGCGAAGCGTGGAAGCAGCAGTCAGAAGGGGAACGGATCTGTGTGCCCA
CAGCTCCTGGAGCCCCACAGGAGCACG**TGA**ATTGCCTCTGCTTACGTTCAGGCCCTGTCCTAAACCCAGCCGTCT
AGCACCCAGTGATCCCATGCCTTTGGGAATCCCAGGATGCTGCCCAACGGGAAATTTGTACATTGGGTGCTATCA
ATGCCACATCACAGGGACCAGCCATCACAGAGCAAAGTGACCTCCACGTCTGATGCTGGGGTCATCAGGACGGAC
CCATCATGGCTGTCTTTTTGCCCCACCCCCTGCCGTCAGTTCTTCCTTTCTCCGTGGCTGGCTTCCCGCACTAGG
GAACGGGTTGTAAATGGGGAACATGACTTCCTTCCGGAGTCCTTGAGCACCTCAGCTAAGGACCGCAGTGCCCTG
TAGAGTTCCTAGATTACCTCACTGGGAATAGCATTGTGCGTGTCCGGAAAAGGGCTCCATTTGGTTCCAGCCCAC
TCCCCTCTGCAAGTGCCACAGCTTCCCTCAGAGCATACTCTCCAGTGGATCCAAGTACTCTCTCTCCTAAAGACA
CCACCTTCCTGCCAGCTGTTTGCCCTTAGGCCAGTACACAGAATTAAAGTGGGGGAGATGGCAGACGCTTTCTGG
GACCTGCCCAAGATATGTATTCTCTGACACTCTTATTTGGTCATAAAACAATAAATGGTGTCAATTTCAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 572

MGQAGCKGLCLSLFDYKTEKYVIAKNKKVGLLYRLLQASILAYLVVWVFLIKKGYQDVDTSLQSAVITKVKGVAF
TNTSDLGQRIWDVADYVIPAQGENVFFVVTNLIVTPNQRQNVCAENEGIPDGACSKDSDCHAGEAVTAGNGVKTG
RCLRRGNLARGTCEIFAWCPLETSSRPEEPFLKEAEDFTIFIKNHIRFPKFNFSKNNVMDVKDRSFLKSCHFGPK
NHYCPIFRLGSIVRWAGSDFQDIALRGGVIGINIEWNCDLDKAASECHPHYSFSRLDNKLSKSVSSGYNFRFARY
YRDAAGVEFRTLMKAYGIRFDVMVNGKGAFFCDLVLIYLIKKREFYRDKKYEEVRGLEDSSQEAEDEASGLGLSE
QLTSGPGLLGMPEQQELQEPPEAKRGSSSQKGNGSVCPQLLEPHRST

FIGURE 573

GTGTGCCTGGTAGATCCCCGGGGCAAGCCCTGTGAGACAGTGTTCCAGAGGCTAAGCTACAATGGCCAGTCCAGT
GTGGTACGGTGCCGGCCACTCACAGGCCGCACACACCAGATTCGAGTCCACCTTCAGTTCTTGGGCCATCCCATT
CTCAACGACCCCATCTACAACTCAGTTGCCTGGGGTCCTTCTCGAGGCCGGGGCGGCTACATTCCCAAGACAAAC
GAGGAGTTGCTACGGGACCTGGTAGCAGAGCACCAGGCCAAACAGAGCCTGGATGTGCTAGATCTCTGTGAGGGT
GACCTGTCCCCAGGACTCACAGACTCTACGGCCCCCTCCTCAGAGTTGGGCAAGGACGACCTGGAAGAGTTGGCT
GCAGCTGCCCAGAAGATGGAGGAAGTAGCTGAGGCAGCCCCTCAGGAGTTGGACACAATAGCCTTGGCATCAGAG
AAGGCAGTTGAAACAGATGTCATGCATCAGAGACAGACCACTCTCTGCAGAGTGCCGGCTGGTGCGACAGGATCC
CTTGCCCCAAGACCTTGTGATGTTCCTACATGCCCTACGCTA**TAA**AGGGCCAGGCTTTGAGTACTTTTCACCAAT
GCCTGCCTGGGCACAGGATGACTGGCAAAAGGACTGAGGGTGTGGCCAATGGAGGGATTGCTTCTTGGGTTGTGA
CAAGGATGGGCTATAGGGCAAGGGCTGACCCCATGGGCTAGTACTTGGGGTTTCTATAGGAATGAGGACGGGCTT
CTAAAGAGACCTGCTCATACTTGCTACCTCCTTCCAGTGGGAATTTGGAGACTTTTTGGTTTGTAAATATATCCC
TTTTTCTAAC

FIGURE 574

VCLVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQFLGHPILNDPIYNSVAWGPSRGRGGYIPKTN
EELLRDLVAEHQAKQSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAAQKMEEVAEAAPQELDTIALASE
KAVETDVMHQRQTTLCRVPAGATGSLAPRPCDVPTCPTL

FIGURE 575

GTCCGGGATTCCCAGCC**ATG**GCAGATTCCTCCGGGCAGCAGGGCAAAGGCCGGCGTGTGCAGCCCCAGTGGTCCC
CTCCTGCTGGGACCCAGCCATGCAGACTCCACCTTTACAACAGCCTCACCAGGAACAAGGAAGTGTTCATACCTC
AAGATGGGAAAAAGGTGACGTGGTATTGCTGTGGGCCAACCGTCTATGACGCATCTCACATGGGGCACGCCAGGT
CCTACATCTCTTTTGATATCTTGAGAAGAGTGTTGAAGGATTACTTCAAATTTGATGTCTTTTATTGCATGAACA
TTACGGATATTGATGACAAGATCATCAAGAGGGCCCGGCAGAACCACCTGTTCGAGCAGTATCGGGAGAAGAGGC
CTGAAGCGGCACAGCTCTTGGAGGATGTTCAGGCCGCCCTGAAGCCATTTTCAGTAAAATTAAATGAGACCACGG
ATCCCGATAAAAAGCAGATGCTCGAACGGATTCAGCACGCAGTGCAGCTTGCCACAGAGCCACTTGAGAAAGCTG
TGCAGTCCAGACTCACGGGAGAGGAAGTCAACAGCTGTGTGGAGGTGTTGCTGGAAGAAGCCAAGGATTTGCTCT
CTGACTGGCTGGATTCTACACTTGGCTGTGATGTCACTGACAATTCCATCTTCTCCAAGCTGCCCAAGTTCTGGG
AGGGGGACTTCCACAGAGACATGGAAGCTCTGAATGTTCTCCCTCCAGATGTCTTAACCCGGGTTAGTGAGTATG
TGCCAGAAATTGTGAACTTTGTCCAGAAGATTGTGGACAACGGTTACGGCTATGTCTCCAATGGGTCTGTCTACT
TTGATACAGCGAAGTTTGCTTCTAGCGAGAAGCACTCCTATGGGAAGCTGGTGCCTGAGGCCGTTGGAGATCAGA
AAGCCCTTCAAGAAGGGGAAGGTGACCTGAGCATCTCTGCAGACCGCCTGAGTGAGAAGCGCTCTCCCAACGACT
TTGCCTTATGGAAGGCCTCTAAGCCCGGAGAACCGTCCTGGCCGTGCCCTTGGGGAAAGGGTCGTCCGGGCTGGC
ATATCGAGTGCTCGGCCATGGCAGGCACCCTCCTAGGGGCTTCGATGGACATTCACGGAGGTGGGTTCGACCTCC
GGTTCCCCCACCATGACAATGAGCTGGCACAGTCGGAGGCCTACTTTGAAAACGACTGCTGGGTCAGGTACTTCC
TGCACACAGGCCACCTGACCATTGCAGGCTGCAAAATGTCAAAGTCACTAAAAAACTTCATCACCATTAAAGATG
CCTTGAAAAAGCACTCAGCACGGCAGTTGCGGCTGGCCTTCCTCATGCACTCGTGGAAGGACACCCTGGACTACT
CCAGCAACACCATGGAGTCAGCGCTTCAATATGAGAAGTTCTTGAATGAGTTTTTCTTAAATGTGAAAGATATCC
TTCGCGCTCCTGTTGACATCACTGGTCAGTTTGAGAAGTGGGGAGAAGAAGAAGCAGAACTGAATAAGAACTTTT
ATGACAAGAAGACAGCAATTCACAAAGCCCTCTGTGACAATGTTGACACCCGCACCGTCATGGAAGAGATGCGGG
CCTTGGTCAGTCAGTGCAACCTCTATATGGCAGCCCGGAAAGCCGTGAGGAAGAGGCCCAACCAGGCTCTGCTGG
AGAACATCGCCCTGTACCTCACCCATATGCTGAAGATCTTTGGGGCCGTAGAAGAGGACAGCTCCCTGGGATTCC
CGGTCGGAGGGCCTGGAACCAGCCTCAGTCTCGAGGCCACAGTCATGCCCTACCTTCAGGTGTTATCAGAATTCC
GAGAAGGAGTGCGGAAGATTGCCCGAGAGCAAAAAGTCCCTGAGATTCTGCAGCTCAGCGATGCCCTGCGGGACA
ACATCCTGCCCGAGCTTGGGGTGCGGTTTGAAGACCACGAAGGACTGCCCACAGTGGTGAAACTGGTAGACAGAA
ACACCTTATTAAAAGAGAGAGAAGAAAAGAGACGGGTTGAAGAGGAGAAGAGGAAGAAGAAAGAGGAGGCGGCCC
GGAGGAAACAGGAACAAGAAGCAGCAAAGCTGGCCAAGATGAAGATTCCCCCCAGTGAGATGTTCTTGTCAGAAA
CCGACAAATACTCCAAGTTTGATGAAAATGGTCTGCCCACACATGACATGGAGGGCAAAGAGCTCAGCAAAGGGC
AAGCCAAGAAGCTGAAGAAGCTCTTCGAGGCTCAGGAGAAGCTCTACAAGGAATATCTGCAGATGGCCCAGAATG
GAAGCTTCCAG**TGA**GGGGGCACAGGACTGACTTTTTAAACCATTGTGGACTAGTGGCTGCTGTCTGCCTCAGTGA
CAATGTC

FIGURE 576

MADSSGQQGKGRRVQPQWSPPAGTQPCRLHLYNSLTRNKEVFIPQDGKKVTWYCCGPTVYDASHMGHARSYISFD
ILRRVLKDYFKFDVFYCMNITDIDDKIIKRARQNHLFEQYREKRPEAAQLLEDVQAALKPFSVKLNETTDPDKKQ
MLERIQHAVQLATEPLEKAVQSRLTGEEVNSCVEVLLEEAKDLLSDWLDSTLGCDVTDNSIFSKLPKFWEGDFHR
DMEALNVLPPDVLTRVSEYVPEIVNFVQKIVDNGYGYVSNGSVYFDTAKFASSEKHSYGKLVPEAVGDQKALQEG
EGDLSISADRLSEKRSPNDFALWKASKPGEPSWPCPWGKGRPGWHIECSAMAGTLLGASMDIHGGGFDLRFPHHD
NELAQSEAYFENDCWVRYFLHTGHLTIAGCKMSKSLKNFITIKDALKKHSARQLRLAFLMHSWKDTLDYSSNTME
SALQYEKFLNEFFLNVKDILRAPVDITGQFEKWGEEEAELNKNFYDKKTAIHKALCDNVDTRTVMEEMRALVSQC
NLYMAARKAVRKRPNQALLENIALYLTHMLKIFGAVEEDSSLGFPVGGPGTSLSLEATVMPYLQVLSEFREGVRK
IAREQKVPEILQLSDALRDNILPELGVRFEDHEGLPTVVKLVDRNTLLKEREEKRRVEEEKRKKKEEAARRKQEQ
EAAKLAKMKIPPSEMFLSETDKYSKFDENGLPTHDMEGKELSKGQAKKLKKLFEAQEKLYKEYLQMAQNGSFQ

FIGURE 577

CAGCGGCGGCCCAGGAGGCAGCCGGTGAGCGCCTGCGAGCAGAGTGGCGGGGGCCGCTGACAGGTCCCGCGCAGC
CCAGCCCAGCCCAGCCACGCGGCTCACAGGTGGGGTCCAAGAGCAGTTTGGAGCAACCCGGCGCTACGGAGAGGG
GTGGACGGCTCTGCACGGGCCTCCTGTCTCCCGCTCGGGCAGAGGGACTCGGGGGACCTCGCTCCTTGGCCGAG
AGAACCTGAACTCGGGCGGAGAGAACGCGCCCAGGCGGGCAAGGGGACCAGAGAAAGCCGGGGCTGGAAGTCACT
GTCGCTCGCCACTGTCTGGAGCGCACGGAGCGCAGAGGCCCGGCAGCCGCGCGTGCCCTCCCGGGGACCGAGCCA
GTGATGCAGGATCGCTGAGCGGAGATCCGCGCCGAGAAGTCTCTCGGGGCCGGGGCTGAGACGCACGCCTTCGAC
ACCGCTGCCAAGACCCCGATTCCGGCGACTCTTGCGGGGAACCGAGGGGCCAAGGCTGCCCCAAGCTCAGGACTT
GGGCGAGTCTAAGACGATGGTTTCTTAAGCACGGACCCGCGTTCCCCTTCCCGCCCCCTCGACTGGAGGCAGGGA
TCCTGCGCGGGGCCCCCGGGATTCCGTTTCCCCGCGGAGCCCCGGCCGCTGCCTCCCGGGACAGTTCGCACGGCC
ACAGGGGCGCACGGCGATGTGGCCTCCGTCCAGCGCGCTGGCCCGCCGGGGGGATGCTCTGGCACCTGTCGGGGT
CCAGGCCTAGCATGGCCGGCGCGTTGCCCGACGTCGCCTCCGGCTAGG**ATG**GCCCCTCCGGGCCCGGCCAGTGCC
CTCTCCACCTCGGCCGAGCCGCTGTCCCGCAGCATCTTCCGGAAGTTCTTGCTGATGCTCTGCTCCCTGCTCACG
TCCCTTTACGTCTTCTACTGCCTGGCCGAGCGCTGCCAGACCCTGTCCGGCCCCGTCGTGGGGCTGTCCGGCGGC
GGCGAGGAGGCGGGGGCCCCTGGTGGCGGCGTCCTGGCCGGAGGCCCGAGGGAGCTGGCGGTGTGGCCGGCGGCG
GCACAGAGAAAGCGCCTCCTGCAACTGCCGCAGTGGCGGAGGCGCCGGCCGCCCGCGCCCCGCGACGACGGCGAG
GAGGCGGCCTGGGAAGAAGAGTCCCCTGGCCTGTCAGGGGGTCCGGGCGGCTCCGGGGCCGGAAGCACCGTGGCC
GAGGCCCCGCCGGGGACCCTGGCGCTGCTCCTGGACGAAGGCAGCAAGCAGCTGCCGCAGGCCATCATCATCGGA
GTGAAGAAGGGCGGCACGCGGGCGCTGCTGGAGTTCCTGCGCGTGCACCCCGACGTGCGCGCCGTGGGCGCCGAG
CCCCACTTCTTCGACCGCAGCTACGACAAGGGCCTCGCCTGGTACCGGGACCTGATGCCCAGAACCCTGGACGGG
CAGATCACCATGGAGAAGACGCCCAGTTACTTCGTCACGCGGGAGGCCCCCGCGCGCATCTCGGCCATGTCCAAG
GACACCAAGCTCATCGTGGTGGTGCGGGACCCGGTGACCAGGGCCATCTCGGACTACACGCAGACGCTGTCCAAG
CGGCCCGACATCCCCACCTTCGAGAGCTTGACGTTCAAAAACAGGACAGCGGGCCTCATCGACACGTCGTGGAGC
GCCATCCAGATCGGCATCTACGCCAAGCACCTGGAGCACTGGCTGCGCCACTTCCCCATCCGCCAGATGCTCTTC
GTGAGCGGCGAGCGGCTCATCAGCGACCCGGCCGGGGAGCTGGGCCGCGTGCAAGACTTCCTGGGCCTCAAGAGG
ATCATCACGGACAAGCACTTCTACTTCAACAAGACCAAGGGCTTCCCCTGCCTGAAGAAGGCGGAGGGCAGCAGC
CGGCCCCATTGCCTGGGCAAGACCAAGGGCAGGACCCATCCTGAGATCGACCGCGAGGTGGTGCGCAGGCTGCGC
GAGTTCTACCGGCCTTTCAACCTCAAGTTCTACCAGATGACCGGGCACGACTTTGGCTGGGATGGA**TAA**CCATAT
AATTTAAAAAGAAAAAAAAAATCAAAATATAATATATTTTTTTACCAATCGGTAGAGAAGAGACAGTTTAATATT
TGTGCTGAAAATATGTTTCAGTATTTTTTTCAATGAATGTTAAGAGATTGTTCTCACTCCCGCCCCATCTTAATG
TATAACCAACACCAAACACGTGGATCAACAGAAAAGGAAAATTTCACTCGTCTAAACACTTTCAATTTTCAGTTT
TTATTTTATGTTCTATATACCCAGTCATAAAGTATAAGCATCAGTTGTCATTAAAAGTTTTCAGAAAATCTTGAG
GTTAAACATCTCTCTCTCTTTTTTTAAAATACAAGGCCCTGATAAAATTGATATCTATCCTTATATTTTTCTCCC
TTTTTCCCGTGCCACTTTTTCTTAAATTATTTCCCAGTTAGTATTATCATATGTTTGTACCCGTCACAGTTTTCA
TAGTGCTTTCAAATACACCTTTTTGATCATTAAAATAAAAAAATAAATCTTGGAAAAAAAAAAAAAAAAA

FIGURE 578

MAPPGPASALSTSAEPLSRSIFRKFLLMLCSLLTSLYVFYCLAERCQTLSGPVVGLSGGGEEAGAPGGGVLAGGP
RELAVWPAAAQRKRLLQLPQWRRRRPPAPRDDGEEAAWEEESPGLSGGPGGSGAGSTVAEAPPGTLALLLDEGSK
QLPQAIIIGVKKGGTRALLEFLRVHPDVRAVGAEPHFFDRSYDKGLAWYRDLMPRTLDGQITMEKTPSYFVTREA
PARISAMSKDTKLIVVVRDPVTRAISDYTQTLSKRPDIPTFESLTFKNRTAGLIDTSWSAIQIGIYAKHLEHWLR
HFPIRQMLFVSGERLISDPAGELGRVQDFLGLKRIITDKHFYFNKTKGFPCLKKAEGSSRPHCLGKTKGRTHPEI
DREVVRRLREFYRPFNLKFYQMTGHDFGWDG

FIGURE 579

GCTGTTGAGAAGCTACCCGCGGGGTTGTAGACCTCGGACCTC**ATG**GCAGAGATAATTCAGGAACGCATAGAAGAT
CGGCTCCCGGAATTGGAACAGCTGGAGCGCATTGGACTGTTCAGTCATGCGGAGATTAAGGCTATCATTAAGAAG
GCTTCCGATCTAGAGTACAAAATCCAGAGAAGAACCCTTTTCAAGGAAGACTTTATCAATTATGTTCAATATGAA
ATTAATCTTTTGGAGCTGATCCGGAGAAGAAGAACACGCATTGGATATTCATTTAAGAAGGATGAGATTGAGAAT
TCTATTGTACACCGGGTACAAGGTGTTTTCCAGCGTGCCTCAGCAAAATGGAAAGACGATGTTCAACTTTGGCTC
TCCTATGTGGCTTTTTGTAAGAAGTGGGCTACTAAAACTCGACTTAGCAAGGTATTCTCTGCCATGTTGGCGATT
CATTCCAACAAACCAGCTTTGTGGATTATGGCAGCCAAATGGGAAATGGAAGATCGATTGTCTTCAGAAAGCGCA
AGGCAACTATTTCTTCGCGCACTGCGCTTTCATCCAGAGTGCCCAAAACTTTATAAAGAATACTTTAGGATGGAG
CTGATGCATGCTGAAAAACTGAGGAAGGAGAAGGAAGAATTTGAAAAAGCCAGTATGGATGTGGAGAATCCTGAT
TATTCTGAAGAAATCCTTAAGGGCGAGTTGGCATGGATCATCTACAAAAATTCTGTAAGCATAATTAAAGGTGCA
GAATTTCACGTGTCACTGCTTTCGATTGCACAGCTATTTGACTTTGCCAAAGATCTACAAAAAGAGATTTATGAT
GACCTTCAGGCTCTACACACAGATGATCCTCTCACTTGGGATTATGTGGCAAGGCGAGAATTAGAGATTGAGTCA
CAGACAGAAGAGCAGCCTACAACGAAACAAGCCAAAGCAGTGGAGGTCGGCCGGAAGGAGGAGAGGTGCTGTGCT
GTGTATGAAGAGGCAGTGAAGACTCTGCCAACAGAGGCCATGTGGAAGTGTTACATCACCTTTTGCTTGGAAAGA
TTTACTAAGAAGTCAAATAGTGGGTTCCTTAGAGGGAAGAGGTTGGAAAGAACCATGACTGTATTCAGGAAGGCA
CATGAACTGAAGCTTCTGTCAGAATGCCAATACAAGCAGTTGAGTGTTTCGTTGCTGTGTTATAACTTCCTGAGG
GAAGCTCTGGAAGTGGCAGTAGCTGGAACTGAATTGTTTAGAGACTCTGGGACAATGTGGCAGCTGAAGCTGCAG
GTGCTGATCGAGTCAAAGAGCCCTGACATAGCCATGCTTTTTGAAGAAGCCTTTGTGCACCTGAAACCCCAGGTT
TGTCTGCCATTGTGGATTTCCTGGGCAGAGTGGAGTGAAGGTGCCAAAAGCCAAGAAGACACTGAGGCAGTCTTT
AAGAAAGCTCTCTTAGCTGTCATAGGTGCCGACTCAGTAACCCTGAAGAATAAGTACCTGGATTGGGCTTATCGA
AGTGGTGGCTACAAAAAGGCCAGAGCTGTGTTTAAAAGTTTACAGGAGAGCCGACCATTTTCAGTTGACTTTTTC
AGGAAAATGATTCAGTTTGAAAAGGAGCAAGAATCCTGCAATATGGCGAACATAAGAGAATATTATGAGAGAGCT
TTGAGAGAGTTTGGATCCGCAGATTCTGATCTTTGGATGGATTATATGAAAGAAGAATTGAACCACCCCCTTGGT
AGACCTGAGAACTGTGGACAGATCTACTGGCGAGCGATGAAAATGTTGCAGGGAGAGTCAGCAGAGGCATTTGTA
GCTAAACATGCTATGCATCAGACTGGCCATTTA**TGA**AGATGAAGAATACCGTCCGCTTTGTGAAATAGTATTGCA
AGCCAGCCCCGTGGGCAAATTTGTATTGAGTCCATCTGTAATTTGCTCAGTGATGGCAGACAAGATGGCTGTCTG
GTTTTGAGACACACACTTTAATTTTATGTTAACTTGTTAAATCTTTTTAAAAATTAAAAAATTTTTATGATTGAA
AAAAAAA

FIGURE 580

MAEIIQERIEDRLPELEQLERIGLFSHAEIKAIIKKASDLEYKIQRRTLFKEDFINYVQYEINLLELIRRRRTRI
GYSFKKDEIENSIVHRVQGVFQRASAKWKDDVQLWLSYVAFCKKWATKTRLSKVFSAMLAIHSNKPALWIMAAKW
EMEDRLSSESARQLFLRALRFHPECPKLYKEYFRMELMHAEKLRKEKEEFEKASMDVENPDYSEEILKGELAWII
YKNSVSIIKGAEFHVSLLSIAQLFDFAKDLQKEIYDDLQALHTDDPLTWDYVARRELEIESQTEEQPTTKQAKAV
EVGRKEERCCAVYEEAVKTLPTEAMWKCYITFCLERFTKKSNSGFLRGKRLERTMTVFRKAHELKLLSECQYKQL
SVSLLCYNFLREALEVAVAGTELFRDSGTMWQLKLQVLIESKSPDIAMLFEEAFVHLKPQVCLPLWISWAEWSEG
AKSQEDTEAVFKKALLAVIGADSVTLKNKYLDWAYRSGGYKKARAVFKSLQESRPFSVDFFRKMIQFEKEQESCN
MANIREYYERALREFGSADSDLWMDYMKEELNHPLGRPENCGQIYWRAMKMLQGESAEAFVAKHAMHQTGHL

FIGURE 581

GGGAGTGGCGTGGCGCAGGG**ATG**GCACAAAAGAAATATCTTCAAGCAAAATTGACCCAGTTTTTAAGGGAAGACA
GGATTCAACTTTGGAAACCTCCATATACAGATGAAAATAAAAAAGTTGGTTTGGCATTAAAGGACCTTGCTAAGC
AGTACTCTGACAGACTAGAATGCTGTGAAAATGAAGTAGAAAAGGTAATAGAAGAAATACGTTGCAAGGCAATTG
AGCGTGGAACAGGAAATGACAATTATAGAACAACGGGAATTGCTACAATCGAGGTGTTTTTACCACCAAGACTAA
AAAAAGATAGGAAAAACTTGTTGGAGACCCGATTGCACATCACTGGCAGAGAACTGAGGTCCAAAATAGCTGAAA
CCTTTGGACTTCAAGAAAATTATATCAAAATTGTCATAAATAAGAAGCAACTACAACTAGGGAAAACCCTTGAAG
AACAAGGCGTGGCTCACAATGTGAAAGCGATGGTGCTTGAACTAAAACAATCTGAAGAGGACGCGAGGAAAAACT
TCCAGTTAGAGGAAGAGGAGCAAAATGAGGCCAAACTCAAAGAAAAACAAATTCAGAGGACCAAGAGAGGACTAG
AAATACTGGCAAAGAGAGCAGCAGAGACAGTGGTGGATCCAGAAATGACACCGTACTTAGACATAGCTAACCAGA
CAGGCAGATCAATCAGAATTCCCCCATCAGAAAGAAAAGCCCTTATGTTAGCTATGGGATATCATGAGAAGGGCA
GAGCTTTCCTGAAAAGAAAAGAATATGGAATAGCCTTGCCATGTCTGTTGGACGCTGACAAATATTTCTGTGAGT
GTTGCAGAGAGCTGCTGGACACAGTGGATAACTATGCCGTCCTCCAGCTGGATATAGTGTGGTGTTACTTCCGCC
TGGAACAGCTGGAATGCCTTGATGATGCAGAAAAAAAATTAAACTTGGCCCAGAAATGCTTTAAAAATTGTTACG
GAGAAAATCATCAGAGACTGGTCCACATAAAAGGAAATTGTGGGAAAGAGAAGGTACTGTTTCTAAGACTCTACT
TACTTCAAGGGATCCGAAACTATCACAGTGGAAATGATGTAGAGGCTTATGAGTATCTTAACAGGCACGTCAGCT
CTTTAAAGAGCTATATATTGATCCATCAAAAGTGGACAATTTGTTGCAGTTGGGGTTTACTGCCCAGGAAGCACC
GGCTTGGCCTGAGGGCGTGTGATGGGAACGTGGATCATGCGGCCACTCATATTACCAACCGCAGAGAGGAACTGG
CCCAAATAAGGAAGGAGGAAAAAGAGAAGAAAAGACGCCGCCTCGAGAACATCAGGTTTCTGAAAGGGATGGGCT
ACTCCACGCACGCGGCCCAGCAGATTCTGCTCAGCAATCCTCAGATGTGGTGGTTAAATGATTCCAATCCTGAAA
CCGACAACCGTCAAGAAAGTCCTTCCCAGGAAAACATTGACCGATTGGTGTACATGGGTTTTGATGCACTCGTGG
CCGAAGCTGCGCTGAGAGTGTTCAGAGGCAACGTCCAGCTGGCCGCCCAGACCCTTGCTCACAACGGAGGAAGCC
TGCCTCCCGAGCTGCCGCTGTCGCCAGAAGACTCTTTGTCCCCGCCAGCCACGTCCCCTTCTGACTCCGCAGGAA
CCTCTAGTGCCTCAACAGACGAAGACATGGAGACAGAGGCCGTCAATGAGATACTGGAAGACATTCCAGAGCATG
AGGAAGACTATCTTGACTCAACTCTGGAAGATGAAGAAATTATTATTGCAGAGTACCTATCCTATGTAGAAAATA
GGAAGTCAGCAACAAAGAAAAAC**TAA**ATAATGAACAGAAATAGCGCTAATTTTCTGCTTATAAATGCTATCATTA
TGAAAAGGCTAATGCAGCTCTTTCTGTTCTTACTTTTTATCTGAATTACAAGTCCTCTTTGGGTGTAGGAGGGGG
TGGGCAGGGGACAAGTCCAGGAGGGGTCCCAGGGCCTTCATGCATGGTCTCGGGGAAGAAGCTTCTTTTGGCCTG
GCGCAAGCCGTTCCATCTGGCTCCCAAGTCTGCGTCCCTAACCCCCTTCCCCAACTTTGGGGGTTTTACCCCCGA
AACAAGGAAA

FIGURE 582

MAQKKYLQAKLTQFLREDRIQLWKPPYTDENKKVGLALKDLAKQYSDRLECCENEVEKVIEEIRCKAIERGTGND
NYRTTGIATIEVFLPPRLKKDRKNLLETRLHITGRELRSKIAETFGLQENYIKIVINKKQLQLGKTLEEQGVAHN
VKAMVLELKQSEEDARKNFQLEEEEQNEAKLKEKQIQRTKRGLEILAKRAAETVVDPEMTPYLDIANQTGRSIRI
PPSERKALMLAMGYHEKGRAFLKRKEYGIALPCLLDADKYFCECCRELLDTVDNYAVLQLDIVWCYFRLEQLECL
DDAEKKLNLAQKCFKNCYGENHQRLVHIKGNCGKEKVLFLRLYLLQGIRNYHSGNDVEAYEYLNRHVSSLKSYIL
IHQKWTICCSWGLLPRKHRLGLRACDGNVDHAATHITNRREELAQIRKEEKEKKRRRLENIRFLKGMGYSTHAAQ
QILLSNPQMWWLNDSNPETDNRQESPSQENIDRLVYMGFDALVAEAALRVFRGNVQLAAQTLAHNGGSLPPELPL
SPEDSLSPPATSPSDSAGTSSASTDEDMETEAVNEILEDIPEHEEDYLDSTLEDEEIIIAEYLSYVENRKSATKK
N

FIGURE 583

GATCAGAGGGCGATCAGCTGGACAGCAACTCAGG**ATG**GCATCAGGCAGGGCACGCTGCACCCGAAAACTCCGGAA
CTGGGTGGTGGAGCAAGTGGAGAGTGGGCAGTTTCCCGGAGTGTGCTGGGATGATACAGCTAAGACCATGTTCCG
GATTCCCTGGAAACATGCAGGCAAGCAGGACTTCCGGGAGGACCAGGATGCTGCCTTCTTCAAGGCCTGGGCAAT
ATTTAAGGGAAAGTATAAGGAGGGGGACACAGGAGGTCCAGCTGTCTGGAAGACTCGCCTGCGCTGTGCACTCAA
CAAGAGTTCTGAATTTAAGGAGGTTCCTGAGAGGGGCCGCATGGATGTTGCTGAGCCCTACAAGGTGTATCAGTT
GCTGCCACCAGGAATCGTCTCTGGCCAGCCAGGGACTCAGAAAGTACCATCAAAGCGACAGCACAGTTCTGTGTC
CTCTGAGAGGAAGGAGGAAGAGGATGCCATGCAGAACTGCACACTCAGTCCCTCTGTGCTCCAGGACTCCCTCAA
TAATGAGGAGGAGGGGGCCAGTGGGGGAGCAGTCCATTCAGACATTGGGAGCAGCAGCAGCAGCAGCAGCCCTGA
GCCACAGGAAGTTACAGACACAACTGAGGCCCCCTTTCAAGGGGATCAGAGGTCCCTGGAGTTTCTGCTTCCTCC
AGAGCCAGACTACTCACTGCTGCTCACCTTCATCTACAACGGGCGCGTGGTGGGCGAGGCCCAGGTGCAAAGCCT
GGATTGCCGCCTTGTGGCTGAGCCCTCAGGCTCTGAGAGCAGCATGGAGCAGGTGCTGTTCCCCAAGCCTGGCCC
ACTGGAGCCCACGCAGCGCCTGCTGAGCCAGCTTGAGAGGGGCATCCTAGTGGCCAGCAACCCCCGAGGCCTCTT
CGTGCAGCGCCTTTGCCCCATCCCCATCTCCTGGAATGCACCCCAGGCTCCACCTGGGCCAGGCCCGCATCTGCT
GCCCAGCAACGAGTGCGTGGAGCTCTTCAGAACCGCCTACTTCTGCAGAGACTTGGTCAGGTACTTTCAGGGCCT
GGGCCCCCCACCGAAGTTCCAGGTAACACTGAATTTCTGGGAAGAGAGCCATGGCTCCAGCCATACTCCACAGAA
TCTTATCACAGTGAAGATGGAGCAGGCCTTTGCCCGATACTTGCTGGAGCAGACTCCAGAGCAGCAGGCAGCCAT
TCTGTCCCTGGTG**TAG**AGCCTGGGGGACCCATCTTCCACCTCACCTCTTTGTTCTTCCTGTCTCCTTTGAAGTAG
ACTCATTCTTCACACGATTGACCTGTCCTCTTTGTGATAATTCTCAGTAGTTGTCCGTGATAATCGTGTCCTGAA
AATCCTCGCACACACTGGCTGGTGGAGAACTCAAGGCTAATTTTTTATCCTTTTTTTTTTTTATTTTTGAGATA
TACGCCCTCTTTCATCTGTAAGGGACTAGGAAATTCCAAATGGTGTGAACCCAGGGGGCCTTTCCCTCTTCCCTG
ACCTCCCAACTCTAAAGCCAAGCACTTTATATTTTTCTCTTAGATATTCACTAAGGACTTAAAATAAAATTTTTT
TGAAAGAGG

FIGURE 584

MASGRARCTRKLRNWVVEQVESGQFPGVCWDDTAKTMFRIPWKHAGKQDFREDQDAAFFKAWAIFKGKYKEGDTG
GPAVWKTRLRCALNKSSEFKEVPERGRMDVAEPYKVYQLLPPGIVSGQPGTQKVPSKRQHSSVSSERKEEEDAMQ
NCTLSPSVLQDSLNNEEEGASGGAVHSDIGSSSSSSSPEPQEVTDTTEAPFQGDQRSLEFLLPPEPDYSLLLTFI
YNGRVVGEAQVQSLDCRLVAEPSGSESSMEQVLFPKPGPLEPTQRLLSQLERGILVASNPRGLFVQRLCPIPISW
NAPQAPPGPGPHLLPSNECVELFRTAYFCRDLVRYFQGLGPPPKFQVTLNFWEESHGSSHTPQNLITVKMEQAFA
RYLLEQTPEQQAAILSLV

FIGURE 585

ATAAAAAATAAAAAAAAGAAAATTAACTTTGGTACCAGGTACAAACCAGTCTGGGAGCAGATCAGCAAAGAAACT
CTTGAAATAAACGGT**<u>TAA</u>**GATAAAAGGAGTAACAAAGGTGTAATACCAACGCATCGGCAGTGGCGCTGACCTTAG
AAGGCTTCCGACAGTCAATCACAATACTTCAGGACCTATCAGAGGTAGGATCTAAGCCTCCCAGAGTCCCCGCAC
GCCCTTGTCAGCTTCCCTGCTCCTCTCCTGATGCTTCCTGGGATCACTTCCGAAATAAATTACTTGCACTT

FIGURE 586

IKNKKKKINFGTRYKPVWEQISKETLEING

FIGURE 587

ATTGAANTTAGGTGACCCNATNGAAGNGCTATNACGTNGCATGCACNGCGTACGTAAGCTCGGAATTCGGCTCGA
GAAAAAAAAAAGTGCCAGCGTA**TGA**GGTAATTAGATTGGTTCTCTCCAGAGGTAACCTGCCAAGAAGAGATGCTA
TAGATGTTACTCCTATACTGTAAAACATTGTGAAATCAGATTACTTTAAAATGATGTATTACAAAGTTATGCAAA
AAAGCAGTTGTGACTATGGAAGCCCAAGGCTTATATCCCAGCTCTGTCTTACACTAAATATGGGTACAGTGTTTC
CACTCTGTCCATAAAATGGGAGCTAATATTCTCCAACCTGTGTGCCTGACATGATGGTTAAAGGGATTAAACAAA
ACAATAGTTTGTAATTTATTCTGTCAGAGCAAACTGCTGGTAAATAAAAGGGACTAAGTTGACGAAAAATAAATT
TTAAAAAACCTAATAAAACAAGTTTGTAATTTATAATTGTATACAAATAAAAGATGTTACAAAAATTGCGCACTT
ATATGTATGTACCATGACATAACTAATTCGTTGAACAAGTTGTGAGACAATCCTTTCTGAGAAAAGGTAGACCTG
TTACATCGTCTGTGGGTTAGGGTCATGTCAGCACGTACCAGGTACATTCTAGCTTTTGTAGAGAAAGTAAAATCT
AGTGTTGAGTATGTAGGCACTGAGCCAGGTGGCCTGCTTAACATAAAAGGACTGATTTCAGGGTGGCTGTGGGAG
CCTTTCTAATGCTCTAATTCTCTAGCCCCTTGCCTGATCCAGCTGATTCCAAGAGCCAAGATTTAGTCTTTCTT
GGTTGGCTTTTTTAAATGCTTTGGGCTTTCCTTTAATGTATCTTCAAAATCATTC

FIGURE 588

LXLGDPXEXLXRXMHXVRKLGIRLEKKKSASV

FIGURE 589

GCGCTGCAGCTCACTTTCTCCCTGTTTGCTGGCCAGCAGGGTTTGTGGCCGCCTCTGCTGTGACGCCACAGCCTG
GTGAGGAGGGGGCTGCAGTTCCTCAGGAAACTGCCAGTGGACAAAGTCATAAACAAGAGTTCCAGTTCCCTGGAA
CCTGAGTCGGGAGGCCTGCAACTCACTTTCTCCCTGTTTGCTGGCCCAGACAGGCCTGTGCTAGAGGGCTGGATA
GTGTGGTAGTGTGGTGGATAGAGTGCTGCCTCTATCCACAACGCAGCCATATGCTGACTGAAGATAACTTTGTGT
CTGGAAGAGCCCTCTGATTTCTTACACTA**ATG**GCCTTACACGAGATGGAGGATTTTACATTTGATGGAACAAAGC
GCTTAAGTGTCAACTACGTGAAGGGAATTCTTCAACCGACAGACACCTGTGACATCTGGGATAAGATCTGGAACT
TCCAAGCCAAGCCTGATGACCTGCTTATTTCTACCTATCCTAAAGCAGGAACAACATGGACTCAGGAGATAGTGG
AATTAATACAAAATGAAGGTGATGTGGAGAAAAGTAAACGGGCACCGACTCATCAACGATTTCCTTTCCTCGAAA
TGAAAATCCCATCCTTAGGATCTGGTTTGGAACAAGCTCATGCAATGCCCTCACCACGGATCCTGAAAACACATC
TTCCCTTTCACTTGCTGCCACCATCCTTGCTAGAGAAAAACTGTAAGATAATCTATGTAGCAAGAAATCCCAAGG
ACAACATGGTGTCCTATTACCATTTCCAAAGAATGAATAAAGCTCTTCCTGCTCCAGGAACATGGGAAGAGTATT
TTGAGACTTTTCTGGCTGGGAAAGTGTGCTGGGGCTCCTGGCATGAACATGTGAAAGGATGGTGGGAAGCCAAAG
ACAAACACCGTATTCTCTATCTCTTCTATGAGGACATGAAGAAGAACCCAAAGCATGAAATTCAGAAGCTGGCAG
AATTTATTGGGAAGAAATTAGATGACAAAGTTCTAGATAAAATTGTCCATTACACTTCGTTTGATGTCATGAAAC
AGAATCCAATGGCAAACTATTCATCGATTCCTGCTGAAATCATGGACCACTCCATTTCTCCATTCATGAGAAAAG
GGGCAGTGGGAGACTGGAAGAAACACTTCACCGTGGCTCAGAATGAGAGATTTGATGAAGATTACAAGAAGAAAA
TGACTGATACCAGACTAACTTTCCACTTCCAGTTC**TAG**TAAGGAAGAAAAACTGAAAATGTTTTAGTTTATTACC
CAGTATATTTGGGTAATAATGAAAGTTTAATTCTCATAACAAATGATATCAGATTCCAGTTATCAGAATAGTTTA
CTGTGTTTGCTCTTATTCACTCTACTAAAAAATTATTTAAAAGGCTGGAGGCAAGGTGGTGACAGGCAGCAGGG
TGGCGACATGGAGAGAGGGAAGCTCAATAAATCACTAGGTACAATCCTGGTATCATTGCCAATTATCATCATATT
TACATTTTCTACAATCATGTGCTTATTAACATATTGGAAATGCTTCAGTCCTCACATGATAATACACTAACATTT
TCAGATTAAGTTTTGGTTCAAGTTAATTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCT
GGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCTGCTTCCTGGGTTCACGCCATTCCCCTGCCTCAGCCTC
CCGAGTAGCTGGGACTATGGGCGCCCACCACCACTCCCGGCTAATTTTTTTTTTTGTATTCTTAGTAGAGACGAG
GTTTCACCGTGTTAGCCAGGATGTTCTCGATCTCCTGACCCCATGATCCACCCGCCTCAGCCTAGACCTGCTGAT
CCAGGGTGTGTGTGAGTTGAGGGTGGGTGGAGGGGTTTGCAGTGTGGGAATGTGGCCCTGCAGTTGACCTGAGCT
GCTTCACATGGTTGTCCATTCTGGGGCTTAAAGAACTGGGACCAGACCAAGTAGAGGCCTTGGTGCTGGTTGGGG
TGGGGCCTGCAGAGTCTTAGTTACTGATTTCATTTTCAATAAATGTAGGTTTGTTACATGAGTTTCCCAATTAAA
AAAAAAATGACTTCTTGTCCAGTGCAAAAAAAAAAAAAAAAAA

FIGURE 590

MALHEMEDFTFDGTKRLSVNYVKGILQPTDTCDIWDKIWNFQAKPDDLLISTYPKAGTTWTQEIVELIQNEGDVE
KSKRAPTHQRFPFLEMKIPSLGSGLEQAHAMPSPRILKTHLPFHLLPPSLLEKNCKIIYVARNPKDNMVSYYHFQ
RMNKALPAPGTWEEYFETFLAGKVCWGSWHEHVKGWWEAKDKHRILYLFYEDMKKNPKHEIQKLAEFIGKKLDDK
VLDKIVHYTSFDVMKQNPMANYSSIPAEIMDHSISPFMRKGAVGDWKKHFTVAQNERFDEDYKKKMTDTRLTFHF
QF

FIGURE 591

TGGAGTCTTTTGAAAATTAAAGTCCAGGATTAAATTATATGTTGTCACCATTCACCACCACTACCACCCTCCCCC
ACCAATCTCTCCCACCGGTTAAACTCGTCTTCTAATCCTGTAGAATCACATGAACTAAATGAAGAAGTAAGAACT
TGAAGGCTCAGACTGACACTGTTACAAACTAGCATCTTCAGATGC**ATG**GTATTTACTTTAAATGTGCTTATATAC
AGTGTAGAGAAGCTCTTGTATAAGAAGACATCTATGCTAGCTAACTTAGTAGTAGTAGAGGGAACATATTCAGTG
AGCTGCCTTTATATCTGTAGTGTCGGAGACTTGTTACTGGTTCATTTGTGGTTATCAGTTGAAGGTTCTGTTCCT
GAGATGTGCAATAGTAGTGTTGAAAGGTATTGTTTAATAGTGATGGGGAACAGACATATTGGACTTTTTTTTCCA
TAT**TAA**ATTATTTAGTTTGCATGCCTGTTTGAAATTGGACCTCTCAGCAGCACTTTGAAATAGTTTTAATTAGGT
TAACATTTGCGTACACTTTAAATAAGCTAGCATATCGATGGCTTGATTTCACCTAGATGCTGTTCAAATTTCTGA
AAGCACAAAGGTATTTCATC

FIGURE 592

MVFTLNVLIYSVEKLLYKKTSMLANLVVVEGTYSVSCLYICSVGDLLLVHLWLSVEGSVPEMCNSSVERYCLIVM
GNRHIGLFFPY

FIGURE 593

GCAGGCTGCTGTCTCACAGAGCGAGAAGGTGTCAGGAGCAGCCCAGTTGTGTCTCTCTCTCTACCTCTGTGAAGG
GCGCGA**ATG**GGCAGAGCAGAACTTCTAGAAGGGAAGATGAGCACCCAGGATCCCTCAGATCTGTGGAGCAGATCC
GATGGAGAGGCTGAGCTGCTCCAGGACTTGGGGTGGTATCACGGCAACCTCACACGCCATGCTGCTGAAGCTCTT
CTCCTCTCAAATGGATGTGACGGCAGCTACCTTCTGAGGGACAGCAATGAGACCACCGGGCTGTACTCTCTCTCT
GTGAGGGCCAAAGATTCTGTTAAACACTTTCATGTTGAATATACTGGATATTCATTTAAATTTGGCTTTAATGAA
TTCTCATCTTTGAAGGATTTTGTCAAGCATTTTGCAAATCAGCCTTTGATTGGAAGCGAGACAGGCACTCTGATG
GTTCTAAAACATCCCTACCCAAGAAAAGTGGAAGAACCCTCCATTTATGAATCTGTCCGGGTTCACACAGCAATG
CAGACAGGAAGAACAGAAGATGACCTTGTGCCCACAGCACCTTCTCTGGGCACCAAAGAAGGTTACCTCACCAAA
CAGGGAGGCCTGGTCAAGACCTGGAAAACAAGATGGTTTACTCTGCACAGGAATGAACTGAAATACTTCAAAGAC
CAGATGTCACCAGAACCAATTCGGATCCTAGACCTAACAGAATGTTCAGCTGTACAATTCGATTATTCACAAGAA
AGGGTAAACTGTTTTTGTTTGGTATTTCCATTCAGGACATTTTATCTCTGTGCAAAGACCGGAGTAGAAGCTGAT
GAGTGGATCAAGATATTACGCTGGAAATTGGTCAAGGACAAAAGCTGTATTTTGTCTGCTCTCTGTATATCTCCC
GAGGAGAAGACTGATCACAAA**TAA**GAAAACAGCTCAACCAAGGGGAAGGCACGATCCGATCTCGGTCGTTCATCT
TTAAATAGATCTTTCTTGCCAAGGAATGCTCTGGCCCAGGAGCAAGGTGGAATGTTTCCCTGACGCTGTGATCTG
CAGCAGGCTTCAAATGAAAACCGACTAAGGATTTTCTTTCAAAAACAAATCAGAAGCAGATGCTGATTGGGACCC
ATATACCACGTTGCTGACTCACGTTGCTGCCCTTCCATGATGTTGCCATCTCCTTGAGAACACTGAAGCAATCAC
CATTCTGATAGAAAGTGCTTAAACCACCACTCTTAGGTCTGCTCACTCTTAGAACACACAATGGAAGAGGAAGGG
TTTTTGTTTTCACTCATTGTGGTCCCCAAGCCTATTGACACTAGTTGCCTAGAGTCCCACTGTGAGTCATGGTCA
GCCTGTCTGACATCCAGGTTGTGCTATTAACCAAGAAGGAAACAGATACTTGGAGGCTTAGATGACTTCTGCAGG
ATTTATATTCAGATAGAAAACATCAAATATTTTCAGGGGAGAGGTTTTTTTTTTTAATTTTTCCCCCTTTATACA
AAAAAAAAGAACATTTCCAAAACTAAAATAGAAAATGCTTGTGGCATTTATTTTCTCTTTTTAAAAGGTTCAGAA
ATTTGGCAGGTCCTTTGCTTCTAATGACAAAACTGTGAGAGCTAGATGTCCTATGGGCAATTAGGTAGTATAATA
AAGGTAAATGAAGGTACAATTTTTAAACCATTATTTTCACCCTGTTGGGGTAAATGTTTTAAAGAGTGAGAAAAC
ATAAATTGAGAAAGGGTGATAAAGTAATAGATAACTTTTAGTTTAATAATAATTATTGTTATTATACTACTAATA
ATAGAGCACTTGTAAGCACTAAGTTATCTTTATCCAACATTTCTCCAAATGGACTGAAAGAAACTTTTCAAGGAC
AGTGTATTATAACAATCCCTTTCCCAGAATTAGTTGTATAGGGTTGGCCCAAGAGATGTAAGAAAAATCTCGCAT
TGCTCCCTAAGCACCCTGGGCCTTATTAAAGAGCAACTTCTATTTCCAGTCGGGGGAGTAACACTAAAGCTACAA
GAAATATGTAATAATGATAGGTAATAATGTGTTCCAAAGCTTTTTCAAACTAGAATAAGGAGGCAAATAGAAGAA
TGAGATACTGATGTCCACAGTTCATTGGCAGAATCTAACCCCTTCTGTTATCTTTTTAATACTATTTTTGTTTA
GATAGAAGTTTCAAAGAAGATAAAAATGCTTGAAGAGCCTGAGAGTAAAAAGATTATGCTGCAAAGCTATGATAT
AAACTGCTCTTGCAGTCCAAAGGGATACCTGATTAAAGAAGTTTCTTATTTAAACATCTCAGACGCAAAAATTAC
ATTAAATTTTTGTATATTTCAACAACATTTTAAATGTATTTTGTTATGTTTGTATTATATAGGATAAAGCAAATG
TCAAGTTAAAATGTATTGTGTTGTTTGTAAAGTAAGAAGTTACTGGCCAGGAGCGGCGGCTCATGCCTGTAATCC
CAGGACTTTGGTAGGCCAAGACAAGCAGATCACTTGAGGTCAGGAGTTCAACATCAGCCTGGCCAACATGATGAA
ACCTTGTCTTTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTCAGGAGG
CTGAGGCAGGAGAATTGCTTGAACCCGGGAGGTGGAGGTTGCAGTGAACCAAGATCGCGGCGCTGCACTCTAGCC
TGGGTGACAGAGTCAGACTCCGTCCCAAAAAAACAAACAAACAAAACAAAACAAAAAAAACAGAAGTTACAAATG
AATACTCACGGATATGTATAGTTTTATGTTTGTTTTCTTAGAAACAAATGTGTTTCTTTGGGTGGGTAATATTGT
GTTTTACTATGTTTACCTTTTATAAAACATAACCTGTTTATTTATATTCTTTGGCTTTGTTTATTAAAAAGCATG
ATTTTGCTGTGCATGTACCATTTTG

FIGURE 594

MGRAELLEGKMSTQDPSDLWSRSDGEAELLQDLGWYHGNLTRHAAEALLLSNGCDGSYLLRDSNETTGLYSLSVR
AKDSVKHFHVEYTGYSFKFGFNEFSSLKDFVKHFANQPLIGSETGTLMVLKHPYPRKVEEPSIYESVRVHTAMQT
GRTEDDLVPTAPSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYSQERV
NCFCLVFPFRTFYLCAKTGVEADEWIKILRWKLVKDKSCILSALCISPEEKTDHK

FIGURE 595

GGTGTGGTAGCCGGCGCCGCGCCCATAGCCGGACGGGGATCTGAGCTGGCAGG**ATG**AATGTGGGGGTGGCACACA
GCGAAGTAAACCCCAACACCCGAGTGATGAATAGCCGAGGCATCTGGCTGGCCTACATCATCTTGGTAGGATTGC
TGCATATGGTTCTACTCAGCATCCCCTTCTTCAGCATTCCTGTTGTCTGGACCCTGACCAACGTCATCCATAACC
TGGCTACGTATGTCTTCCTTCATACGGTGAAAGGGACACCCTTTGAGACTCCTGACCAAGGAAAGGCTCGGCTAC
TGACACACTGGGAGCAAATGGACTATGGGCTCCAGTTTACCTCTTCCCGCAAGTTCCTCAGCATCTCTCCTATTG
TGCTCTATCTCCTGGCCAGCTTCTATACCAAGTATGATGCTGCGCACTTCCTCATCAACACAGCCTCATTGCTAA
GTGTACTGCTGCCGAAGTTGCCCCAGTTCCATGGGGTTCGTGTCTTTGGCATCAACAAATAC**TGA**GGGATGGGTT
TTGGGACAGCTCCATGGGCATGGGGAAGGCACTGAAACAGAGGACTATAAAACACCAAAAAAAAAAAAAAAAAA
AAAAAAAAA

FIGURE 596

MNVGVAHSEVNPNTRVMNSRGIWLAYIILVGLLHMVLLSIPFFSIPVVWTLTNVIHNLATYVFLHTVKGTPFETP
DQGKARLLTHWEQMDYGLQFTSSRKFLSISPIVLYLLASFYTKYDAAHFLINTASLLSVLLPKLPQFHGVRVFGI
NKY

FIGURE 597

CGCTCATTCCTGACCCCGCAGTGGGCGCG**ATG**GCGGAGGCTGTACTGAGGGTCGCCCGGCGGCAGCTGAGCCAGC
GCGGCGGGTCTGGAGCCCCCATCCTCCTGCGGCAGATGTTCGAGCCTGTGAGCTGCACCTTCACGTACCTGCTGG
GTGACAGAGAGTCCCGGGAGGCCGTTCTGATCGACCCAGTCCTGGAAACAGCGCCTCGGGATGCCCAGCTGATCA
AGGAGCTGGGGCTGCGGCTGCTCTATGCTGTGAATACCCACTGCCACGCGGACCACATTACAGGCTCGGGGCTGC
TCCGTTCCCTCCTCCCTGGCTGCCAGTCTGTCATCTCCCGCCTTAGTGGGGCCCAGGCTGACTTACACATTGAGG
ATGGAGACTCCATCCGCTTCGGGCGCTTCGCGTTGGAGACCAGGGCCAGCCCTGGCCACACCCCAGGCTGTGTCA
CCTTCGTCCTGAATGACCACAGCATGGCCTTCACTGGAGATGCCCTGTTGATCCGTGGGTGTGGGCGGACAGACT
TCCAGCAAGGCTGTGCCAAGACCTTGTACCACTCGGTCCATGAAAAGATCTTCACACTTCCAGGAGACTGTCTGA
TCTACCCTGCTCACGATTACCATGGGTTCACAGTGTCCACCGTGGAGGAGGAGAGGACTCTGAACCCTCGGCTCA
CCCTCAGCTGTGAGGAGTTTGTCAAAATCATGGGCAACCTGAACTTGCCTAAACCTCAGCAGATAGACTTTGCTG
TTCCAGCCAACATGCGCTGTGGGGTGCAGACACCCACTGCC**TGA**TCTCACTTCTGTCAGATGCTCCCATCCACTA
TTAATGCACTAGGTGGGAGGAGAGGGCGGCAATGACACTGCACCTCTCCTTTCCCACCGCATTCCCTGGAGCTCC
CTAAATAAAACTTTTTTTAACGTGAAAAAAAAAAAAAAAA

FIGURE 598

MAEAVLRVARRQLSQRGGSGAPILLRQMFEPVSCTFTYLLGDRESREAVLIDPVLETAPRDAQLIKELGLRLLYA
VNTHCHADHITGSGLLRSLLPGCQSVISRLSGAQADLHIEDGDSIRFGRFALETRASPGHTPGCVTFVLNDHSMA
FTGDALLIRGCGRTDFQQGCAKTLYHSVHEKIFTLPGDCLIYPAHDYHGFTVSTVEEERTLNPRLTLSCEEFVKI
MGNLNLPKPQQIDFAVPANMRCGVQTPTA

FIGURE 599

GGCTGTTGAGCTTGGTGATGAACTACAAATAGATGCCATAGATGATCAAAAATGTGATATTTTGGTTCAGGAAGA
ACTTCTAGCTTCACCTAAGAAACTCTTAGAAGATACTTTATTTCCTTCCTCAAAGAAGCTCAAGAAAGACAACCA
AGAGAGCTCAGACGCTGAGCTTAGTAGTAGTGAGTACATAAAAACAGATTTGGATGCGATGGATATTAAGGGCCA
GGAATCAAGCAGTGATCAAGAGCAGGTTGATGTGGAATCCATTGATTTTAGCAAAGAGAACAAAATGGACATGAC
TAGTCCAGAGCAGTCTAGAAATGTGCTACAGTTTACTGAAGAAAAAGAAGCTTTTATCTCTGAAGAGGAGATTGC
AAAATACATGAAGCGTGGAAAAGGAAAGTATTATTGCAAAATTTGTTGCTGTCGTGCTATGAAAAAAGGTGCTGT
TTTGCATCATTTGGTTAATAAGCATAATGTTCATAGCCCTTACAAATGCACAATCTGTGGAAAGGCTTTTCTTTT
GGAATCTCTCCTTAAAAATCATGTAGCAGCCCATGGGCAAAGTTTACTTAAATGTCCACGTTGTAATTTTGAATC
AAATTTCCCAAGAGGTTTTAAGAAACATTTAACTCATTGTCAAAGCCGGCATAATGAAGAGGCAAATAAAAAGCT
AATGGAAGCTCTTGAACCGCCACTGGAGGAGCAGCAAATTTGATAACACAGTGTGAATATTTGTTCTACAAAGGT
GTTTGTTGGAACCATTCTTTGTAAGTATAGCTTATCAGATAGCATAGTTGGATCAGTAGATGACATGTATGGTGT
ACCGTGTTTCACTGTCTCAGTTGTGTTACTAAGAATGAGCATTTGATCATTTTTTTCTGGTCTCTGTCTATGTGA
CTATCTTGTAAGTCAATAAATTTCTGTATAGTCCAGATGGATTAAACTTCTCATTTCTTTTAAATATGTATGAAT
AATAATACAAGGAAGTAGGCATTCCATTTAATAATCAAGAGCAAGTTGTACTCAAAGCATTCAGTTAAAGTGTAT
CTGTGTGTGGAACTAATTTCAGACAATAGAAAATATTAGTTGAAATGTTTAAGAATTAGGCATGAAAAATAAATT
TGAGAAATTTTGTTTCCTTACATGTATTTTTAAATCATAAGAGTTATTTTCTATCTGATGTAAAATTAGTTTATA
AATCTTAATCAGCTTCTAGATGTTTATTAGCTTTTATGTCATGAAATGTTGGAGTCTCAGGGTTGCTGATTTTCT
GCTAATGGGAAAAATTGACTAAGTCTTTAAAATAGTTTGCAGCCTTCTCCCACAGGAGACAAGTGAAAGATAAGT
GTGATTTTAGATCTTTCTTGTCCATAGTTGTTTTCAGTGGAGTCTTCCATTCTGTATCTTACCCTAAGATCTGGT
TCTTCCCTCCCCATCCCCACCCCCCACCCACCGCCTGCCAGCTCACACTAATAGATGATTCTTAATTGCCAAATG
TGTTAGAGTTTGTATATCCTACTCCTGGGCCTTACATGTCGCCTGTTGGGGCTTAAGACCAGGTTGATAAGTAGG
AACTGAAAGTCTTCCAGATTCACAGTAGAAAATTTTATAGACATTTCTGTTAAAGAAATATATCGATTTTATGTT
TTTCAATTATGTTACTGTAAATACCTTGTACCTGTTCATGGATTATTTTATTCTAAAATATTTTGTCAAATGTGT
ATCAACCAAATTAAAAAGAAAGGTTTTCATGTCAAAAAAAAAAAAAAAAAAA

FIGURE 600

AVELGDELQIDAIDDQKCDILVQEELLASPKKLLEDTLFPSSKKLKKDNQESSDAELSSSEYIKTDLDAMDIKGQ
ESSSDQEQVDVESIDFSKENKMDMTSPEQSRNVLQFTEEKEAFISEEEIAKYMKRGKGKYYCKICCCRAMKKGAV
LHHLVNKHNVHSPYKCTICGKAFLLESLLKNHVAAHGQSLLKCPRCNFESNFPRGFKKHLTHCQSRHNEEANKKL
MEALEPPLEEQQI

FIGURE 601

GGCCCTCGGGCCAAGATTCGGCACGAGGCGAACGGAGCAGCTGCTGCAGCAGGGCCC**ATG**GCGGACACCCAGTAC
ATCCTGCCCAATGACATCGGCGTGTCTAGCCTGGACTGCCGTGAGGCCTTCCGCCTGCTGTCACCCACAGAGCGC
CTCTATGCCTACCACCTGTCCCGTGCCGCCTGGTACGGAGGCCTGGCTGTGCTGCTTCAGACCTCCCCTGAGGCC
CCCTACATCTATGCTCTGCTCAGCCGCCTCTTCCGCGCCCAGGACCCCGACCAGCTGCGCCAACATGCCCTGGCT
GAAGGCCTTACCGAGGAGGAGTATCAGGCGTTCCTGGTCTATGCCGCGGGTGTTTACTCCAACATGGGCAACTAC
AAGTCCTTTGGTGACACCAAGTTTGTTCCCAACTTGCCCAAGGAAAAGCTGGAACGGGTGATCCTAGGGAGTGAG
GCTGCTCAGCAGCACCCAGAAGAAGTCAGGGGCCTCTGGCATACCTGCGGGGAGCTTATGTTCTCTCTGGAGCCA
AGGCTTCGACACCTCGGACTGGGGAAGGAGGGAATCACCACCTATTTCTCTGGGAATTGTACCATGGAAGATGCC
AAATTGGCCCAGGACTTTCTGGACTCACAGAACCTCAGTGCCTACAACACCCGGCTCTTCAAAGAGGTCGATGGA
GAAGGGAAGCCCTACTACGAGGTGCGGCTGGCTTCTGTGCTTGGCTCAGAGCCTTCCCTGGACTCTGAGGTGACT
TCCAAGCTGAAGAGCTATGAATTCCGGGGAAGCCCTTTCCAGGTGACCCGGGGGGACTACGCGCCCATCCTCCAG
AAGGTGGTGGAGCAGCTGGAGAAAGCCAAGGCCTATGCAGCCAACAGCCACCAGGGGCAGATGCTGGCCCAGTAT
ATAGAGAGCTTCACCCAGGGCTCCATCGAGGCCCACAAGAGGGGCTCCCGCTTCTGGATCCAGGACAAAGGCCCC
ATCGTGGAGAGTTACATCGGGTTCATCGAGAGCTACCGCGACCCCTTTGGTTCCCGAGGAGAATTTGAAGGTTTC
GTAGCTGTGGTGAACAAGGCCATGAGTGCCAAGTTTGAGCGGCTGGTGGCGAGCGCAGAGCAGCTGCTGAAGGAG
CTGCCCTGGCCCCCAACCTTTGAGAAGGACAAGTTCCTCACCCCTGACTTCACCTCCCTGGATGTTCTCACCTTC
GCTGGCTCCGGCATCCCTGCCGGCATCAACATCCCCAACTACGATGATCTGAGGCAGACGGAAGGCTTTAAGAAC
GTGTCGCTGGGGAATGTGCTGGCTGTGGCCTACGCCACGCAGCGGGAGAAGCTTACCTTTCTGGAGGAGGATGAC
AAGGACCTGTACATCCTCTGGAAGGGGCCCTCCTTCGATGTGCAGGTGGGCCTGCACGAGCTGCTGGGCCATGGC
AGTGGCAAGCTCTTCGTACAGGACGAAAAAGGAGCATTCAACTTTGACCAGGAAACAGTGATCAACCCAGAGACG
GGCGAGCAGATTCAGAGCTGGTATCGGAGCGGGGAGACCTGGGATAGCAAGTTCAGCACCATCGCCTCCAGCTAC
GAAGAGTGCCGGGCTGAGAGCGTGGGTCTCTACCTCTGTCTCCACCCGCAAGTGCTGGAGATCTTTGGCTTTGAG
GGGGCTGATGCGGAGGACGTGATCTACGTGAACTGGCTCAACATGGTTCGGGCCGGGCTGCTCGCTCTGGAGTTC
TACACACCTGAGGCCTTCAACTGGCGACAGGCCCATATGCAGGCCCGGTTTGTGATCCTGAGAGTCTTGCTGGAG
GCTGGCGAGGGACTCGTTACCATCACTCCCACCACAGGCTCCGATGGGCGCCCAGATGCCCGGGTCCGCCTCGAC
CGCAGCAAGATCCGGTCTGTGGGCAAGCCTGCTCTAGAGCGCTTCCTGCGGAGACTTCAGGTGCTGAAGTCCACA
GGGGATGTGGCCGGAGGGCGGGCCCTGTACGAGGGGTATGCAACGGTCACTGATGCGCCCCCCGAGTGCTTCCTC
ACCCTCAGGGACACGGTGCTGCTGCGTAAGGAATCTCGGAAGCTCATTGTTCAGCCCAACACTCACCTTGAAGGC
TCAGACGTGCAGCTTCTGGAATACGAGGCGTCAGCTGCTGGCCTCATCCGATCCTTCTCTGAGCGTTTCCCAGAG
GATGGACCCGAGTTGGAGGAGATCCTCACACAGCTGGCCACAGCCGATGCCCGATTCTGGAAGGGCCCCCAGTGAG
GCCCCATCTGGCCAAGCT**TGA**GGAAGATGTGTGGCCTTGCCCCCAATTCCATCAGACCAAGGCTGCAAGTGGCCC
TCCATTCGTGTGTGTATTTAGGGGCTGGGGAGGGGGAGGGGCAGGAGCTTGGACCTTGGTACTACCTCAGCTGAG
GGTGGTGACACAACCCCTTCCATTTGTCAGCACTTTCCAGCCTGCCAATTGCTTCCCCTCTGTGATCTCATTTCA
TCTGCACTGCCATACGTGGAGTGAGCAAGACAGGGCTTACCATCCTGTCTACCAGATGAGGAAATGGCAGTTCTG
AGAAGTCACTGGTCTAGATCCCGCAGGTGGCACGTGACAGCTAGGGTTCAAAACGTTCTCACCAAATCCAATGCT
CCTCACATATTAATTTTATAACCAGACAAATAAATATTAGAGACAACCACCAAAAAAAAAAAAAA

FIGURE 602

MADTQYILPNDIGVSSLDCREAFRLLSPTERLYAYHLSRAAWYGGLAVLLQTSPEAPYIYALLSRLFRAQDPDQL
RQHALAEGLTEEEYQAFLVYAAGVYSNMGNYKSFGDTKFVPNLPKEKLERVILGSEAAQQHPEEVRGLWHTCGEL
MFSLEPRLRHLGLGKEGITTYFSGNCTMEDAKLAQDFLDSQNLSAYNTRLFKEVDGEGKPYYEVRLASVLGSEPS
LDSEVTSKLKSYEFRGSPFQVTRGDYAPILQKVVEQLEKAKAYAANSHQGQMLAQYIESFTQGSIEAHKRGSRFW
IQDKGPIVESYIGFIESYRDPFGSRGEFEGFVAVVNKAMSAKFERLVASAEQLLKELPWPPTFEKDKFLTPDFTS
LDVLTFAGSGIPAGINIPNYDDLRQTEGFKNVSLGNVLAVAYATQREKLTFLEEDDKDLYILWKGPSFDVQVGLH
ELLGHGSGKLFVQDEKGAFNFDQETVINPETGEQIQSWYRSGETWDSKFSTIASSYEECRAESVGLYLCLHPQVL
EIFGFEGADAEDVIYVNWLNMVRAGLLALEFYTPEAFNWRQAHMQARFVILRVLLEAGEGLVTITPTTGSDGRPD
ARVRLDRSKIRSVGKPALERFLRRLQVLKSTGDVAGGRALYEGYATVTDAPPECFLTLRDTVLLRKESRKLIVQP
NTHLEGSDVQLLEYEASAAGLIRSFSERFPEDGPELEEILTQLATADARFWKGPSEAPSGQA

FIGURE 603

CCCGCTCTCAGGCACTGCTGGAGAACCGAGACCGACTTCTTTCTCTTTACCCTCATTGGCGCTTCTCTCCTGCAG
TCCGCCTCTGGGCCCTGCCGCATTTCTTGAGACTTAAAGTGGCATTCTAAAGGCAATTTAAAAATC**ATG**TCAAGC
TCAGTTGAACAGAAAAAAGGGCCTACAAGACAGCGCAAATGTGGCTTTTGTAAGTCAAATAGAGACAAGGAATGT
GGACAGTTACTAATATCTGAAAACCAGAAGGTGGCAGCGCACCATAAGTGCATGCTCTTTTCATCTGCTTTGGTA
TCATCACACTCTGATAATGAAAGTCTTGGTGGATTTTCTATTGAAGATGTCCAAAAGGAAATTAAAAGAGGCACG
AAGCTGATGTGTTCTTTGTGCCATTGTCCTGGAGCAACAATTGGTTGTGATGTGAAAACATGTCACAGGACATAC
CACTACCACTGTGCATTGCATGATAAAGCTCAAATACGAGAGAAACCTTCACAAGGAATTTACATGGCCTATTGC
CGAAAACACAAGAAAACTGCACATAACTCCGAAGCAGCTGATTTAGAAGAAAGTTTTAATGAACATGAACTGGAG
CCCTCATCACCTAAAAGTAAAAAGAAAAGTCGCAAAGGAAGGCCAAGAAAAACTAATTTTAAAGGGCTGTCAGAA
GATACCAGGTCCACATCCTCCCATGGAACAGATGAAATGGAAAGTAGTTCCTATAGAGATAGGTCTCCACACAGA
AGCAGCCCTAGTGACACCAGGCCTAAATGTGGATTTTGCCATGTAGGGGAGGAAGAAAATGAAGCACGAGGAAAA
CTGCATATATTTAATGCCAAGAAGGCAGCTGCCCATTATAAGTGCATGTTGTTTTCTTCTGGCACAGTCCAGCTC
ACAACAACATCAAGAGCAGAATTTGGAGACTTTGATATTAAAACTGTACTTCAGGAGATTAAACGAGGAAAAAGA
ATGGTCTGTAGTTTTTATATTTGTTATGCAACATTACACTTGATTTGCTGCTTTAAATTTAGAGTACATCCCAAA
TTTATCCAGTCATCAGAAAATTTAAAG**TAG**TTCGTATGTTAAAGCAAAGTATATATTTGACTTATTTGTAATATA
ATAAAGGATGCTGATGTTACGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 604

MSSSVEQKKGPTRQRKCGFCKSNRDKECGQLLISENQKVAAHHKCMLFSSALVSSHSDNESLGGFSIEDVQKEIK
RGTKLMCSLCHCPGATIGCDVKTCHRTYHYHCALHDKAQIREKPSQGIYMAYCRKHKKTAHNSEAADLEESFNEH
ELEPSSPKSKKKSRKGRPRKTNFKGLSEDTRSTSSHGTDEMESSSYRDRSPHRSSPSDTRPKCGFCHVGEEENEA
RGKLHIFNAKKAAAHYKCMLFSSGTVQLTTTSRAEFGDFDIKTVLQEIKRGKRMVCSFYICYATLHLICCFKFRV
HPKFIQSSENLK

FIGURE 605

CTCGAGAGCTCCGCC**ATG**GCCGCTCTCACCCGGGACCCCCAGTTCCAGAAGCTGCAGCAATGGTACCGCGAGCAC
CGCTCCGAGCTGAACCTGCGCCGCCTCTTCGATGCCAACAAGGACCGCTTCAACCACTTCAGCTTGACCCTCAAC
ACCAACCATGGGCATATCCTGGTGGATTACTCCAAGAACCTGGTGACGGAGGACGTGATGCGGATGCTGGTGGAC
TTGGCCAAGTCCAGGGGCGTGGAGGCCGCCCGGGAGCGGATGTTCAATGGTGAGAAGATCAACTACACCGAGGGT
CGAGCCGTGCTGCACGTGGCTCTGCGGAACCGGTCAAACACACCCATCCTGGTAGACGGCAAGGATGTGATGCCA
GAGGTCAACAAGGTTCTGGACAAGATGAAGTCTTTCTGCCAGCGTGTCCGGAGCGGTGACTGGAAGGGGTACACA
GGCAAGACCATCACGGACGTCATCAACATTGGCATTGTCGGCTCCGACCTGGGACCCCTCATGGTGACTGAAGCC
CTTAAGCCATACTCTTCAGGAGGTCCCCGCGTCTGGTATGTCTCCAACATTGATGGAACTCACATTGCCAAAACC
CTGGCCCAGCTGAACCCGGAGTCCTCCCTGTTCATCATTGCCTCCAAGACCTTTACTACCCAGGAGACCATCACG
AATGCAGAGACGGCGAAGGAGTGGTTTCTCCAGGCGGCCAAGGATCCTTCTGCAGTGGCGAAGCACTTTGTTGCC
CTGTCTACTAACACAACCAAAGTGAAGGAGTTTGGAATTGACCCTCAAAACATGTTCGAGTTCTGGGATTGGGTG
GGAGGACGCTACTCGCTGTGGTCGGCCATCGGACTCTCCATTGCCCTGCACGTGGGTTTTGACAACTTCGAGCAG
CTGCTCTCGGGGGCTCACTGGATGGACCAGCACTTCCGCACGACGCCCCTGGAGAAGAACGCCCCCGTCTTGCTG
GCCCTGCTGGGTATCTGGTACATCAACTGCTTTGGGTGTGAGACACACGCCATGCTGCCCTATGACCAGTACCTG
CACCGCTTTGCTGCGTACTTCCAGCAGGGCGACATGGAGTCCAATGGGAAATACATCACCAAATCTGGAACCCGT
GTGGACCACCAGACAGGCCCCATTGTGTGGGGGGAGCCAGGGACCAATGGCCAGCATGCTTTTTACCAGCTCATC
CACCAAGGCACCAAGATGATACCCTGTGACTTCCTCATCCCGGTCCAGACCCAGCACCCCATACGGAAGGGTCTG
CATCACAAGATCCTCCTGGCCAACTTCTTGGCCCAGACAGAGGCCCTGATGAGGGGAAAATCGACGGAGGAGGCC
CGAAAGGAGCTCCAGGCTGCGGGCAAGAGTCCAGAGGACCTTGAGAGGCTGCTGCCACATAAGGTCTTTGAAGGA
AATCGCCCAACCAACTCTATTGTGTTCACCAAGCTCACACCATTCATGCTTGGAGCCTTGGTCGCCATGTATGAG
CACAAGATCTTCGTTCAGGGCATCATCTGGGACATCAACAGCTTTGACCAGTGGGGAGTGGAGCTGGGAAAGCAG
CTGGCTAAGAAAATAGAGCCTGAGCTTGATGGCAGTGCTCAAGTGACCTCTCACGACGCTTCTACCAATGGGCTC
ATCAACTTCATCAAGCAGCAGCGCGAGGCCAGAGTCCAA**TAA**ACTCGTGCTCATCTGCAGCCTCCTCTGTGACTC
CCCTTTCTCTTCTCGTCCCTCCTCCCCGGAGCCGGCACTGCATGTTCCTGGACACCACCCAGAGCACCCTCTGGT
TGTGGGCTTGGACCACGAGCCCTTAGCAGGGAAGGCTGGTCTCCCCCAGCCTAACCCCCAGCCCCTCCATGTCTA
TGCTCCCTCTGTGTTAGAATTGGCTGAAGTGTTTTTGTGCAGCTGACTTTTCTGACCCATGTTCACGTTGTTCAC
ATCCCATGTAGAAAAACAAAGATGCCACGGAGGAGGT

FIGURE 606

MAALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTLNTNHGHILVDYSKNLVTEDVMRMLVDLAKSR
GVEAARERMFNGEKINYTEGRAVLHVALRNRSNTPILVDGKDVMPEVNKVLDKMKSFCQRVRSGDWKGYTGKTIT
DVINIGIVGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHIAKTLAQLNPESSLFIIASKTFTTQETITNAETA
KEWFLQAAKDPSAVAKHFVALSTNTTKVKEFGIDPQNMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGA
HWMDQHFRTTPLEKNAPVLLALLGIWYINCFGCETHAMLPYDQYLHRFAAYFQQGDMESNGKYITKSGTRVDHQT
GPIVWGEPGTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMRGKSTEEARKELQ
AAGKSPEDLERLLPHKVFEGNRPTNSIVFTKLTPFMLGALVAMYEHKIFVQGIIWDINSFDQWGVELGKQLAKKI
EPELDGSAQVTSHDASTNGLINFIKQQREARVQ

FIGURE 607

GTGTATTTGCATATTTTAAGTATCTACCATCTAATATTTATTAATACAATTTTTTCTTAATTTCTTAGACTTGTG
ACTATTTGAAACAAATTATAACACTGTATTGTAGGATTTATAATTTGTAGTTGTAAAATTTATAACACATGGAAT
AAGAAGATAAATGGAACTGTTCTGTAGCAAATTTTTCATGTTTTATATTTAAGACAGTATAGTATTAACTCTAAA
AGTATGGTGGATATGTTAAAGATTCATATTGTATTCCCTGCAGCAACCACTAAAAAATGCAAAGAAGTGTAATGT
AAATGCTAAAAAAGGAGATAATTATAAAATATTTATTTGCANNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNCTAATTGTATAGCTTTTAGAACAAAATACAGCTC
AGGAATATGAAAAACCAAGCACACATCCTGGATAAAATTCATAAACCTGCTCAATGAGAGAAAAGTTGGACACAA
AATTGTACTTTATGTATTTTGTATTTTATTCCAGGCAAAATAATCCTATGGTGAAAAAAAATCAACAAGATAATC
TCTGCATGAGAAAAAGGACCAAAGACAAGTGAATTTTCTGAGGGTGATGAAAGTGTTGCTTCGAAAAGGGGTGAA
GTTTATATGGGTCTATTTATTTGTCTAACATGTACAGTTAAGGTTTATGCCTTGCAATGTATGTACATCTTCACA
AAAAAAATCTTAAAAAAATTAAATGGGTGGGGGTAGGGAAAGGGTTGAAGTATAGATGAAGCAGAAGTGGTACAT
GATTAGTAGTTGAAGCTGGGGGCAGGTCTATATATTTTATTTTTATGTCTTTAATAGCATTTGTATAAATGTACA
ATATTCGTTTACA**<u>ATG</u>**TTAGCTCAGGATCTTGTTTACCTTTGGACAGGGAGGGAGGGAGAAATTTATTTTCTGGG
TAGGAG

FIGURE 608

MLAQDLVYLWTGREGEIYFLGR

FIGURE 609

GCGGCCGCGGAGGAGGAGGAAGGGGAGGAGGGCGAGGCGGGAGGTGCAGGAGGGACCCTCGCCATGGGTCCACGG
GCCTAGAGTGGCGGAAGATACCGGCCTGGTGCCAAACTGGCTACTGCTGCTTCCTGTGGCCTCC**ATG**GCTGAGGA
CTGGCTGGACTGCCCGGCCCTGGGCCCTGGCTGGAAGCGCCGCGAAGTCTTTCGCAAGTCAGGGGCCACCTGTGG
ACGCTCAGACACCTATTACCAGAGCCCCACAGGAGACAGGATCCGAAGCAAAGTTGAGCTGACTCGATACCTGGG
CCCTGCGTGTGATCTCACCCTCTTCGACTTCAAACAAGGCATCTTGTGCTATCCAGCCCCCAAGGCCCATCCCGT
GGCGGTTGCCAGCAAGAAGCGAAAGAAGCCTTCAAGGCCAGCCAAGACTCGGAAACGTCAGGTTGGACCCCAGAG
TGGTGAGGTCAGGAAGGAGGCCCCGAGGGATGAGACCAAGGCTGACACTGACACAGCCCCAGCTTCATTCCCTGC
TCCTGGGTGCTGTGAGAACTGTGGAATCAGCTTCTCAGGGGATGGCACCCAAAGGCAGCGGCTCAAAACGTTGTG
CAAAGACTGTCGAGCACAGAGAATTGCCTTCAACCGGGAACAGAGAATGTTTAAGCGTGTGGGCTGTGGGGAGTG
TGCAGCCTGCCAGGTAACAGAAGACTGTGGGGCCTGCTCCACCTGCCTCCTGCAGCTGCCCCATGATGTGGCATC
GGGGCTGTTCTGCAAGTGTGAACGGAGACGCTGCCTCCGGATTGTGGAAAGGAGCCGAGGGTGTGGAGTATGCCG
GGGCTGTCAGACCCAAGAGGATTGTGGCCATTGCCCCATCTGCCTTCGCCCTCCCCGCCCTGGTCTCAGGCGCCA
GTGGAAATGTGTCCAGCGACGTTGCCTACGGGGTAAACATGCCCGCCGCAAGGGAGGCTGTGACTCCAAGATGGC
TGCCAGGCGGCGCCCCGGAGCCCAGCCACTGCCTCCACCACCCCCATCACAGTCCCCAGAGCCCACAGAGCCGCA
CCCCAGAGCCCTGGCCCCCTCGCCACCTGCCGAGTTCATCTATTACTGTGTAGACGAGGACGAGCTACAGCCCTA
CACGAACCGCCGGCAGAACCGCAAGTGCGGGGCCTGTGCAGCCTGCCTACGGCGGAATGGATGTGGCCGCTGCGA
CTTCTGCTGCGACAAGCCCAAATTCGGGGGCAGCAACCAGAAGCGCCAGAAGTGTCGTTGGCGCCAATGCCTGCA
GTTTGCCATGAAGCGGCTGCTGCCCAGTGTCTGGTCAGAGTCTGAGGATGGGGCAGGATCGCCCCCACCTTACCG
TCGTCGAAAGAGGCCCAGCTCTGCCCGACGGCACCATCTTGGCCCTACCTTGAAGCCCACCTTGGCTACACGCAC
AGCCCAACCAGACCATACCCAGGCTCCAACGAAGCAGGAAGCAGGTGGTGGCTTTGTGCTGCCCCCGCCTGGCAC
TGACCTTGTGTTTTTACGGGAAGGCGCAAGCAGTCCTGTGCAGGTGCCGGGCCCTGTTGCAGCTTCCACAGAAGC
CCTGTTGCAGGAGGCCCAGTGCTCTGGCCTGAGTTGGGTTGTGGCCTTACCCCAGGTGAAGCAAGAGAAGGCGGA
TACCCAGGACGAGTGGACACCAGGCACAGCTGTCCTGACTTCTCCCGTATTGGTGCCTGGCTGCCCTAGCAAGGC
AGTAGACCCAGGCCTGCCTTCTGTGAAGCAAGAGCCACCTGACCCAGAGGAGGACAAGGAGGAGAACAAGGATGA
TTCTGCCTCCAAATTGGCCCCAGAGGAAGAGGCAGGAGGGGCTGGCACACCCGTGATCACGGAGATTTTCAGCCT
GGGTGGAACCCGCTTCCGAGATACAGCAGTCTGGTTGCCAAGGTCCAAAGACCTTAAAAAACCTGGAGCTAGAAA
GCAG**TAG**ACTGGAGGCTTCTACAGACTGTAGGATTCAAGTCTGCAGGGCAGGCACTCGGGAAGGGAAGATGGATG
TAAAGTGTGGGAGACCGAGGACACAGTGGAGCCCACGAGCACGAGCTGGAACCCACGAGGATGGCCTGGAACCCA
TGTCAGTCTCTCACCACCTCCAGCTTCGATGATGTGGGTGTCCTGCAGAAGAAGCTGGTGCCCTTCCTCACAGAG
TTAAATATGCATCTGGCCCAGGAATTAGAGAAGCTGAAAGGATGATCCTGGGGAAGGTGGAGCAGCTGCAGGCCT
GGCTGCAGGCCTGACTACTGCCCACACCAACGAGGTGATCTAGCAGATACATGGCAACGTGTGAACTGCAACAAC
GCCTGGTGCCCCAGCACCAACCTTCCAAGTGTAAAAACAATGTGCTGCTGCTTCACTTCCGCCCTCCGGTTATCA
AGCAAAATGTCTCTTGTGGCCCATCTTACTGGAAGAGAGTTCCGGGAAACATAGCCTCACCAAGGTGACACATTA
CAAAGCCACCCTACCATGAATCCGCTCCCAAGGGTCTCACTGCTCACCTGAGGATAACTCAATATAACTATGTTG
CTGAAAATGCAAAGCTGAAGACCATGGATTTCATGGTGATTCCAGCAAGTACAGAGATTCTATGAAGCCCACCCA
GAAAAAACTTGCTGGTCCTGGCTATTTTTGTGTCATTTATTCAAGTATTGAGAACCTGGCCTGTGGTAGGCACTG
TACTTAATACTAGGATACAGAAATGCAAAAGATACGGCCCATGCAATTTTATTAAATGCATCAATATGTATTACA
AATGGTGAATGGATTTCCAACTTTATCATGGAATTTAATGCTGAATATATAGAATTCAGAAAATTGTTGGGAGGA
CAGCCCTTTTGTGAACCTTGTTTGGGGCACAGTAGGAATTGGAAATAATTTAGTTTCTATCTCTAAGCTGTTCTA
TTTTAAAATTATTTTTAAATTTTTATTGTCCCACTT

FIGURE 610

MAEDWLDCPALGPGWKRREVFRKSGATCGRSDTYYQSPTGDRIRSKVELTRYLGPACDLTLFDFKQGILCYPAPK
AHPVAVASKKRKKPSRPAKTRKRQVGPQSGEVRKEAPRDETKADTDTAPASFPAPGCCENCGISFSGDGTQRQRL
KTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTEDCGACSTCLLQLPHDVASGLFCKCERRRCLRIVERSRGC
GVCRGCQTQEDCGHCPICLRPPRPGLRRQWKCVQRRCLRGKHARRKGGCDSKMAARRRPGAQPLPPPPPSQSPEP
TEPHPRALAPSPPAEFIYYCVDEDELQPYTNRRQNRKCGACAACLRRNGCGRCDFCCDKPKFGGSNQKRQKCRWR
QCLQFAMKRLLPSVWSESEDGAGSPPPYRRRKRPSSARRHHLGPTLKPTLATRTAQPDHTQAPTKQEAGGGFVLP
PPGTDLVFLREGASSPVQVPGPVAASTEALLQEAQCSGLSWVVALPQVKQEKADTQDEWTPGTAVLTSPVLVPGC
PSKAVDPGLPSVKQEPPDPEEDKEENKDDSASKLAPEEEAGGAGTPVITEIFSLGGTRFRDTAVWLPRSKDLKKP
GARKQ

FIGURE 611

CCCATTGTGTCGGACAATTATTTCTAGAGTCTTTTTCCAAACAGAATTGAACAATGCCACAAAAACTTTCTTTAC
TAAAGAATATTTGAAAATAAAACAAAGCTTTCAGAAATCCAACTCTGCAAAATGGCCCCTACCAAGCTGCAGAAA
AGCATTTCATCTTTTTGGAGGTTTCCGCAGACATGCAGCTCCAGTTACAAGAAGGCAGTTCCCACACGGTGCACA
CAGGATGGATTACCTGCACTTTGAGGATGATAGCCCGTGGATGGTGGTT**TGA**CATGGATATGGTGATCATATATA
TTTATTCAGTGAACTGGGTCATTGGATTCATTGTTTTCTGCTTTTTTTGCTATTTTTTCTTTCCGTTTTAGGAAT
TTCATACCTTACTACAATTGACCAATCATAAATGATGTAAATAACAATTGCTTAAACAATTTTT

FIGURE 612

PLCRTIISRVFFQTELNNATKTFFTKEYLKIKQSFQKSNSAKWPLPSCRKAFHLFGGFRRHAAPVTRRQFPHGAH
RMDYLHFEDDSPWMVV

FIGURE 613

AGAAGTTAGGGGCTGCAGCGGCGCTGGCTTTAGGTGAACGACGTGGTGAGGAGTGGGTTTCGGGCATGAGAAGTC
ACAGGGCCGTTTCCTAGTCTCTCTTCACTTCTTTGGGTCTTCTCAGAGAAAGAAGGCTGCCGTGGGTAGGCTGGG
GGCGGAGACTATCGGGAAGAGAAAATTACTTTTCCCACTGAAACACACCCAAGTATATGCCCAGCCTTC**ATG**AAA
GTGAACAGAGAAACGAAGCGCCTTTATGTGGGTGGCCTTAGCCAGGACATTTCTGAGGCAGACCTACAAAATCAG
TTCAGCAGATTTGGAGAAGTTTCGGATGTGGAGATCATCACACGGAAAGATGACCAAGGAAACCCACAGAAAGTT
TTTGCATATATCAACATCAGTGTAGCAGAAGCGGACCTGAAAAAATGTATATCTGTTTTAAATAAAACAAAATGG
AAAGGTGGAACATTACAAATTCAACTAGCAAAAGAAAGCTTTCTGCACAGATTGGCCCAAGAGAGAGAAGCAGCA
AAAGCTAAGAAAGAAGAATCAACAACAGGTAACGCCAACTTGTTAGAAAAGACAGGAGGAGTGGATTTCCATATG
AAAGCTGTGCCAGGGACAGAAGTGCCAGGGCATAAGAATTGGGTTGTGAGCAAATTTGGAAGAGTCTTACCTGTT
CTTCACCTTAAAAATCAACATAAACGTAAAATCATCAAATATGATCCCTCAAAGTACTGCCACAACCTGAAGAAG
ATAGGGGAGGATTTCTCAAACACCATTCCTATATCCAGCCTGACTTGGGAATTAGAAGGAGGGAATGACCCTATG
AGTAAGAAACGGCGAGGAGAGTTCTCTGACTTTCATGGCCCTCCCAAGAAGATAATAAAAGTGCAGAAGGATGAG
AGTTCCACTGGGTCTCTGGCCATGAGTACAAGGCCCAGGAGGGTAATAGAGAGACCACCCTTAACACAGCAACAG
GCTGCACAAAAAAGAACTTGTGATTCCATTACTCCTTCTAAATCATCTCCTGTACCTGTTTCTGATACTCAGAAA
CTTAAAAATCTACCTTTTAAGACTTCTGGCTTGGAAACTGCCAAGAAGAGAAACAGCATTTCTGATGATGATACT
GATTCTGAAGATGAATTGAGAATGATGATTGCGAAAGAGGAAAACTTACAGAGAACTACACAACCCTCAATAAAT
GAATCTGAAAGTGATCCTTTTGAAGTTGTAAGGGATGATTTCAAATCAGGCGTTCACAAACTGCATTCTTTAATA
GGTTTAGGTATCAAAAATCGTGTCTCTTGCCATGATAGTGATGATGATATTATGAGAAATGATCGTGAGTATGAC
TCAGGAGATACAGATGAAATTATTGCGATGAAAAAAAATGTTGCTAAGGTCAAAAACAGTACAGAATTTTCACAA
ATGGAAAAATCTACGAAGAAAACTTCTTTCAAAAAATAGAGAAAACTGTGAGCTTTCTGATCACTGTATTAAACTA
C

FIGURE 614

MKVNRETKRLYVGGLSQDISEADLQNQFSRFGEVSDVEIITRKDDQGNPQKVFAYINISVAEADLKKCISVLNKT
KWKGGTLQIQLAKESFLHRLAQEREAAKAKKEESTTGNANLLEKTGGVDFHMKAVPGTEVPGHKNWVVSKFGRVL
PVLHLKNQHKRKIIKYDPSKYCHNLKKIGEDFSNTIPISSLTWELEGGNDPMSKKRRGEFSDFHGPPKKIIKVQK
DESSTGSLAMSTRPRRVIERPPLTQQQAAQKRTCDSITPSKSSPVPVSDTQKLKNLPFKTSGLETAKKRNSISDD
DTDSEDELRMMIAKEENLQRTTQPSINESESDPFEVVRDDFKSGVHKLHSLIGLGIKNRVSCHDSDDDIMRNDRE
YDSGDTDEIIAMKKNVAKVKNSTEFSQMEKSTKKTSFKNRENCELSDHCIKL

FIGURE 615

CTTATGCATCGGATTTATTTTTCCAAATCAAGAGGACAGTGATAGATGCATTTTCCCCAGGCTGTCTCAGAAAGG
TCGCTAAATGTATACTGTTGTCAGAATTGCTGAGATCTCCCCCCACTTTGGTTTTTGCAGCAGTAAAAACTCTTT
CCACTGTGACTTATTTTCCCCAGGCTGTCTCAGAAAGGTCGCTAAATGTATACTGTTGTCAGAATTGCTGAGATC
TCCCCCCACTTTTGGTTTTTGCAGCAGTAAAAACTCTTTCCACTGTGACTTATTTTCTCTCTCAGGCAGCCAGCC
ACCTGGTCCCTTGTGCTGACTCTAGCACAGTGGCCAGGATCCAATACGAGTCCAGGGGTGACCGCAGGATGGTGG
GGGCAGCGGGCTTCTCCACCTACCCCAGCCACCAAGGCCCTGACGCACTGCCTCCTGCACCTTCAGCACATCCCT
GTGCACAGCTGGAAGGGTGCATGGCCCGCTCACCTTTGTTCAGATGGGTGGAAACGCTGATGATACCAGCTCCTC
CTGCCGTGCCCCTGCCACGGAGCAGGCATTGTGAACTGGCTGGTGTTTGCAGTCCCACGTGGCATGGCCTCCAGC
CCAACCCACAGTGGAGACTGGAGACAGGGCAATGAGTCTGGTCGGGGGCACGTGGACATGCCCCATAGGGGCCCC
ACCCAGACTTAACAGGCAAGGTCCTGGGCATTGCGCGACGCAGGACTCAATGCTAAAGCAAGCCTGCCTGGCTCT
GTGCCAGGGCCCCTCTTCTGATTTACACATCCCATTTTTACACAGACCCTTCCTTCTTAATAAAGGCTGACAGTT
CTGTTGGCAGCCAAGAACCCACACCATGAAGACAGGGAGTGAGGGGCCTTTGTGCCCAACTCCAGCACAGCTGCG
TTCTGGGGTGTGTGAGAGGCATGTTCGTGTCTGTGCGCTGGTGGTCTCGTGAGACAGTTCCGAGGACGGGGAAAT
TGCAGGGTGGTGGGGGCGTGAGGCTTATATGTGGAACTGATGCAGAGTTCGCCTGCAGACGGATCTGGATATACA
CTATGTATAATTGTTACGTGTAATTTAAAATATATCTGTTTGCCATCGTCATGAGAAGATTATATGTAAGGCTCT
GAAGGGAGAGGGAGATGTACATTCTGCCAGGCTCCTGGGGACCTTATCCGAGTCATGAAATTGATGACTGTTGAT
CCAGTGGTGCAAGAAGCTACACTCCATGTGTCATCACGCTTATGACTCCTAATGTATTTTTAAGGCAAAAAATGT
CAGCCGACTCCATCTTCACCCCTCGATTCCTCGAGTCCAGCCTTTCTGTGCCAGTGCTTCACTGAGCCACAACGC
TCTCGCCATCGGGACCCGGCTGGGCCTGGAGTCTCGGGGCACAGTTGCCATGGAGCCCTCCTGGGTCATTCTACA
AATGTGCTGAGTGCCAGCTGAAAACCCCACAGGAGATGGAGTACCTTGGCCAAGCTTAAAGAGAAGATTTTCTCA
GGGTATTTATTAGTGTGTCCAGCAGGGTCAGGAAGCAGGATGGAAAGATGCATTCAGACTGTTAATTTATTAACA
AGGCAAATGATTTTGTGTTTCTTGATGACAGACTATTAAGTTTGGGACTTATTTTCCCATTTGAGAAGTTATAAT
ATATATTTAAGATGATAAGTTTCCTGCTTAAGTTGTGCCTTTCAGCTTCAATGAGTTTAAGGAGCACTAAGGGTA
ATGATACCAATGAGGGTTGGTTTATTATCAAACCTGAATAGCTGTGGTTTCTCCAGTAAATATTTTCTTCTACTG
AACATGGAGCCATTATTAAGAGTTGTGTGTTTTTTATTATGTACATTTGTATATTTTTTTGCTTGTTTGATGTTC
TATTTTTCTAATAGTTTTCTTTTAGTTTCTTAAAGTTGTGATACTAGATTTAGATTCTGATGCTAACTGCAAATC
AGGTTGGTCTCTGCTGGGTCTCTCCTGCTTTTATTTACTTTAAGGACAAGTGTAGTTGTCGTCCACCACCTTTC
AAAAAATGTGAAACTGCCCTGCCTCCCCTTTTTGCTGACAACACTGTGTACATTGACCACTTCCTACCATACTTT
ATGTTGTAAAATCAAACTCTTTTGTGGTACATTATCTCATGCTTCTGCAAATTCGAATAAATTCTATGGCTTCCA
TGTGAAAAAAA

FIGURE 616

MIPMRVGLLSNLNSCGFSSKYFLLLNMEPLLRVVCFLLCTFVYFFACLMFYFSNSFLLVSKVVILDLDSDANCKS
GWSLLGLSCFYFTLRTSVVVVHHLSKNVKLPCLPFLLTTLCTLTTSYHTLCCKIKLFCGTLSHASANSNKFYGFH
VK

FIGURE 617

CTGCTCGCGGCCGCCACCGCCGGGCCCCGGCCGTCCCTGGCTCCCCTCCTGCCTCGAGAAGGGCAGGGCTTCTCA
GAGGCTTGGCGGGAAAAAAGAACGGAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTTCGGGGCTTTATCTAA
CTCGCTGTAGTAATTCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGGGTGGAAGAGCCGGGCGAGCA
GAGCTGCGCTGCGGGCGTCCTGGGAAGGGAGATCCGGAGCGAATAGGGGGCTTCGCCTCTGGCCCAGCCCTCCCG
CTTGATCCCCCAGGCCAGCGGTCCGCAACCCTTGCCGCATCCACGAAACTTTGCCCATAGCAGCGGGCGGGCACT
TTGCACTGGAACTTACAACACCCGAGCAAGGACGCGACTCTCCCGACGCGGGGAGGCTATTCTGCCCATTTGGGG
ACACTTCCCCGCCGCTGCCAGGACCCGCTTCTCTGAAAGGCTCTCCTTGCAGCTGCTTAGACGCTGGATTTTTTT
CGGGTAGTGGAAAACCAGCAGCCTCCCGCGACG**ATG**CCCCTCAACGTTAGCTTCACCAACAGGAACTATGACCTC
GACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGAGGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAG
CTGCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATTCGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGC
CGCCGCTCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTTCTCCCTTCGGGGAGACAACGACGGCGGT
GGCGGGAGCTTCTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTGGGAGGAGACATGGTGAACCAGAGT
TTCATCTGCGACCCGGACGACGAGACCTTCATCAAAAACATCATCATCCAGGACTGTATGTGGAGCGGCTTCTCG
GCCGCCGCCAAGCTCGTCTCAGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAGCGGCAGCCCGAACCCC
GCCCGCGGCCACAGCGTCTGCTCCACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCTCAGAGTGCATC
GACCCCTCGGTGGTCTTCCCCTACCCTCTCAACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACTCCAGC
GCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCGACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTG
CTCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTGAGGAGGAACAAGAAGATGAGGAAGAAATCGATGTT
GTTTCTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGTCTGGATCACCTTCTGCTGGAGGCCACAGCAAA
CCTCCTCACAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACATCAGCACAACTACGCAGCGCCTCCCTCC
ACTCGGAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGTCCTGAGACAGATCAGCAACAAC
CGAAAATGCACCAGCCCCAGGTCCTCGGACACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCTTGGAGCGC
CAGAGGAGGAACGAGCTAAAACGGAGCTTTTTTGCCCTGCGTGACCAGATCCCGGAGTTGGAAAACAATGAAAAG
GCCCCCAAGGTAGTTATCCTTAAAAAAGCCACAGCATACATCCTGTCCGTCCAAGCAGAGGAGCAAAAGCTCATT
TCTGAAGAGGACTTGTTGCGGAAACGACGAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACTCTTGTGCG
TAAGGAAAAGTAAGGAAAACGATTCCTTCTAACAGAAATGTCCTGAGCAATCACCTATGAACTTGTTTCAAATGC
ATGATCAAATGCAACCTCACAACCTTGGCTGAGTCTTGAGACTGAAAGATTTAGCCATAATGTAAACTGCCTCAA
ATTGGACTTTGGGCATAAAAGAACTTTTTATGCTTACCATCTTTTTTTTTCTTTAACAGATTTGTATTTAAGA
ATTGTTTTTAAAAAATTTTAA

FIGURE 618

MPLNVSFTNRNYDLDYDSVQPYFYCDEEENFYQQQQQSELQPPAPSEDIWKKFELLPTPPLSPSRRSGLCSPSYV
AVTPFSLRGDNDGGGGSFSTADQLEMVTELLGGDMVNQSFICDPDDETFIKNIIIQDCMWSGFSAAAKLVSEKLA
SYQAARKDSGSPNPARGHSVCSTSSLYLQDLSAAASECIDPSVVFPYPLNDSSSPKSCASQDSSAFSPSSDSLLS
STESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEEIDVVSVEKRQAPGKRSESGSPSAGGHSKPPHSPLVLKRC
HVSTHQHNYAAPPSTRKDYPAAKRVKLDSVRVLRQISNNRKCTSPRSSDTEENVKRRTHNVLERQRRNELKRSFF
ALRDQIPELENNEKAPKVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQLRNSCA

FIGURE 619

GTGGAGCCAAGATTTAAACCCACAATCTTAGCCACTAATCTGGGGACAGTGCAGACTACTGAATCCTTGGATGGA
AGACAGACTGAGACCCTATCCAGCTGCTGCCCCATCTCCAAGAGCCTCGCCCTGCTGGAAGTGCACTGCTAGTCT
GGTTCATCAGCCACTCTGCACAGGACCCCTGCCCAGGACCCAGGGTCTGCATTTTAGGCCATCCTTGCTGGATAG
GCCCAGAGCCCAGGGTCCCCACCTGCCTGTAGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNGAATGATGGGGCATGATGAGGAAGAGGCAGAAAATGGGAAGGAAGTATAGGATCAAGA
TGGGGGCATCCTAAGGAGGGGGCAACTGCCAGCCGGTGCCAGCGTGCCTTCCAATATTCAGCCATCTCCTCATGA
AGCCTGGGATGTGATTCTTGTGCCTCTAGCTCTTTCCTGAGGGGCACTGGTACCTCCAGGACCTGGAGTGTACTG
GAAGAAATGGTGCAGTCCAGGTACAGCATGGACCCCAGATCACCCCCACCCCACTCCCTTTCAGTGATTATTGTC
TTATGAACTAGGAGGGGGAGTGGGGCAGAGATGCCTCTTTCATGGCTCCCTGCACACACAGAACCCCTTTGTACT
GGGCACTTCTACTCCCAAGGACCCTGACTTGCACCCAGCAGCTAAGGTCATCTCACCCCCACCTCCCACCTGCCC
CTGGGCCAGCAGGAGGGGCTTGGCCATATGTAGGCGAGACAGGACTTCTTGAAGCTGAAAGATTTCCCACCCCAT
AAAAGAGCCAGAATGTGACAACCAGGAGCGCTGATACCTGGGGAAGGGAGACTGGCTCTGGTCGTGTGATTCCGG
GTTTAGGGCTCTGGGCCATTCCCCCTCAGCCAGCTGGTGACAGAGACTGGCCCACCGCCTGCTGAGAGGGCCATC
TCACCTACAGTGAGAACAGAGCCCCCACCCCAGCCTGGCTTGGACACTCTGAGGATGGGCCCAAGCAGCCACCTA
CCAGGACTCTTGGCCCGGGGCCACACCCAGTGCTGCTAGCAGCCCCACCTTCTCCTGAAGTAGCCAGGTGTGCTC
TGCCTCCAGGGCCTGCAATGGCCCCCCAACACCATCTGCTCTCCCTGCAGATGCTGCAGCTGCTCCAAGCAGGCC
CCTAGTTGCTGGTGGCTCTGGCCCAGCTCTTCTGAGTCTCTTGTTCACCTCAGTGAGTATCAGCAACTGCTCCTG
CAGACGGACTGTGTCCTGAGCCTGGGCAGGGGTCTCAGCTGCTGGCATGGAGACTCTGGGTCCCGAAGCTCCTGG
GCCCTGCCTCCATCCCAGCTCTGCTCTTGGATCTGCAGGCCTGGCACCAGCATCTCCTGTAGATACACTTGGTCC
AGAATCCTGGGGTCTCCTTCCAGCTTCCAGACCACACTGGGGTGGTCTTGGCAGACCGTTGATGCCTCAGGGCAT
GTTGTGGCAGGGTCCTGGCCCCAACTCAAGTTATGACTCTGAACAAGCTCTCCTCTGCTCTCTGGTCTCAGTTTT
CCCATCTGAACCAGGAGGGAAGTCACTGAATGATCCCAGGGTATTCCCAAATGTTGGAAGAGGATCCCTCTCTTG
GCTGGACTAAGCCCCTGCGCTGCCTTCCTTCTCTAGATAATGCTTCAATAATGAGGACCAGAGAATAAAGTGTGG
GGCAGAGTCAAAGGTACAGCAGGGCCAGTGCGCAGGGCCTGCCATGCACCCACTTGGGGGATCCCCAGGCTGGGC
TCTGGGCCAACAGGCTGTTGGGTCATTTGGTCCAAATGCCGCTAGGCCTTTTCCACTTCTGTCTGCAGCAGCAGG
ATCCTGTGGGTAGAAGGG**ATG**GTCTGCCTGTTCCCTGCCACCCCACCCCTCCCCCACAGCCCAGCCCCACTCACT
TGTCTTCTATGTTCTGGTCTGGCCTCCTCCACTCAGCCTGTCCCTGGGATCCCTGCATCTGGTGCCTCTCCTGCT
CCAGGCAGGCCAGGGAGCACTCCACCTGCTAGGAGGAGGCTGAGTGGGAGGGCTGAAGGCAGCACAGAGCCTCAG
ATAGGTAGGGCTAGCTTCCCTGCCTCCCACCAGGCAGGGCAGTGTCTGCAGCCTTTGATAACGCAGGCGGACTGG
CAGCCAG

FIGURE 620

MVCLFPATPPLPHSPAPLTCLLCSGLASSTQPVPGIPASGASPAPGRPGSTPPARRRLSGRAEGSTEPQIGRASF
PASHQAGQCLQPLITQADWQ

FIGURE 621

GTGAGCCGTCTACGAAGCCCGGGCTTGGCCTGGGCGACACTGAGCGGCTTTAACCGGCGGCGTCCAGCCGGCTCC
GCCAGCGCTGCCGCCGCCCTCGAGGCTCCCTCTGACTGAAGGCGCGCTGAGCATCGCGGCATTAGGGGCTCCTGG
TCCCTCAAACATCCAGGGAAGCCATTTTCAGGGACTAGGTACTGACCCCCGCGAGCCGCCACAGCCACAGCCCGC
GCTCCGGGCCGAACGCCCGAGCTCAAGAGCTCCCGAGCTTCCGTCGGGCGGCGGCCTCACAGCTGGGGGCCCTGA
GGCGGAAGGCGCAGCCGCTCAGCTGCGGACCGGGGGCGTGGCGAGGGCGCACAGGTTCTGTTTTCGCCGGCCCG
GGGCCGCTTTCGGTTTCGTTTCCCGCCGGCGTCTCCACCCTGCGAGAGCCGCCCGCCAGCCAGCGTCCGCCGCCG
TCCGCGTCGCGCCACCCGCGGTCCGACGGGAGCAGGCCCAGCGGCC**ATG**GCCCAGGCCGGCGTCGTCGGTGAGGT
CACCCAGGTGCTGTGCGCGGCCGGGGGCGCCCTGGAGTTGCCCGAGCTGCGGCGCCGCTTGCGGATGGGCTTGAG
CGCCGACGCGCTGGAGCGGCTGCTGCGGCAGCGTGGGCGCTTCGTGGTGGCGGTGCGGGCGGGCGGCGCAGCCGC
GGCCCCGGAGCGCGTGGTGCTGGCCGCCTCGCCGCTGCGCCTGTGTCGCGCGCACCAGGGCTCCAAGCCGGGCTG
CGTGGGGCTCTGCGCGCAGCTCCACCTCTGCAGGTTCATGGTCTACGGCGCCTGCAAGTTCCTGAGAGCCGGGAA
GAACTGTAGGAATAGTCACAGCTTGACAACCGAACACAACCTGAGTGTGCTGAGAACTCATGGCGTTGACCACCT
GAGCTATAATGAGCTATGCCAACTCTTGTTTCAGAACGACCCCTGGCTTTTGCCAGAAATTTGCCAACATTACAA
CAAAGGAGATGGACCCCACGGCTCTTGTGCCTTTCAAAAGCAGTGCATCAAGCTCCATATCTGCCAGTATTTTTT
ACAGGGGGAATGCAAGTTTGGCACTAGCTGTAAGAGATCCCATGATTTCTCTAATTCTGAGAATCTGGAAAAATT
GGAGAAGTTGGGTATGAGCTCAGACCTGGTGAGCAGGCTGCCTACCATTTATAGAAATGCACATGACATCAAGAA
TAAGAGCTCTGCCCCCAGCAGAGTGCCTCCTCTTTTGTCCCACAGGGGACTTCTGAAAGAAAAGACAGTTCAGG
TTCTGTGTCCCCAAACACTCTTAGCCAGGAGGAGGGTGATCAGATCTGTTTGTACCATATCCGGAAAAGTTGTAG
CTTTCAAGATAAGTGCCATAGAGTTCATTTCCATTTGCCGTATCGATGGCAATTCTTGGATAGAGGCAAATGGGA
GGATTTGGACAACATGGAACTTATTGAAGAGGCATATTGCAATCCCAAAATAGAAAGGATCCTGTGCTCTGAGTC
AGCCAGTACCTTTCACTCTCATTGTCTGAACTTTAACGCCATGACTTACGGTGCTACCCAGGCTCGCCGCCTCTC
CACGGCCTCCTCTGTCACCAAACCTCCACACTTCATCCTCACCACTGACTGGATTTGGTACTGGAGTGATGAGTT
TGGTTCTTGGCAGGAATATGGAAGACAGGGCACGGTGCACCCTGTGACCACTGTCAGCAGTAGCGACGTGGAGAA
GGCCTACCTGGCCTACTGTACACCGGGGTCTGACGGCCAGGCAGCCACCTTGAAGTTCCAGGCCGGAAAGCACAA
CTACGAGTTAGATTTCAAAGCCTTCGTTCAGAAAAACCTGGTCTATGGCACAACTAAAAAGGTTTGCCGCAGACC
CAAATACGTGTCTCCCCAGGATGTGACGACCATGCAAACCTGCAATACCAAGTTTCCAGGCCCGAAGAGCATCCC
AGACTATTGGGACTCCTCTGCCCTGCCAGACCCAGGCTTTCAGAAGATCACCCTTAGTTCTTCCTCGGAAGAGTA
TCAGAAGGTCTGGAACCTCTTTAACCGCACGCTGCCTTTTTACTTTGTTCAGAAGATTGAGCGAGTACAGAACCT
GGCCCTCTGGGAAGTCTACCAGTGGCAAAAAGGACAGATGCAGAAGCAGAACGGAGGGAAGGCCGTGGACGAGCG
GCAGCTGTTCCACGGCACCAGCGCCATTTTTGTGGACGCCATCTGCCAGCAGAACTTTGACTGGCGGGTCTGTGG
TGTTCATGGCACTTCCTACGGCAAGGGGAGCTACTTTGCCCGAGATGCTGCATATTCCCACCACTACAGCAAATC
CGACACGCAGACCCACACGATGTTCCTGGCCCGGGTGCTGGTGGGCGAGTTCGTCAGGGGCAATGCCTCCTTTGT
CCGTCCACCGGCCAAGGAGGGCTGGAGCAACGCCTTCTATGATAGCTGCGTGAACAGTGTGTCCGACCCCTCCAT
CTTTGTGATCTTTGAGAAACACCAGGTCTACCCAGAGTATGTCATCCAGTACACCACCTCCTCCAAGCCCTCGGT
CACACCCTCCATCCTGCTGGCCTTGGGCTCCCTGTTCAGCAGCCGACAG**TGA**GTGCACAGGAGTGTTCCAGGCCT
TTCACCTGCTCTGCCTTGAAATGGCTATTTGGGCCTTTCCTTTTCTTTTTAAACAGAAACTTTTAATGAACTGTT
CTCTTAACATTGACCTCTCAATGAAGTTATGTTCTTAATCTCTTGCTAATAATGATTTTTACTTTTAAGTCACTT
TTGGGTTCACTAGTGGACTAACCAGAAGTGATTGTAGTTGAGTCCAGTTTTGCTTTTTAATAATGTGTTGAAGTT
TTAGTTTTTACTCTTTGTTGACTTTGCTGCTTATTGGCACCAGGGACAGAGTTTCTAGATACAATTTTATGGATT
GGTTTTAATTTTTATGAGTTTGTCTCTGCAGTGATTCGGTTTCTCAGAGTCTCATGGCATCATAGTTTTTCCAGA
ATGACACAGTAGCCACCGGTGGATGACAGCCCACGGGCGGCACAGTCACTTCTGCCTGTTGCTCTGACACCAACC
CAGGCAGCTCTGCTGTGGCTTCTCCTGGGCTCTGGCATTAGTTGGTCTGTGTCACATTGTCAGAACAGGTGGCTG
CTGTGTGGTGCCATCGAGTCCCTGCTGGTTCCCCTTGTCCTGGGAGGGTCACCCATTGCCCAAGGAAGTGCATCC
ACCTGGCAGGTGACCTGGAGGAGTAGCTTCCCCGAGGACCCCCAGGCTTGGCCTGTGATTGCGCAAACCCACATT
TCCTAAGCACACTGGACACCCTTCGAGTGTGGGTTTTAACATCCCTGTGAGATTGAATACTTGTGCCACACATGT
CACAAAAGAGTATGGAAATAAAAGAAAATTTATCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 622

MAQAGVVGEVTQVLCAAGGALELPELRRRLRMGLSADALERLLRQRGRFVVAVRAGGAAAAPERVVLAASPLRLC
RAHQGSKPGCVGLCAQLHLCRFMVYGACKFLRAGKNCRNSHSLTTEHNLSVLRTHGVDHLSYNELCQLLFQNDPW
LLPEICQHYNKGDGPHGSCAFQKQCIKLHICQYFLQGECKFGTSCKRSHDFSNSENLEKLEKLGMSSDLVSRLPT
IYRNAHDIKNKSSAPSRVPPLFVPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCHRVHFHLPYR
WQFLDRGKWEDLDNMELIEEAYCNPKIERILCSESASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTT
DWIWYWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAYCTPGSDGQAATLKFQAGKHNYELDFKAFVQKNLVY
GTTKKVCRRPKYVSPQDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEEYQKVWNLFNRTLPFYF
VQKIERVQNLALWEVYQWQKGQMQKQNGGKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYFARD
AAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKEGWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVI
QYTTSSKPSVTPSILLALGSLFSSRQ

FIGURE 623

TCCCTTATTCAATCAAAGGTAATGTATATTACTTCCAAAGTATAGGAGTATTAATTTAAGCTGACCAAAAAAAGA
GGACCCAGATACTCGTTTCCAAAGATGTTTTGAATCCACCTATTTCTCAAAAGGCCAAATTTCATTTTACAGCTC
TTGTGAAACCAGGCAAGCAGTGTAAATTTTAAAATGCAGCAGTGGGATATCTTCAAATGTAGCAGTGAGATTTTT
AAAATGTAGTTGTTTCAAAACTGATCAGTGACCGTCTAAAATACGGGCTCCTTGAGGACATCCTGCGCCTGGTTC
ATCCTTTTTGCACTCTCAAAGTCTAGCCTTCCCAG**ATG**GGACCTCAGTCCCAGCCCCCCTACACTGCCATCCCCC
AGATCTTTAGGGCAGTGGGGTTCATTGAACAAGGTTGCAGGCTACAAACTTGGCAAAGTTTATAC**TAA**CACCTCA
TTCCATCCCACCTCCCATCTTAAAAAGGAAACCGTTAAGTATCTTATTCTAGTGACTTCAATAAAGGAACTAATT
TATAAGACAGCCAAGAACAATTAAAGTCATAAAGGGCCAAACATTTTATTTTCATCTAAGAACCGTTTGCAGGGG
TGGTCCGATCTTTTGGCTTCCCTGGGCCACACTAGAACTGTCTTGGGCCACACGTAAAATACATTAACTAGCTGA
TGAGCTTTTTTTTCC

FIGURE 624

MGPQSQPPYTAIPQIFRAVGFIEQGCRLQTWQSLY

FIGURE 625A

GGCCACCGGAGCGGCCCGGCGACGATCGCTGACAGCTTCCCCTGCCCTTCCCGTCGGTCGGGCCGCCAGCCGCCG
CAGCCCTCGGCCTGCACGCAGCCACCGGCCCCGCTCCCGGAGCCCAGCGCCGCCGAGGCCGCAGCCGCCCGGCCA
GTAAGGCGGCGCCGCCCGCGGCCACCGCGGGCCCTGCCGTTCCCTCCGCCGCGCTGCGCCATGGCGCGGCGCTGA
CTGGCCTGGCCCGGCCCCGCCGCGCTCCCGCTCGCCCCGACCCGCACTCGGGCCCGCCCGGGCTCCGGCCTGCCG
CCGCCTCTTCCTTCTCCAGCCGGCAGGCCCCGCCGCTTAGGAGGGAGAGCCCACCCGCGCCAGGAGGCCGAACGC
GGACTCGCCACCCGGCTTCAGA**ATG**GCAGAAGATGATCCATATTTGGGAAGGCCTGAACAAATGTTTCATTTGGA
TCCTTCTTTGACTCATACAATATTTAATCCAGAAGTATTTCAACCACAGATGGCACTGCCAACAGATGGCCCATA
CCTTCAAATATTAGAGCAACCTAAACAGAGAGGATTTCGTTTCCGTTATGTATGTGAAGGCCCATCCCATGGTGG
ACTACCTGGTGCCTCTAGTGAAAAGAACAAGAAGTCTTACCCTCAGGTCAAAATCTGCAACTATGTGGGACCAGC
AAAGGTTATTGTTCAGTTGGTCACAAATGGAAAAAATATCCACCTGCATGCCCACAGCCTGGTGGGAAAACACTG
TGAGGATGGGATCTGCACTGTAACTGCTGGACCCAAGGACATGGTGGTCGGCTTCGCAAACCTGGGTATACTTCA
TGTGACAAAGAAAAAAGTATTTGAAACACTGGAAGCACGAATGACAGAGGCGTGTATAAGGGGCTATAATCCTGG
ACTCTTGGTGCACCCTGACCTTGCCTATTTGCAAGCAGAAGGTGGAGGGGACCGGCAGCTGGGAGATCGGGAAAA
AGAGCTAATCCGCCAAGCAGCTCTGCAGCAGACCAAGGAGATGGACCTCAGCGTGGTGCGGCTCATGTTTACAGC
TTTTCTTCCGGATAGCACTGGCAGCTTCACAAGGCGCCTGGAACCCGTGGTATCAGACGCCATCTATGACAGTAA
AGCCCCCAATGCATCCAACTTGAAAATTGTAAGAATGGACAGGACAGCTGGATGTGTGACTGGAGGGGAGGAAAT
TTATCTTCTTTGTGACAAAGTTCAGAAAGATGACATCCAGATTCGATTTTATGAAGAGGAAGAAAATGGTGGAGT
CTGGGAAGGATTTGGAGATTTTTCCCCCACAGATGTTCATAGACAATTTGCCATTGTCTTCAAAACTCCAAAGTA
TAAAGATATTAATATTACAAAACCAGCCTCTGTGTTTGTCCAGCTTCGGAGGAAATCTGACTTGGAAACTAGTGA
ACCAAAACCTTTCCTCTACTATCCTGAAATCAAAGATAAAGAAGAAGTGCAGAGGAAACGTCAGAAGCTCATGCC
CAATTTTTCGGATAGTTTCGGCGGTGGTAGTGGTGCCGGAGCTGGAGGCGGAGGCATGTTTGGTAGTGGCGGTGG
AGGAGGGGGCACTGGAAGTACAGGTCCAGGGTATAGCTTCCCACACTATGGATTTCCTACTTATGGTGGGATTAC
TTTCCATCCTGGAACTACTAAATCTAATGCTGGGATGAAGCATGGAACCATGGACACTGAATCTAAAAAGGACCC
TGAAGGTTGTGACAAAAGTGATGACAAAAACACTGTAAACCTCTTTGGGAAAGTTATTGAAACCACAGAGCAAGA
TCAGGAGCCCAGCGAGGCCACCGTTGGGAATGGTGAGGTCACTCTAACGTATGCAACAGGAACAAAAGAAGAGAG
TGCTGGAGTTCAGGATAACCTCTTTCTAGAGAAGGCTATGCAGCTTGCAAAGAGGCATGCCAATGCCCTTTTCGA
CTACGCGGTGACAGGAGACGTGAAGATGCTGCTGGCCGTCCAGCGCCATCTCACTGCTGTGCAGGATGAGAATGG
GGACAGTGTCTTACACTTAGCAATCATCCACCTTCATTCTCAACTTGTGAGGGATCTACTAGAAGTCACATCTGG
TTTGATTTCTGATGACATTATCAACATGAGAAATGATCTGTACCAGACGCCCTTGCACTTGGCAGTGATCACTAA
GCAGGAAGATGTGGTGGAGGATTTGCTGAGGGCTGGGGCCGACCTGAGCCTTCTGGACCGCTTGGGTAACTCTGT
TTTGCACCTAGCTGCCAAAGAAGGACATGATAAAGTTCTCAGTATCTTACTCAAGCACAAAAAGGCAGCACTACT
TCTTGACCACCCCAACGGGGACGGTCTGAATGCCATTCATCTAGCCATGATGAGCAATAGCCTGCCATGTTTGCT
GCTGCTGGTGGCCGCTGGGGCTGACGTCAATGCTCAGGAGCAGAAGTCCGGGCGCACAGCACTGCACCTGGCTGT
GGAGCACGACAACATCTCATTGGCAGGCTGCCTGCTCCTGGAGGGTGATGCCCATGTGGACAGTACTACCTACGA
TGGAACCACACCCCTGCATATAGCAGCTGGGAGAGGGTCCACCAGGCTGGCAGCTCTTCTCAAAGCAGCAGGAGC
AGATCCCCTGGTGGAGAACTTTGAGCCTCTCTATGACCTGGATGACTCTTGGGAAAATGCAGGAGAGGATGAAGG
AGTTGTGCCTGGAACCACGCCTCTAGATATGGCCACCAGCTGGCAGGTATTTGACATATTAAATGGGAAACCATA
TGAGCCAGAGTTTACATCTGATGATTTACTAGCACAAGGAGACATGAAACAGCTGGCTGAAGATGTGAAGCTGCA
GCTGTATAAGTTACTAGAAATTCCTGATCCAGACAAAAACTGGGCTACTCTGGCGCAGAAATTAGGTCTGGGGAT
ACTTAATAATGCCTTCCGGCTGAGTCCTGCTCCTTCCAAAACACTTATGGACAACTATGAGGTCTCTGGGGGTAC
AGTCAGAGAGCTGGTGGAGGCCCTGAGACAAATGGGCTACACCGAAGCAATTGAAGTGATCCAGGCAGCCTCCAG
CCCAGTGAAGACCACCTCTCAGGCCCACTCGCTGCCTCTCTCGCCTGCCTCCACAAGGCAGCAAATAGACGAGCT
CCGAGACAGTGACAGTGTCTGCGACACGGGCGTGGAGACATCCTTCCGCAAACTCAGCTTTACCGAGTCTCTGAC
CAGTGGTGCCTCACTGCTAACTCTCAACAAAATGCCCCATGATTATGGGCAGGAAGGACCTCTAGAAGGCAAAAT
T**TAG**CCTGCTGACAATTTCCCACACCGTGTAAACCAAAGCCCTAAAATTCCACTGCGTTGTCCACAAGACAGAAG
CTGAAGTGCATCCAAAGGTGCTCAGAGAGCCGGCCCGCCTGAATCATTCTCGATTTAACTCGAGACCTTTTCAAC
TTGGCTTCCTTTCTTGGTTCATAAATGAATTTTAGTTTGGTTCACTTACAGATAGTATCTAGCAATCACAACACT
GGCTGAGCGGATGCATCTGGGGATGAGGTTGCTTACTAAGCTTTGCCAGCTGCTGCTGGATCACAGCTGCTTTCT

FIGURE 625B

GTTGTCATTGCTGTTGTCCCTCTGC

FIGURE 626

MAEDDPYLGRPEQMFHLDPSLTHTIFNPEVFQPQMALPTDGPYLQILEQPKQRGFRFRYVCEGPSHGGLPGASSE
KNKKSYPQVKICNYVGPAKVIVQLVTNGKNIHLHAHSLVGKHCEDGICTVTAGPKDMVVGFANLGILHVTKKKVF
ETLEARMTEACIRGYNPGLLVHPDLAYLQAEGGGDRQLGDREKELIRQAALQQTKEMDLSVVRLMFTAFLPDSTG
SFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEENGGVWEGFGDF
SPTDVHRQFAIVFKTPKYKDINITKPASVFVQLRRKSDLETSEPKPFLYYPEIKDKEEVQRKRQKLMPNFSDSFG
GGSGAGAGGGGMFGSGGGGGGTGSTGPGYSFPHYGFPTYGGITFHPGTTKSNAGMKHGTMDTESKKDPEGCDKSD
DKNTVNLFGKVIETTEQDQEPSEATVGNGEVTLTYATGTKEESAGVQDNLFLEKAMQLAKRHANALFDYAVTGDV
KMLLAVQRHLTAVQDENGDSVLHLAIIHLHSQLVRDLLEVTSGLISDDIINMRNDLYQTPLHLAVITKQEDVVED
LLRAGADLSLLDRLGNSVLHLAAKEGHDKVLSILLKHKKAALLLDHPNGDGLNAIHLAMMSNSLPCLLLLVAAGA
DVNAQEQKSGRTALHLAVEHDNISLAGCLLLEGDAHVDSTTYDGTTPLHIAAGRGSTRLAALLKAAGADPLVENF
EPLYDLDDSWENAGEDEGVVPGTTPLDMATSWQVFDILNGKPYEPEFTSDDLLAQGDMKQLAEDVKLQLYKLLEI
PDPDKNWATLAQKLGLGILNNAFRLSPAPSKTLMDNYEVSGGTVRELVEALRQMGYTEAIEVIQAASSPVKTTSQ
AHSLPLSPASTRQQIDELRDSDSVCDTGVETSFRKLSFTESLTSGASLLTLNKMPHDYGQEGPLEGKI

FIGURE 627

AGCAAAGTATTCCTGTGTTGCTGGAAGGCAGAGATGCTCTCGTGAGATCCCAGACGGGCTCAGGTAAAACTCTTG
CCTATTGCATCCCTGTGGTCCAGTCCCTTCAAGCA**ATG**GAGTCAAAAATACAGCGCAGTGATGGCCCCTATGCCC
TGGTGCTCGTGCCAACGAGAGAGCTAGCTCTACAAAGCTTTGACACTGTCCAGAAACTGCTTAAGCCTTTCACCT
GGATTGTGCCTGGAGTGTTAATGGGAGGAGAGAAGAGAAAATCAGAAAAGGCCAGACTCCGCAAAGGAATAAATA
TCCTTATCTCAACTCCTGGACGCCTGGTGGATCATATAAAATCCACAAAGAACATTCATTTTAGTCGGCTGCGGT
GGTTGGTGTTTGATGAAGCAGACAGAATCTTGGATTTGGGTTTTGAAAAGGACATCACAGTGATACTTAATGCTG
TAAATGCTGAATGCCAAAAACGACAGAATGTCTTGCTATCAGCGACACTCACAGAAGGTGTAACGCGGCTAGCTG
ATATCAGTTTGCATGATCCAGTCAGTATTTCTGTCCTGGACAAGAGCCATGACCAGTTGAACCCAAAGGACAAAG
CGGTCCAGGAGGTCTGTCCTCCACCAGCTGGCGACAAGCTGGACAGCTTTGCAATACCAGAGAGTCTCAAGCAGC
ATGTGACTGTGGTTCCCAGCAAACTGAGGCTCGTCTGCCTAGCGGCCTTCATCCTTCAGAAATGCAAGTTTGAGG
AAGACCAGAAGATGGTTGTCTTTTTCTCAAGTTGCGAGCTGGTGGAGTTCCACTACAGCCTCTTCCTACAGACCC
TGCTGAGCAGCTCAGGGGCGCCGGCATCAGGGCAGTTGCCATCTGCCTCCATGCGATTAAAATTCCTACGGCTGC
ATGGCGGCATGGAGCAGGAGGAAAGAACAGCAGTGTTTCAGGAATTTTCACATTCCAGAAGAGGCGTCCTTCTTT
GCACGGATGTTGCAGCTCGGGGCTTAGATCTCCCTCAAGTCACGTGGATTGTTCAGTACAACGCTCCATCTTCAC
CTGCAGAATACATCCACCGGATTGGAAGAACCGCCCGGATTGGCTGCCATGGGAGCAGCCTGCTCATTTTGGCTC
CTTCGGAGGCAGAATATGTCAACTCGTTGGCTTCTCACAAAATCAACGTTTCTGAGATTAAGATGGAAGATATTT
TGTGTGTTCTGACAAGAGATGATTGTTTTAAAGGGAAACGATGGGGAGCCCAGAAATCCCATGCTGTTGGCCCCC
AGGAAATCCGAGAGCGAGCCACAGTCTTGCAGACGGTATTTGAAGATTACGTGCACTCCAGTGAGAGGAGGGTCT
CCTGGGCAAAGAAAGCTCTGCAGTCCTTCATCCAAGCCTACGCCACCTACCCCAGGGAGCTGAAGCACATCTTCC
ACGTCCGATCCCTCCACCTTGGGCATGTGGCGAAGAGCTTCGGACTAAGAGATGCCCCCAGGAATCTTAGTGCCT
TGACTAGAAAGAAGAGGAAAGCACACGTGAAAAGGCCTGACCTTCATAAGAAGACCCAGAGTAAACACAGCCTCG
CTGAAATCCTACGTTCGGAATACTCAAGCGGCATGGAGGCCGACATCGCCAAGGTCAAAAAGCAAAACGCACCTG
GAGAGCCTGGTGGCCGGCCCCTGCAGCACAGTCTGCAGCCGACACCCTGCTTTGGCCGTGGGAAAACATTAAAAT
GGAGAAAAACCCAAAAAGGTGTACAGCGGGACAGCAAGACTTCCCAGAAAGTT**TAA**AATCTCTCTGGGTCTTCGA
GTGGAACCTGGAAGCCCCGGGTGGCAGTGGATTGATGTCCAGTTCTTGTCAGAGGAGGCTTGTGAAAAATAACTG
CGCCTTTGCCTGAATACCACGTCCCCAAGAATCAGAGGGGCCACAGCCCTTCTCCTCCATGGGAGGCCCTGGAGC
CTGATAGAAATCAGTGGTGTGGGGCACTGTAGAGACTAGCCAGCTCCCGACGGAAGGGGTCTGTGTCTTGTATTG
ATCCCATCAGTGCCCGGCACTCCCTTCACCCAGGTGCTGACGTGCCGGGGTTGAGCTGGCACCCCGGGATGTGAT
GTAAGAACGCCCTGCGCGTCAGCCTGGAACGGGCTTGATTGCTGCCCTTAACTGTGTTCTGAAGTTTCACAGCTT
GGCTTCAGCCTATCAGCGCATACATTGGCATGAATTTTGTGAATTAGGGTGTTAAAAACTGGAATTGAATTTGTA
CAAAAAGAGAATATATTTATCACTAATTATTTTCTTAATGTAGGAATGTACCGTTAAAAAGGACCAAAAGTTTTT
GGTCTGGGTCAAAAAATACGAATGTGTTCTC

FIGURE 628

MESKIQRSDGPYALVLVPTRELALQSFDTVQKLLKPFTWIVPGVLMGGEKRKSEKARLRKGINILISTPGRLVDH
IKSTKNIHFSRLRWLVFDEADRILDLGFEKDITVILNAVNAECQKRQNVLLSATLTEGVTRLADISLHDPVSISV
LDKSHDQLNPKDKAVQEVCPPPAGDKLDSFAIPESLKQHVTVVPSKLRLVCLAAFILQKCKFEEDQKMVVFFSSC
ELVEFHYSLFLQTLLSSSGAPASGQLPSASMRLKFLRLHGGMEQEERTAVFQEFSHSRRGVLLCTDVAARGLDLP
QVTWIVQYNAPSSPAEYIHRIGRTARIGCHGSSLLILAPSEAEYVNSLASHKINVSEIKMEDILCVLTRDDCFKG
KRWGAQKSHAVGPQEIRERATVLQTVFEDYVHSSERRVSWAKKALQSFIQAYATYPRELKHIFHVRSLHLGHVAK
SFGLRDAPRNLSALTRKKRKAHVKRPDLHKKTQSKHSLAEILRSEYSSGMEADIAKVKKQNAPGEPGGRPLQHSL
QPTPCFGRGKTLKWRKTQKGVQRDSKTSQKV

FIGURE 629

AGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCAGCAGCAGCAGCAGCAGGAGAC
CTTCTCTG**ATG**GATGACCTCTGTGAAGCAAATGGCACTTTTGCCATCAGCTTATTTAAAATATTGGGGGAAGAGG
ACAACTCAAGAAACGTATTCTTCTCTCCCATGAGCATCTCCTCTGCCCTGGCCATGGTCTTCATGGGGGCAAAGG
GAAGCACTGCAGCCCAGATGTCCCAGGCACTTTGTTTATACAAAGACGGAGATATTCACCGAGGTTTCCAGTCAC
TTCTCAGTGAAGTTAACAGAACTGGCACTCAGTACTTGCTTAGAACTGCCAACAGACTCTTTGGAGAAAAGACGT
GTGATTTCCTTCCAGACTTTAAAGAATACTGTCAGAAGTTCTATCAGGCAGAGCTGGAGGAGTTGTCCTTTGCTG
AAGACACTGAAGAGTGCAGGAAGCATATAAATGACTGGGTGGCAGAGAAGACTGAAGGTAAGATTTCAGAGGTAC
TGGATGCTGGGACAGTCGATCCCCTGACAAAGCTAGTCCTTGTGAATGCCATTTATTTCAAGGGAAAGTGGAATG
AGCAATTTGACAGAAAGTACACAAGGGGAATGCTCTTTAAAACCAACGAGGAAAAAAAGACAGTGCAGATGATGT
TTAAGGAAGCTAAGTTTAAAATGGGGTATGCGGATGAGGTACACACCCAGGTCCTGGAGCTGCCCTATGTGGAAG
AGGAGCTGAGCATGGTCATTCTGCTTCCCGATGACAACACGGACCTCGCCGTGGTGGAAAAAGCACTTACATATG
AGAAATTCAAAGCCTGGACAAATTCAGAAAAGTTGACAAAAAGTAAGGTTCAAGTTTTCCTTCCCAGATTAAAGC
TGGAGGAGAGTTATGACTTGGAGCCTTTCCTTCGAAGATTAGGAATGATCGATGCTTTTGACGAAGCCAAGGCAG
ACTTTTCTGGAATGTCAACTGAGAAGAATGTGCCTCTGTCCAAGGTTGCCCACAAGTGCTTCGTGGAGGTCAATG
AGGAAGGCACAGAGGCTGCCGCAGCCACTGCTGTGGTCAGGAATTCCCGGTGCAGCAGAATGGAGCCAAGATTCT
GTGCAGACCACCCTTTTCTTTTCTTCATCAGGCGCCACAAAACCAACTGCATCTTGTTCTGTGGCAGGTTCTCTT
CTCCG**TAA**AGAGGAGCAATTGCTGTACATACCCTCCTTTCCTTCTACCTATCTTGCCTTAATTAACATTCCCTGT
GACCTAGTTGGTGCAGTGGCTTGAATGCCAAAATAAAGCGTGTGCACTGG

FIGURE 630

MDDLCEANGTFAISLFKILGEEDNSRNVFFSPMSISSALAMVFMGAKGSTAAQMSQALCLYKDGDIHRGFQSLLS
EVNRTGTQYLLRTANRLFGEKTCDFLPDFKEYCQKFYQAELEELSFAEDTEECRKHINDWVAEKTEGKISEVLDA
GTVDPLTKLVLVNAIYFKGKWNEQFDRKYTRGMLFKTNEEKKTVQMMFKEAKFKMGYADEVHTQVLELPYVEEEL
SMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLTKSKVQVFLPRLKLEESYDLEPFLRRLGMIDAFDEAKADFS
GMSTEKNVPLSKVAHKCFVEVNEEGTEAAAATAVVRNSRCSRMEPRFCADHPFLFFIRRHKTNCILFCGRFSSP

FIGURE 631

AAATCAGTTTTCTCCACCTGCACCACTGCATAGCACAGATACAGAAACCATCCTATTTCAGGATTTGAATGCAAA
ACTTACCTTCTTACTCTAAAG**ATG**AATGATCAGGGAGAGATTTATTCAACCCTGAGATTTTTGCAGTCTCCTTCA
GAGTCACAGAATAGATTAAGGCCTGATGATACTCAAAGGCCTGGGAAAACTGATGACAAAGAATTTTCAGTGCCC
TGGCACCTCATTGCAGTGACTCTTGGGATCCTCTGTTTACTTCTTCTGATGATAGTCACAGTGTTGGTGACAAAT
ATCTTTCAGTGTATTCAAGAAAAACATCAACGGCAGGAAATTCTAAGAAACTGTAGTGAAAAGTACATCATGCAA
AATGACAACTACTTAAAAGAGCAGATTTTGACAAATAAGACTTTAAAATATGACGTTCTCAAAAATAGCTTTCAG
CAGAAAAAGGAACTGGATTCACGCCTTATACAAAAGAACAGATGTCATAGAGAAAATGAGATCGTTTTTAAAGTT
TTGCAAAATACAGGCAAATTCTCTGAAGACCACGGGTCCTGTTGTGGAGTAAACTGTTATTATTTTACCATGCAG
AAGAAAGACTGGAAGGGATGTAAACAGACTTGTCAACATTGTAGATCATCCCTTTTGAAGATAGATGACAAAGAT
GAACTCGTATTTTACATTCACTTTTATTCTCTTGGACTCTGTTTCTCAATGTTGGACCTAAGATAT**TGA**AGACAG
GCTGGAGTCCAGAGCCTTCATTCAATCTCAGATTTATGAAAATAATTACTGGATCGGATTATCATATGATGAAAG
GGAAAGTAAGTGGAAATGGATTGATAATGGCACATCTCCTGGAATTAATTCTACAATAATGCGTTTTTCTTCTGG
GAGAGGAGAATGTGCATTTTTGACCTCAACAAGAATGGCAACTATTGATTGCATTCAAACGTACAATTGTATCTG
TGGGAAGAGAATAGACTCTATTTTCTCTGATTCGGTGTGCGCCAAGAAGAAAAGGTGAAAATGGAATGTTTTCTT
TTTTTGTTTCCCATAATAATTTCTGATTATAAATCATTGCTTTTAACTGTGGGACTTAGTTAATTCTTCAAAAGA
TAAAGATGAACAGGAAGAAAAAGAAAATTATTTTGGACTATGACTTTAAAGATCAGATGCCATCTTTCTTCCTGG
AGAAGAGGAGATTTTCTCTTTTGAGAGTGGTTGTTCCTTCCTT

FIGURE 632

MNDQGEIYSTLRFLQSPSESQNRLRPDDTQRPGKTDDKEFSVPWHLIAVTLGILCLLLLMIVTVLVTNIFQCIQE
KHQRQEILRNCSEKYIMQNDNYLKEQILTNKTLKYDVLKNSFQQKKELDSRLIQKNRCHRENEIVFKVLQNTGKF
SEDHGSCCGVNCYYFTMQKKDWKGCKQTCQHCRSSLLKIDDKDELVFYIHFYSLGLCFSMLDLRY

FIGURE 633

CGAGTAAAGTTTGCAAAGAGGCGCGGGAGGCGGCAGCCGCAGCGAGGAGGCGGCGGGGAAGAAGCGCAGTCTCCG
GGTTGGGGGCGGGGGCGGGGGGGGCGCCAAGGAGCCGGGTGGGGGGCGGCGGCCAGC**ATG**CGGCCCCGCAGCGCC
CTGCCCCGCCTGCTGCTGCCGCTGCTGCTGCTGCCCGCCGCCGGGCCGGCCCAGTTCCACGGGGAGAAGGGCATC
TCCATCCCGGACCACGGCTTCTGCCAGCCCATCTCCATCCCGCTGTGCACGGACATCGCCTACAACCAGACCATC
ATGCCCAACCTTCTGGGCCACACGAACCAGGAGGACGCAGGCCTAGAGGTGCACCAGTTCTATCCGCTGGTGAAG
GTGCAGTGCTCGCCCGAACTGCGCTTCTTCCTGTGCTCCATGTACGCACCCGTGTGCACCGTGCTGGAACAGGCC
ATCCCGCCGTGCCGCTCTATCTGTGAGCGCGCGCGCCAGGGCTGCGAAGCCCTCATGAACAAGTTCGGTTTTCAG
TGGCCCGAGCGCCTGCGCTGCGAGCACTTCCCGCGCCACGGCGCCGAGCAGATCTGCGTCGGCCAGAACCACTCC
GAGGACGGAGCTCCCGCGCTACTCACCACCGCGCCGCCGCCGGGACTGCAGCCGGGTGCCGGGGGCACCCCGGGT
GGCCCGGGCGGCGGCGGCGCTCCCCCGCGCTACGCCACGCTGGAGCACCCCTTCCACTGCCCGCGCGTCCTCAAG
GTGCCATCCTATCTCAGCTACAAGTTTCTGGGCGAGCGTGATTGTGCTGCGCCCTGCGAACCTGCGCGGCCCGAT
GGTTCCATGTTCTTCTCACAGGAGGAGACGCGTTTCGCGCGCCTCTGGATCCTCACCTGGTCGGTGCTGTGCTGC
GCTTCCACCTTCTTCACTGTCACCACGTACTTGGTAGACATGCAGCGCTTCCGCTACCCAGAGCGGCCTATCATT
TTTCTGTCGGGCTGCTACACCATGGTGTCGGTGGCCTACATCGCGGGCTTCGTGCTCCAGGAGCGCGTGGTGTGC
AACGAGCGCTTCTCCGAGGACGGTTACCGCACGGTGGTGCAGGGCACCAAGAAGGAGGGCTGCACCATCCTCTTC
ATGATGCTCTACTTCTTCAGCATGGCCAGCTCCATCTGGTGGGTCATCCTGTCGCTCACCTGGTTCCTGGCAGCC
GGCATGAAGTGGGGCCACGAGGCCATCGAGGCCAACTCTCAGTACTTCCACCTGGCCGCCTGGGCCGTGCCGGCC
GTCAAGACCATCACCATCCTGGCCATGGGCCAGATCGACGGCGACCTGCTGAGCGGCGTGTGCTTCGTAGGCCTC
AACAGCCTGGACCCGCTGCGGGGCTTCGTGCTAGCGCCGCTCTTCGTGTACCTGTTCATCGGCACGTCCTTCCTC
CTGGCCGGCTTCGTGTCGCTCTTCCGCATCCGCACCATCATGAAGCACGACGGCACCAAGACCGAAAAGCTGGAG
CGGCTCATGGTGCGCATCGGCGTCTTCTCCGTGCTCTACACAGTGCCCGCCACCATCGTCATCGCTTGCTACTTC
TACGAGCAGGCCTTCCGCGAGCACTGGGAGCGCTCGTGGGTGAGCCAGCACTGCAAGAGCCTGGCCATCCCGTGC
CCGGCGCACTACACGCCGCGCATGTCGCCCGACTTCACGGTCTACATGATCAAATACCTCATGACGCTCATCGTG
GGCATCACGTCGGGCTTCTGGATCTGGTCGGGCAAGACGCTGCACTCGTGGAGGAAGTTCTACACTCGCCTCACC
AACAGCCGACACGGTGAGACCACCGTG**TGA**GGGACGCCCCCAGGCCGGAACCGCGCGGCGCTTTCCTCCGCCCGG
GGTGGGGCCCCTACAGACTCCGTATTTTATTTTTTTAAATAAAAAACGATCGAAACCATTTCACTTTTAGGTTGC
TTTTTAAAAGAGAACTCTCTGCCCAACACCCCC

FIGURE 634

MRPRSALPRLLLPLLLLPAAGPAQFHGEKGISIPDHGFCQPISIPLCTDIAYNQTIMPNLLGHTNQEDAGLEVHQ
FYPLVKVQCSPELRFFLCSMYAPVCTVLEQAIPPCRSICERARQGCEALMNKFGFQWPERLRCEHFPRHGAEQIC
VGQNHSEDGAPALLTTAPPPGLQPGAGGTPGGPGGGGAPPRYATLEHPFHCPRVLKVPSYLSYKFLGERDCAAPC
EPARPDGSMFFSQEETRFARLWILTWSVLCCASTFFTVTTYLVDMQRFRYPERPIIFLSGCYTMVSVAYIAGFVL
QERVVCNERFSEDGYRTVVQGTKKEGCTILFMMLYFFSMASSIWWVILSLTWFLAAGMKWGHEAIEANSQYFHLA
AWAVPAVKTITILAMGQIDGDLLSGVCFVGLNSLDPLRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGT
KTEKLERLMVRIGVFSVLYTVPATIVIACYFYEQAFREHWERSWVSQHCKSLAIPCPAHYTPRMSPDFTVYMIKY
LMTLIVGITSGFWIWSGKTLHSWRKFYTRLTNSRHGETTV

FIGURE 635

CGGGCGCGGGGCTTTTGCTGACCGCCGTGTCCCCCAGGCCGGCGCGACCGTGCCCCTGGAGGTGGTGCTGCTGCG
CAAGGTGGGCGCGGCGGGCGGCGCGCGCGGCGTCATCCGCCTGCTGGACTGGTTCGAGCGGCCCGACGGCTTCCT
GCTGGTGCTGGAGCGGCCCGAGCCGGCGCAGGACCTCTTCGACTTTATCACGGAGCGCGGCGCCCTGGACGAGCC
GCTGGCGCGCCGCTTCTTCGCGCAGGTGCTGGCCGCCGTGCGCCACTGCCACAGCTGCGGGGTCGTGCACCGCGA
CATTAAGGACGAAAATCTGCTTGTGGACCTGCGCTCCGGAGAGCTCAAGCTCATCGACTTCGGTTCGGGTGCGCT
GCTCAAGGACACGGTCTACACCGACTTCGACGGCACCCGAGTGTACAGCCCCCCGGAGTGGATCCGCTACCACCG
CTACCACGGGCGCTCGGCCACCGTGTGGTCGCTGGGCGTGCTTCTCTACGATATGGTGTGTGGGGACATCCCCTT
CGAGCAGGACGAGGAGATCCTCCGAGGCCGCCTGCTCTTCCGGAGGAGGGTCTCTCCAGAGCGGCCGTCGCTGGA
TCAGATTGCGGCCCATCCCTGGATGCTGGGGGCTGACGGGGGCGTCCCGGAGAGCTGTGACCTGCGGCTGTGCAC
CCTCGACCCTGATGACGTGGCCAGCACCACGTCCAGCAGCGAGAGCTTGTGAGGAGCTGCACCTGACTGGGAGC**T**
AGGGGACCACCTGCCTTGGCCAGACCTGGGACGCCCCCAGACCCTGACTTTCTCCTGCGTGGGCCGTCTCCTCCT
GCGGAAGCAGTGACCTCTGACCCCTGGTGACCTTCGCTTTGAGTGCCTTTTGAACGCTGGTCCCGCGGGACTTGG
TTTTCTCAAGCTCTGTCTGTCCAAAGACGCTCCGGTCGAGGTCCCGCCTGCCCTGGGTGGATACTTGAACCCCAG
ACGCCCCTCTGTGCTGCTGTGTCCGGAGGCGGCCTTCCCATCTGCCTGCCCACCCGGAGCTCTTTACGCCGGCGC
AGGGTCCCAAGCCCACCTCCCGCCCTCAGTCCTGCGGTGTGCGTCTGGGCACGTCCTGCACACACAATGCAAGTC
CTGGCCTCCGCGCCCGCCCGCCCACGCGAGCCGTACCCGCCGCCAACTCTGTTATTTATGGTGTGACCCCTGGAG
GTGCCCTCGGCCCACCGGGGCTATTTATTGTTTAATTTATTTGTTGAGGTTATTTCCTCTGAGCAGTCTGCCTCT
CCCAAGCCCCAGGGGACAGTGGGGAGGCAGGGGAGGGGGTGGCTGTGGTCCAGGGACCCCAGGCCCTGATTCCTG
TGCCTGGCGTCTGTCCCGGCCCCGCCTGTCAGAAGATGAACATGTATAGTGGCTAACTTAAGGGGAGTGGGTGAC
CCTGACACTTCCAGGCACTGTGCCCAGGGTTTGGGTTTTAAATTATTGACTTTGTACAGTCTGCTTGTGGGCTCT
GAAAGCTGGGGTGGGGCCAGAGCCTGAGCGTTTAATTTATTCAGTACCTGTGTTTGTGTGAATGCGGTGTGTGCA
GGCATCGCAGATGGGGGTTCTTTCAGTTCAAAAGTGAGATGTCTGGAGATCATATTTTTTTATACAGGTATTTCA
ATTAAAATGTTTTTGTACATAGTGG

FIGURE 636

GAGLLLTAVSPRPARPCPWRWCCCARWARRAARAASSACWTGSSGPTASCWCWSGPSRRRTSSTLSRSAAPWTSR
WRAASSRRCWPPCATATAAGSCTATLRTKICLWTCAPESSSSSTSVRVRCSRTRSTPTSTAPECTAPRSGSATTA
TTGARPPCGRWACFSTIWCVGTSPSSRTRRSSEAACSSGGGSLQSGRRWIRLRPIPGCWGLTGASRRAVTCGCAP
STLMTWPAPRPAARACEELHLTGS

FIGURE 637

ATGCTAGACAAGGTACT**ATG**CCTGTATCTCTGCTGAAGGCTCATGAAGCTGAAATGTGGGAAGTTCACTTTCACC
CATCCAACCCAGAACATCTTTTTACCTGCTCTGAAGATGGATCCCTCTGGCACTGGGATGCTTCCACAGATGTAC
CTGAAAAGTCGTCACTCTTTCACCAAGGAGGAAGAAGCAGTACTTTTTTGTCTCATAGCATTAGTAACCAAGCTA
ATGTTCACCAGTCTGTCATTAGCTCCTGGCTCAGCACTGATCCTGCAAAAGACCGAATTGAAATCACAAGCTTAC
TTCCCAGTAGGTCTCTGTCTGTGAACACTTTGGATGTTTTAGGTCCTTGTCTTGTTTGTGGAACCGATGCAGAAG
CAATTTATGTTACTAGACATCTTTTTTCG**TAG**AAGTACTATAATTATAAGATTTCAGATAGAACATGCAATTAGC
CTTTTGAAATCCAGCTTCTGTGCAAAATTTTAGTATCAGAAAATACGAGATTTGCAGGGGAAACATCAGTAAACT
ACCATTAATGTCAATGCCCAGTTTTGACTTTTGTTAGCCTGACACTCCCAAACAGTTGTAGAATCCGATAGATGA
CTGATGGCAAAAGATTGTGAACATGTGGAAGAAAATCAGTGGGATTCTGGTGCTGATGAATAGGTTGCCTTCAGA
GTATTATTGACAGACAGCTTGTGGAACTAATTCTTTATTTTTGATGTTGTGGGAATTAACACATCAATGGTGGTT
ATGGGAACTACCAATGGGTTCCTACAATTTTTATCAGTAGTATGTGGCATATACACCTTCCTAGTGGCAGTTGCC
AATGTTAATGATTATTCTTTTTATTGCAAGTATTTCCTATGATCCTTCCACACTTTATTTCCTTAATAATAATAA
ACTTTTTCAGAAAGAATTGAGTAGAGCAAAAATGACAAAGATGTGTAGCTGTGTTCAATTTTTTTTTTTTTTTTT
TTTGAGGCAGAGTCTTGCTCTGCTGGAGTGCGGTGGTGCAATCTCGGCTCACTGCAACCTCCACCTCCCAGGTTC
AAGCAATTCTCCTGCCTCAGTCTCCTGAGTAGCTGGAACTACAGGTGTGCGCCACCACGCCCAGCTAATTTTTGT
AATTTTAGTAGAGACAGAGTTTCACCATGTTGGCCAGGATGGTCTCGATCTCTTGACCTCATGATCCACCCGCCT
CGACCTCCCAAAGTGCTGTGATTACAGGTGTGAGCCACTGCACCCGGCCTGAAATTTTTTTAAGGTGAAAATGTT
TTGACAAGTTCCTTTTTCAGAATAGGTTTTTGAGCAGAACTCTTTCAGCTTGTTAGACCCAACTTTGCTTTTGTT
TAGCTTCACAGCATAGCTGAAAGTTGCCAAACTGGACATTGTGCAATAAAGTAGAATTCTATATTGATAAGCAAA
CTATTTCCAAACTAAAAATGTGATAGATAAAAGTGTGATTAATCAAATGATATGATCAGAGTAAAGAATTTTGCC
ATTTTGATCCTTTTACTTTGTTTTAGCCACCTATAGTGTTACCAACCATCTTTATCCTTGTCTGCAGGGATAATA
ATGAACTAATGTAGTGTTTTAAGATAATTTAATGATACTATCTTTCCAAACTTTGTTAGATTTTAAATGTATTAT
TGACCTGAGACCTTAATGACAAATCACTGCTATTAGACAATTGAAGTGTTCATTTACTTTGTAATTCCAATAATC
ATAGTTATGGAATTATGGTAAGGTTTTGCTTTTCTGTCCTAATAAATATATATATTTTTTGAGATGGAGTTTTGC
TCTTGTTGCTGAGGCAGGAGAGTTGCTCGAGCCCGGGAGGCAGAGGTTGCAGTGACCCAGGATCGTGCCACTTCA
CTCCAGCCTGGGCAAAAGAGCAAAACGCCATCTCAAAAAATATACATATATAAGGAGATAAAGTTTCCCATTTTC
CAATACAGTTTCACATTTGAACAGCCCTAATTGATACAACTTTATGGCAGGGTTTTAGTGTGTGAGTGGGATCCA
AAACACTCAATCCTGTAAAAGGGTACAGTCCTATTGTATGTTAGTTAACACACTGATGATGTGAGCCTGTGAGAT
GAGCCAATCACCAGTTGTTATGTTCGAATCTGCTTTGTGTTGGGACGCTTTAATGTAGGGTTTCACTAAATAAAT
GAATTTTCATATACTGAACTG

FIGURE 638

MPVSLLKAHEAEMWEVHFHPSNPEHLFTCSEDGSLWHWDASTDVPEKSSLFHQGGRSSTFLSHSISNQANVHQSV
ISSWLSTDPAKDRIEITSLLPSRSLSVNTLDVLGPCLVCGTDAEAIYVTRHLFS

FIGURE 639

GTGCTTTACTGCGCGCTCTGGTACTGCTGTGGCTCCCCGTCCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCT
CCCCGCACAGCCTACTGATTCCCCTGCCGCCCTTGCTCACCTCCTGCTCGCC**ATG**GAGTCGCTGGTTTTCGCGCG
GCGCTCCGGCCCCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGGCTGATCAAGTCGCCCAAGCC
CCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAGCACAACCTGCGGCACCGCTACGAGTTCCTGGAGAC
CCTGGGCAAAGGCACCTACGGGAAGGTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAAT
CCGGAAGGACAAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCACTCAA
CCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTGATCGTCATGGAGTATGCCAG
CCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAGCTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCA
GATCGTCTCTGCCGTGCACTATTGCCATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTT
GGATGCCAATGGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTGCAGAC
ATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCCAGAGGTGGACAG
CTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGCACCATGCCCTTTGATGGGCATGACCATAAGATCCT
AGTGAAACAGATCAGCAACGGGGCCTACCGGGAGCCACCTAAACCCTCTGATGCCTGTGGCCTGATCCGGTGGCT
GTTGATGGTGAACCCCACCCGCCGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCTACGC
CACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGTGACTCTGCCCGCGCCTCCATGGC
TGACTGGCTCCGGCGTTCCTCCCGCCCCCTCCTGGAGAATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGC
ACCTGGTGGGGGAAGCACCACCCCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACAT
GGCCCAGTCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAGCTGCCAAA
GGGCATTCTCAAGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTACAGGAGGACCCTCCGGAGCTCAGCCCAATCCC
TGCGAGCCCAGGGCAGGCTGCCCCGCTGCTCCCCAAGAAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGG
CTACTACTCCTCTCCCGAGCCCAGTGAATCTGGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGAGTGGGGATCC
CAAGGAGCAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACTCAATGGCAAGTT
CTCCCAGACAGCCTTGGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGATGAACTCGCCCCACCTCGCCCCCT
GGCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAGGACAGCATCCTGTCCTCTGAGTCCTTTGACCAGCTGGA
CTTGCCTGAACGGCTCCCAGAGCCCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCC
CCCCTCAGAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGAC
AGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCAAAGCTCACC**TGA**GTGGAGTAGGC
ATTGCCCCAGCCCGGTCAGGCTCTCAGATGCAGCTGGTTGCACCCCGAGGGGAGATGCCTTCTCCCCCACCTCCC
AGGACCTGCATCCCAGCTCAGAAGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAG
GCAAATGAAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGAGAGGGGAA
CGGGAATGCCCGCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGGGGGGCCACAGAGACCTGGAAAGAGA
ACTCTCCCAGGGCCCATCTCCTGCATCCCATGAATACTCTGTACACATGGTGCCTTCTAAGGACAGCTCCTTCCC
TACTCATTCCCTGCCCAAGTGGGGCCAGACCTCTTTACACACACATTCCCGTTCCTACCAACCACCAGAACTGGA
TGGTGGCACCCCTAATGTGCATGAGGCATCCTGGGAATGGTCTGGAGTAACGCTTCGTTATTTTTATTTTTATTT
TTATTTATTTATTTATTTTTTTGAGACGGAGTTTCGCTCTTGGTGCCCAGGCTAGAGTGCAATGGCGCGATCTCA
GCTCACCTCAACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCTAGTAGCTGGGATTACAGGC
GCCCGCCACCATGCCCGGCTAATTTTGTATTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCA
AACTCCCGACCTCAGGTGATCCACCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCC
CACCTAACCCTTCCTTATTTAGCCTAGGAGTAAGAGAACACAATCTCTGTTTCTTCAATGGTTCTCTTCCCTTTT
CCATCCTCCAAACCTGGCCTGAGCCTCCTGAAGTTGCTGCTGTGAATCTGAAAGACTTGAAAAGCCTCCGCCTGC
TGTGTGGACTTCATCTCAAGGGGCCCAGCCTCCTCTGGACTCCACCTTGGACCTCAGTGACTCAGAACTTCTGCC
TCTAAGCTGCTCTAAAGTCCAGACTATGGATGTGTTCTCTAGGCCTTCAGGACTCTAGAATGTCCATATTTATTT
TTATGTTCTTGGCTTTGTGTTTTAGGAAAAGTGAATCTTGCTGTTTTCAATAATGTGAATGCTATGTTCTGGGAA
AATCCACTATGACATCTAAGTTTTGTGTACAGAGAGATATTTTTGCAACTATTTCCACCTCCTCCCACAACCCCC
CACACTCCACTCCACACTCTTGAGTCTCTTTACCTAATGGTCTCTACCTAATGGACCTCCGTGGCCAAAAAGTAC
CATTAAAACCAGAAAGGTGATTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 640

MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKARESSG
RLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERQQLSER
EARHFFRQIVSAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKP
YTGPEVDSWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASH
WWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQHAPGGGSTTPGLERQHSLK
KSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVSASAEGVQEDPPELSPIPASPGQAAPLLPKKGILK
KPRQRESGYYSSPEPSESGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLD
ELAPPRPLARASRPSGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPL
GDSCFSLTDCQEVTATYRQALRVCSKLT

FIGURE 641

GTTTTCTACTTTGCCCGCCCACAGATGTAGTTTTCTCTGCGCGTGTGCGTTTTCCCTCCTCCCCCGCCCTCAGGG
TCCACGGCCACCATGGCGTATTAGGGGCAGCAGTGCCTGCGGCAGCATTGGCCTTTGCAGCGGCGGCAGCAGCAC
CAGGCTCTGCAGCGGCAACCCCCAGCGGCTTAAGCCATGGCGTGAGTACCGGGGCGGGTCGTCCAGCTGTGCTCC
TGGGGCCGGCGCGGGTTTTGGATTGGTGGGGTGCGGCCTGGGGCCAGGGCGGTGCCGCCAAGGGGGAAGCGATTT
AACGAGCGCCCGGGACGCGTGGTCTTTGCTTGGGTGTCCCCGAGACGCTCGCGTGCCTGGGATCGGGAAAGCGTA
GTCGGGTGCCCGGACTGCTTCCCCAGGAGCCCTACAGCCCTCGGACCCCGAGCCCCGCAAGGTCCCAGGGGTCTT
GGCTGTTGCCCCACGAAACGTGCAGGAACCAAGATGGCGGCGGCAGGGCGGCGGCGCGGGCGTGAGTCAAGGGCG
GGCGGTGGGCGGGGCGCGGCCGCTGGCCGTATTTGGACGTGGGGACGGAGCGCTTTCCTCTTGGCGGCCGGTGGA
AGAATCCCCTGGTCTCCGTGAGCGTCCATTTTGTGGAACCTGAGTTGCAAGCAGGGAGGGGCAAATACAACTGCC
CTGTTCCCGATTCTCTAGATGGCCGATCTAGAGAAGTCCCGCCTCATAAGTGGAAGGATGAAATTCTCAGAACAG
CTAACCTCTAATGGGAGTTGGCTTCTGATTCTCATTCAGGCTTCTCACGGCATTCAGCAGCAGCGTTGCTGTAAC
CGACAAAGACACCTTCGAATTAAGCACATTCCTCGATTCCAGCAAAGCACCGCAAC**ATG**ACCGAAATGAGCTTCC
TGAGCAGCGAGGTGTTGGTGGGGGACTTGATGTCCCCCTTCGACCCGTCGGGTTTGGGGGCTGAAGAAAGCCTAG
GTCTCTTAGATGATTACCTGGAGGTGGCCAAGCACTTCAAACCTCATGGGTTCTCCAGCGACAAGGCTAAGGCGG
GCTCCTCCGAATGGCTGGCTGTGGATGGGTTGGTCAGTCCCTCCAACAACAGCAAGGAGGATGCCTTCTCCGGGA
CAGATTGGATGTTGGAGAAAATGGATTTGAAGGAGTTCGACTTGGATGCCCTGTTGGGTATAGATGACCTGGAAA
CCATGCCAGATGACCTTCTGACCACGTTGGATGACACTTGTGATCTCTTTGCCCCCCTAGTCCAGGAGACTAATA
AGCAGCCCCCCCAGACGGTGAACCCAATTGGCCATCTCCCAGAAAGTTTAACAAAACCCGACCAGGTTGCCCCCT
TCACCTTCTTACAACCTCTTCCCCTTTCCCCAGGGGTCCTGTCCTCCACTCCAGATCATTCCTTTAGTTTAGAGC
TGGGCAGTGAAGTGGATATCACTGAAGGAGATAGGAAGCCAGACTACACTGCTTACGTTGCCATGATCCCTCAGT
GCATAAAGGAGGAAGACACCCCTTCAGATAATGATAGTGGCATCTGTATGAGCCCAGAGTCCTATCTGGGGTCTC
CTCAGCACAGCCCCTCTACCAGGGGCTCTCCAAATAGGAGCCTCCCATCTCCAGGTGTTCTCTGTGGGTCTGCCC
GTCCCAAACCTTACGATCCTCCTGGAGAGAAGATGGTAGCAGCAAAAGTAAAGGGTGAGAAACTGGATAAGAAGC
TGAAAAAAATGGAGCAAAACAAGACAGCAGCCACTAGGTACCGCCAGAAGAAGAGGGCGGAGCAGGAGGCTCTTA
CTGGTGAGTGCAAAGAGCTGGAAAAGAAGAACGAGGCTCTAAAAGAGAGGGCGGATTCCCTGGCCAAGGAGATCC
AGTACCTGAAAGATTTGATAGAAGAGGTCCGCAAGGCAAGGGGGAAGAAAAGGGTCCCC**TAG**TTGAGGATAGTCA
GGAGCGTCAATGTGCTTGTACATAGAGTGCTGTAGCTGTGTGTTCCAATAAATTATTTTGTAGGG

FIGURE 642

MTEMSFLSSEVLVGDLMSPFDPSGLGAEESLGLLDDYLEVAKHFKPHGFSSDKAKAGSSEWLAVDGLVSPSNNSK
EDAFSGTDWMLEKMDLKEFDLDALLGIDDLETMPDDLLTTLDDTCDLFAPLVQETNKQPPQTVNPIGHLPESLTK
PDQVAPFTFLQPLPLSPGVLSSTPDHSFSLELGSEVDITEGDRKPDYTAYVAMIPQCIKEEDTPSDNDSGICMSP
ESYLGSPQHSPSTRGSPNRSLPSPGVLCGSARPKPYDPPGEKMVAAKVKGEKLDKKLKKMEQNKTAATRYRQKKR
AEQEALTGECKELEKKNEALKERADSLAKEIQYLKDLIEEVRKARGKKRVP

FIGURE 643

CGGCAGCCAGCTGAGAGCA**ATG**GGAAATGGGGAGTCCCAGCTGTCCTCGGTGCCTGCTCAGAAGCTGGGTTGGTT
TATCCAGGAATACCTGAAGCCCTACGAAGAATGTCAGACACTGATCGACGAGATGGTGAACACCATCTGTGACGT
CTGCAGGAACCCCGAACAGTTCCCCCTGGTGCAGGGAGTGGCCATAGGTGGCTCCTATGGACGGAAAACAGTCTT
AAGAGGCAACTCCGATGGTACCCTTGTCCTTTTCTTCAGTGACTTAAAACAATTCCAGGATCAGAAGAGAAGCCA
ACGTGACATCCTCGATAAAACTGGGGATAAGCTGAAGTTCTGTCTGTTCACGAAGTGGTTGAAAAACAATTTCGA
GATCCAGAAGTCCCTTGATGGGTCCACCATCCAGGTGTTCACAAAAAATCAGAGAATCTCTTTCGAGGTGCTGGC
CGCCTTCAACGCTCTGAGCTTAAATGATAATCCCAGCCCCTGGATCTATCGAGAGCTCAAAAGATCCTTGGATAA
GACAAATGCCAGTCCTGGTGAGTTTGCAGTCTGCTTCACTGAACTCCAGCAGAAGTTTTTTGACAACCGTCCTGG
AAAACTAAAGGATTTGATCCTCTTGATAAAGCACTGGCATCAACAGTGCCAGAAAAAAATCAAGGATTTACCCTC
GCTGTCTCCGTATGCCCTGGAGCTGCTTACGGTGTATGCCTGGGAACAGGGGTGCAGAAAAGACAACTTTGACAT
TGCTGAAGGCGTCAGAACGGTTCTGGAGCTGATCAAATGCCAGGAGAAGCTGTGTATCTATTGGATGGTCAACTA
CAACTTTGAAGATGAGACCATCAGGAACATCCTGCTGCACCAGCTCCAATCAGCGAGGCCAGTAATCTTGGATCC
AGTTGACCCAACCAATAATGTGAGTGGAGATAAAATATGCTGGCAATGGCTGAAAAAAGAAGCTCAAACCTGGTT
GACTTCTCCCAACCTGGATAATGAGTTACCTGCACCATCTTGGAATGTCCTGCCTGCACCACTCTTCACGACCCC
AGGCCACCTTCTGGATAAGTTCATCAAGGAGTTTCTCCAGCCCAACAAATGCTTCCTAGAGCAGATTGACAGTGC
TGTTAACATCATCCGTACATTCCTTAAAGAAAACTGCTTCCGACAATCAACAGCCAAGATCCAGATTGTCCGGGG
AGGATCAACCGCCAAAGGCACAGCTCTGAAGACTGGCTCTGATGCCGATCTCGTCGTGTTCCATAACTCACTTAA
AAGCTACACCTCCCAAAAAAACGAGCGGCACAAAATCGTCAAGGAAATCCATGAACAGCTGAAAGCCTTTTGGAG
GGAGAAGGAGGAGGAGCTTGAAGTCAGCTTTGAGCCTCCCAAGTGGAAGGCTCCCAGGGTGCTGAGCTTCTCTCT
GAAATCCAAAGTCCTCAACGAAAGTGTCAGCTTTGATGTGCTTCCTGCCTTTAATGCACTGGGTCAGCTGAGTTC
TGGCTCCACACCCAGCCCCGAGGTTTATGCAGGGCTCATTGATCTGTATAAATCCTCGGACCTCCCGGGAGGAGA
GTTTTCTACCTGTTTCACAGTCCTGCAGCGAAACTTCATTCGCTCCCGGCCCACCAAACTAAAGGATTTAATTCG
CCTGGTGAAGCACTGGTACAAAGAGTGTGAAAGGAAACTGAAGCCAAAGGGGTCTTTGCCCCCAAAGTATGCCTT
GGAGCTGCTCACCATCTATGCCTGGGAGCAGGGGAGTGGAGTGCCGGATTTTGACACTGCAGAAGGTTTCCGGAC
AGTCCTGGAGCTGGTCACACAATATCAGCAGCTCGGCATCTTCTGGAAGGTCAATTACAACTTTGAAGATGAGAC
CGTGAGGAAGTTTCTACTGAGCCAGTTGCAGAAAACCAGGCCTGTGATCTTGGACCCAGGCGAACCCACAGGTGA
CGTGGGTGGAGGGGACCGTTGGTGTTGGCATCTTCTGGACAAAGAAGCAAAGGTTAGGTTATCCTCTCCCTGCTT
CAAGGATGGGACTGGAAACCCAATACCACCTTGGAAAGTGCCGACAATGCAGACACCAGGAAGTTGTGGAGCTAG
GATCCATCCTATTGTCAATGAGATGTTCTCATCCAGAAGCCATAGAATCCTGAATAATAATTCTAAAAGAAACTT
CTGGAGATCATCTGGCAATCGCTTT**TAA**AGACTCGGCTCACCGTGAGAAAGAGTCACTCACATCCATTCTTCCCT
TGATGGTCCCTATTCCTCCTTCCCTTGCCTTCTTGGACTTCTTGAAATCAATCAAGACTGCAAACCCTTTCATAA
AGCTGCCTTGCTGAACTCCTCTCTGCAGGAGCCCTGCTTAAAATAGTTGATGTCATCACTTTATGTGCATCTTAT
TTCTGTCAACTTGTATTTTTTTTTCTTGTATTTTTCCAATTAGCTCCTCCTTTTTCCTTCCAGTCTAAAAAAGGA
ATCCTCTGTGTCTTCAAAGCAAAGCTCTTTACTTTCCCCTTGGTTCTCATAACTCTGTGATCTTGCTCTCGGTGC
TTCCAACTCATCCACGTCCTGTCTGTTTCCTCTGTATACAAAACCCTTTCTGCCCCTGCTGACACAGACATCCTC
TATGCCAGCAGCCAGGCCAACCCTTTCATTAGAACTTCAAGCTCTCCAAAGGCTCAGATTATAACTGTTGTCATA
TTTATATGAGGCTGTTGTCTTTTCCTTCTGAGCCTGCCTTTATCCCCCCACCCAGGAGTATCCTCTTGCCAAAGC
AAAAGACTTTTTCCTTGGCTTTAGCCTTAAAGATACTTGAAGGTCTAGGTGCTTTAACCTCACATACCCTCACTT
AAACTTTTATCACTGTTGCATATACCAGTTGTGATACAATAAAGAATGTATCTGG

FIGURE 644

MGNGESQLSSVPAQKLGWFIQEYLKPYEECQTLIDEMVNTICDVCRNPEQFPLVQGVAIGGSYGRKTVLRGNSDG
TLVLFFSDLKQFQDQKRSQRDILDKTGDKLKFCLFTKWLKNNFEIQKSLDGSTIQVFTKNQRISFEVLAAFNALS
LNDNPSPWIYRELKRSLDKTNASPGEFAVCFTELQQKFFDNRPGKLKDLILLIKHWHQQCQKKIKDLPSLSPYAL
ELLTVYAWEQGCRKDNFDIAEGVRTVLELIKCQEKLCIYWMVNYNFEDETIRNILLHQLQSARPVILDPVDPTNN
VSGDKICWQWLKKEAQTWLTSPNLDNELPAPSWNVLPAPLFTTPGHLLDKFIKEFLQPNKCFLEQIDSAVNIIRT
FLKENCFRQSTAKIQIVRGGSTAKGTALKTGSDADLVVFHNSLKSYTSQKNERHKIVKEIHEQLKAFWREKEEEL
EVSFEPPKWKAPRVLSFSLKSKVLNESVSFDVLPAFNALGQLSSGSTPSPEVYAGLIDLYKSSDLPGGEFSTCFT
VLQRNFIRSRPTKLKDLIRLVKHWYKECERKLKPKGSLPPKYALELLTIYAWEQGSGVPDFDTAEGFRTVLELVT
QYQQLGIFWKVNYNFEDETVRKFLLSQLQKTRPVILDPGEPTGDVGGGDRWCWHLLDKEAKVRLSSPCFKDGTGN
PIPPWKVPTMQTPGSCGARIHPIVNEMFSSRSHRILNNNSKRNFWRSSGNRF

FIGURE 645

TGTTAGGCAGCAACAGTGCTGATGCTGGACTGTGGCAGGCAGAGGGTGCTATCCTGACACACTTCACCTTAGTGC
AGGAAACTTCAATTTGGTGGAAGAAAGGCGATTTCGAGGTTCCAATCTGGGCGACACTTCCCAGTTGGAGAGTCA
GCAAAAGGGAGAGGGCAATTCCAAGAAGAGGGAAAAGCTTGTGCACAGTGTACCTCCTTTATTCCTGAAGCCCGG
GCAGTGCTTGACCTGGTCGACCAGTGCCCAAAACAGATCCAGAAAGGAAAGTTCCAGGTTGTTGCCATCGAAGGA
CTGGATGCCACGGGTAAAACCACGGTGACCCAGTCAGTGGCAGATTCACTTAAGGCTGTCCTCTTAAAGTCACCA
CCCTCTTGCATTGGCCAGTGGAGGAAGATCTTTGATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTG
GGCAATTATATTGTGGCCTCCGAAATAGCTAAAGAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCAC
AGCACGGCCACCTATGCCATAGCCACTGAGGTGAGTGGGGGTCTCCAGCACCTGCCCCCAGCCCATCACCCTGTG
TACCAGTGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTGCTCACTGTGAGTCCTGAGGAGAGGTTGCAG
AGGCTGCAGGGCCGGGGCATGGAGAAGACCAGGGAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAG
GTAGAAATGTCCTACCAGCGGATGGAGAATCCTGGCTGCCATGTGGTTGATGCCAGCCCCTCCAGAGAAAAGGTC
CTGCAGACGGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCG**TAG**TTACTCTGGCCAGGTGCCACGTCTAAC
TAGATTAGATGTTGTTTGAAACATCTACATCCACCATTTGTTATGCAGTGTTCCCAAATTTCTGTTCTACAAGCA
TGTTGTGTGGCAGAAAACTGGAGACCAGGCATCTTAATTTTACTTCAGCCATCGTACCCTCTTCTGACTGATGGA
CCCGTCATCACAAAGGTCCCTCTCATCATGTTCCAGTGAGAGGCCAGCGATTGCTTTCTTCCTGGCATAGTAAAC
ATTTCTTGGAACATATGTTTCACTTAATCACTACCAAATATCTGGAAGACCTGTCTTACTCAGACAGCACCAGG
TGTACAGAAGCAGCAGACAAGATCTTCCAGATCAGCAGGGAGACCCCGGAGCCTCTGCTTCTCCTACACTGGCAT
GCTGATGAGATCGTGACATGCCCACATTGGCTTCTTCCACATCTGGTTGCACTCGTCATGATGGGCTCGCTGCAT
CTCCCTCAGTCCCAAATTCTAGAGCCAAGTGTTCCTGCAGAGGCTGTCTATGTGTCCTGGCTGCCCAAGGACACT
CCTGCAGAGCCATTTTTGGGTAAGGAACACTTACAAAGAAGGCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTT
TGATAGGCTTCTGAGTCATATATAAAGACATTCAAGCCAAGATGCTCCAACTGCAAATATACCAACCTTCTCTGA
ATTATATTTTGCTTATTTATATTTCTTTTCTTTTTTTCTAAAGTATGGCTCTGAATAGAATGCACATTTTCCATT
GAACTGGATGCATTTCATTTAGCCAATCCAGTAATTTATTTATATTAATCTATACATAATATGTTTCCTCAGCAT
AGGAGCTATGATTCATTAATTAAAAGTGGAGTCAAAACGCTAAATGCAATGTTTGTTGTGTATTTTCATTACACA
AACTTAATTTGTCTTGTTAAATAAGTACAGTGGATCTTGGAGTGGGATTTCTTGGTAAATTATCTTGCACTTGAA
TGTCTCATGATTACATATGAAATCGCTTTGACATATCTTTAGACAGAAAAAAGTAGCTGAGTGAGGGGGAAATTA
TAGAGCTGTGTGACTTTAGGGAGTAGGTTGAACCAGGTGATTACCTAAAATTCCTTCCAGTTCAAAGGCAGATAA
ATCTGTAAATTATTTTATCCTATCTACCATTTCTTAAGAAGACATTACTCCAAAATAATTAAATTTAAGGCTTTA
TCAGGTCTGCATATAGAATCTTAAATTCTAATAAAGTTTCATGTTAATGTCATAGGATTTTTAAAAGAGCTATAG
GTAATTTCTATATAATATGTGTATATTAAAATGTAATTGATTTCAGTTGAAAGTATTTTAAAGCTGATAAATAGC
ATTAGGGTTCTTTGCAATGTGGTATCTAGCTGTATTATTGGTTTTATTTACTTTAAACATTTTGAAAAGCTTATA
CTGGCAGCCTAGAAAAACAAACAATTAATGTATCTTTATGTCCCTGGCACATGAATAAACTTTGCTGTGGTTTAC
TAATCTATGCTGTCATCCTGGGTACATATTGATTTGTCTGAAAAGTGCTTTCTCAGATTCCCCTTTTAATATTGT
GATGTAAAGGAGGGAAATTTTGGTAAAGGAAGTTGAAAGGTGTGAGCTGGCAGGCTAAGTGGAATTTGTGGTTAG
AGTGCTTTCAGAGAAA

FIGURE 646

LGSNSADAGLWQAEGAILTHFTLVQETSIWWKKGDFEVPIWATLPSWRVSKRERAIPRRGKSLCTVYLLYIPEAR
AVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFYSL
GNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTVSPEERLQ
RLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSEP

FIGURE 647

AAGGGGTAAATACCCATTATCAGAAAGTTTATTTTCCCTCATGATGGAAGCT**<u>TAA</u>**TAAAGGGTTTCTATATTTTG
GACACCCAGAGAATTGCTCAAATGTGATTTTAGTGTAATAGGTCTTTCTTTTTTCATTGAGTTGATTTTTAAGCA
TTTAATACATTGCCTTGTACAACTCCAAGCTTCTCTATAGTCAAGAGCCCAAGCTAGATATTTTGTGGGAAACTT
AACTTTAAATTCCAAACCTTTGCTGAAATTGACATTGTCACTTTTTGTGCTGTGCCTTGGATTTGTATTCTTACT
CTTCTTGAGGAAAGATAGAAGGCAGTTGAACTTTGTGACCAAGAGCGTTTCATTGGCAGTCCCTGCATGATTGAT
AATTTGTAGATACAATATTATTGCATTTCTTTACATGTATTCATTTTCCTGAAGAGTATTATCTTGTGCTTTTAA
TAAAATAACATGTG

FIGURE 648

RGKYPLSESLFSLMMEA

FIGURE 649

AAGCTGCCGCAGTTAGTTGGAGTCTAAGGACTCGTGACAATCTTCGGGTGCCCTTCGAGAGAAAAGGGGAGG**ATG**

CCACTGGAGTCATCCTCTTCAATGCCACTATCCTTCCCATCTCTCTTACCCTCAGTACCACACAATACTAACCCT
TCCCCTCCTCTGATGTCTTACATCACCTCCCAGGAGATGAAGTGTATTCTTCACTGGTTTGCCAATTGGTCAGGT
CCCCAGCGTGAACGTTTCCTAGAGGACCTGGTGGCTAAGGCAGTGCCAGAAAAATTACAACCACTGCTGGATAGT
CTGGAGCAGCTTAGTGTGTCTGGGGCAGACCGACCACCTTCTATCTTTGAGTGCCAGCTACATCTTTGGGATCAG
TGGTTTCGAGGCTGGGCTGAGCAGGAGCGCAATGAATTTGTCAGACAGCTGGAGTTCAGTGAGCCAGACTTCGTG
GCAAAGTTTTACCAAGCAGTGGCTGCTACAGCTGGTAAGGAC**TGA**TAGGCATTCAGACCAAAGAAGATAACCATA
GCTGATGGAGCCATGACTCTCTACAATGATAACTCAATTCAAATGTGTCGCCTAAAGCTCTGGAACTGGTATTCC
AACCAGCTGACCGAACTCACTGACCAGTACAGGCATGGTTATTTCAATATTAATAGCATGTCAACTGGACTCCTA
TTTGTAAATGTTATCAATCTAAGCAATCCAGCTCATCAGTCTACTAGTTTGCTTCTTTCCGAGAGATGTCAAGTC
CTCAAGAATTTGATGGCTTCTTCTGCAGCTATAACCACAAGGAACCTACACATTGTAACTCAAGTCCACTGCTGG
CTCATGAAATGTGTAAAGTAGAACCCTCCTTCCCGAGAAATAAGACAGGACAATAAAAGGTGGCGTTTTTGTACT
TTACCTGGATTCCATTGGCTGGTTTTACCACTCCTATCAGATTGTAGTGTAATTGTGTGATACGCAAACCATTAG
TTTACCCAGTGATGATTTAATAAAATTATGAAAAATCAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAA

FIGURE 650

MPLESSSSMPLSFPSLLPSVPHNTNPSPPLMSYITSQEMKCILHWFANWSGPQRERFLEDLVAKAVPEKLQPLLD
SLEQLSVSGADRPPSIFECQLHLWDQWFRGWAEQERNEFVRQLEFSEPDFVAKFYQAVAATAGKD

FIGURE 651A

GGGACCGACGACACGCCCCCCTCTCCTCCTTTGTTCCGGGGGTCGGCGGCCGCTCTCCTGCCAGAGCTCGGGATC
TCGGCCCCGGGAGGCGGGCGCTCGGGCGCAGCCGCGAAG**ATG**CCGTTGGAACTGACGCAGAGCCGAGTGCAGAAG
ATCTGGGTGCCCGTGGACCACAGGCCCTCGTTGCCCAGATCCTGTGGGCCAAAGCTGACCAACTCCCCCACCGTC
ATCGTCATGGTGGGCCTCCCCGCCCGGGGCAAGACCTACATCTCCAAGAAGCTGACTCGCTACCTCAACTGGATT
GGCGTCCCCACAAAAGTGTTCAACGTCGGGGAGTATCGCCGGGAGGCTGTGAAGCAGTACAGCTCCTACAACTTC
TTCCGCCCCGACAATGAGGAAGCCATGAAAGTCCGGAAGCAATGTGCCTTAGCTGCCTTGAGAGATGTCAAAAGC
TACCTGGCGAAAGAAGGGGGACAAATTGCGGTTTTCGATGCCACCAATACTACTAGAGAGAGGAGACACATGATC
CTTCATTTTGCCAAAGAAAATGACTTTAAAGCGTTTTTCATCGAGTCGGTGTGCGACGACCCTACAGTTGTGGCC
TCCAATATCATGGAAGTTAAAATCTCCAGCCCGGATTACAAAGACTGCAACTCGGCAGAAGCCATGGACGACTTC
ATGAAGAGGATCAGTTGCTATGAAGCCAGCTACCAGCCCCTCGACCCCGACAAATGCGACAGGGACTTGTCGCTG
ATCAAGGTGATTGACGTGGGCCGGAGGTTCCTGGTGAACCGGGTGCAGGACCACATCCAGAGCCGCATCGTGTAC
TACCTGATGAACATCCACGTGCAGCCGCGTACCATCTACCTGTGCCGGCACGGCGAGAACGAGCACAACCTCCAG
GGCCGCATCGGGGGCGACTCAGGCCTGTCCAGCCGGGGCAAGAAGTTTGCCAGTGCTCTGAGCAAGTTCGTGGAG
GAGCAGAACCTGAAGGACCTGCGCGTGTGGACCAGCCAGCTGAAGAGCACCATCCAGACGGCCGAGGCGCTGCGG
CTGCCCTACGAGCAGTGGAAGGCGCTCAATGAGATCGACGCGGGCGTCTGTGAGGAGCTGACCTACGAGGAGATC
AGGGACACCTACCCTGAGGAGTATGCGCTGCGGGAGCAGGACAAGTACTATTACCGCTACCCCACCGGGGAGTCC
TACCAGGACCTGGTCCAGCGCTTGGAGCCAGTGATCATGGAGCTGGAGCGGCAGGAGAATGTGCTGGTCATCTGC
CACCAGGCCGTCCTGCGCTGCCTGCTTGCCTACTTCCTGGATAAGAGTGCAGAGGAGATGCCCTACCTGAAATGC
CCTCTTCACACCGTCCTGAAACTGACGCCTGTCGCTTATGGCTGCCGTGTGGAATCCATCTACCTGAACGTGGAG
TCCGTCTGCACACACCGGGAGAGGTCAGAGGATGCAAAGAAGGGACCTAACCCGCTCATGAGACGCAATAGTGTC
ACCCCGCTAGCCAGCCCCGAACCCACCAAAAAGCCTCGCATCAACAGCTTTGAGGAGCATGTGGCCTCCACCTCG
GCCGCCCTGCCCAGCTGCCTGCCCCCGGAGGTGCCCACGCAGCTGCCTGGACAAAACATGAAAGGCTCCCGGAGC
AGCGCTGACTCCTCCAGGAAACAC**TGA**GGCAGACGTGTCGGTTCCATTCCATTTCCATTTCTGCAGCTTAGCTTG
TGTCCTGCCCTCCGCCCGAGGCAAAACGTATCCTGAGGACTTCTTCCGGAGAGGGTGGGGTGGAGCAGCGGGGGA
GCCTTGGCCGAAGAGAACCATGCTTGGCACCGTCTGTGTCCCCTCGGCCGCTGGACACCAGAAAGCCACGTGGGT
CCCTGGCGCCTGCCTTTAGCCTGGGGGCCCCCACCTCCACTCTCTGGGTTCCTAGGAATGTCCAGCCTCGGAGAC
CTTCACAAAGCCTTGGGAGGGTGATGAGTGCTGGTCCTGACAAGAGGCCGCTGGGGACACTGTCCGTTTTGTTTC
GTTTCTGTGATCTCCCGGCACGTTTGGAGCTGGGAAGACCACACTGGTGGCAGAATCCTAAAATTAAAGGAGGCA
GCCTCCTAGTTGCTGAAAGTTAAGGAATGTGTAAAACCTCCACGTGACTGTTTGGTGCATCTTGACCTGGGAAGA
CGCCTCATGGGAACGAACTTGGACAGGTGTTGGGTTGACCCCTCTTCTGCAGGAAGTCCCTGAGCTGAGACGCAA
AGTTGGCTGGGTGGTGGTCGGCACCCTGGCTCCTGCAGGTCCACACACCTTCCAGGCCTGTGGCCTGCCTCCAAA
GATGTGCAAGGGCAGGCTGGCTGCACGGGGAGAGGGAAGTATTTTGCCGAAATATGAGAACTGGGGCCTCCTGCT
CCCAGGGAGCTCCAGGGCCCCTCTCTCCTCCCACCTGGACTTGGGGGGAACTGAGAAACACTTTCCTGGAGCTGC
TGGCTTTTGCACTTTTTTGATGGCAGAAGTGTGACCTGAGAGTCCCACCTTCTCTTCAGGAACGTAGATGTCGGG
GTGTCTTGCCCTGGGGGGCTTGGAACCTCTGAAGGTGGGGAGCGGAACACCTGGCATCCTTCCCCAGCACTTGCA
TTACGGTCCCTGCTCTTCCAAGGTGGGGACAGTGGCCCAAGCAAGGCCTCACACGCAGCCACTTCTTCAAGAGCT
GCCTGCACACTGTCTTGGAGCATCTGCCTTGTGCCTGGCACTCTGCCGGTGCCTTGGGAAGGTCGGTAAGAGTGG
ACTTTGTCCTGGGCTTCCCTTCATGGCGTCTAGACACTTTTGTGGTGATGGAAAGCATGGGACCTGTCGTCTCAG
CCTGTTGGTTTCTCCTCATTGCCTCAAACCCTGGGGTAGGTGGAACGGGGGGTCTCGTGCCCAGATGAAACCATT
TGGAAACTCGGCAGCAGAGTTTGTCCAAATGACCCTTTTCAGGATGTCTCAAAGCTTGTGCCAAAGGTCACTTTT
CTTTCCTGCCTTCTGCTGTGAGCCCTGAGATCCTCCTCCCAGCTCAAGGGACAGGTCCTGGGTGAGGGTGGGAGA
TTTAGACACCTGAAACTGGGCGTGGAGAGAAGAGCCGTTGCTGTTTGTTTTTGGGAAGAGCTTTTAAAGAATGC
ATATTTTTTTACCTGGTTGGAATTGAGTAGGAACTGAGGCTGTGCTTCAGGTATGGTACAATCAAGTGGGGGATT
TTCATGCTGAACCCATTCAAAGCCCTCCCCGTCCCCGCATTTCCAGGCCACCCTTTGGCTGGCGTCTGCTGGAGA
GGATGTCTCTGTCGCATTCCCGTGCAGCTCAGCTCGCGCAGGTTTTCTCTCTCTCCCTGGATGTTGAGCTCTCAT
CAGAATATGTGGGTGGGGGGTGGACGTGCACGGGTGCATGATTGTGCTTAACTTGGTTGTATTTTTCGATTTGAC
ATGGAAGCCTGTTGCTTTGCTCTAGAGAATAGTTTCTCGTGTCCCCTTCGCACGCCTCATTCTTTGAACCTCATC
TCTGATGTTTGATACAGATGGGGGCTTGATAGCTGTGGTCCCCTTTCCCTTCTGACTACGTGAAAATCAATACCT

FIGURE 651B

AAATACAGAAGCCTTGGTCTAAACACCGAGACTTTTAGTTTGCGAAGGGGCTTAGATAGGGAGAGAGGTAACATG
AATCTGGACAGGGGAGGGAGATACTATAGAAAGGAGAACACTGCATACTTTGCAAAGCCAGTGACCTCCTTTTGA
AGGGGACATTGGACGGGGGCCGGGGGCGGGGGTTCGGTTTGACTACCGTCATGAACTTTTGGCGTATACTGATTC
CTCCAACTCTCCACCCCACAAAATAACGGGGACCAATATTTTTAACTTTGCCTATTTGTTTTTGGGTGAGTTTCC
CCCCTCCATTATTCTGTCCTGAGACCACGGGCAAAGCTCTTCCATTTTGAGAGAGAAGAAAAACTGTTTGGAACC
ACACCAATGATATTTTTCTTTGTAATACTTGAAATTTATTTTTTTATTATTTTGATAGCAGATGTGCTATTTATT
TATTTAATATATGTATAAGGAGTCCTAAACAATAGAAAGCTGTAGAAGCTGTAGAGATAGGCTTCAGTTGTTAAT
TGGTTTGGAGCCTCCTATGTGTGACTTATGACTCTCTGTGTTCTGTGTATTTGTCTGAATTAATGACCTGGGATA
TAAAGCTATGCTAGCTTTCAAACAGGAGATGCCTTCAGAAAGCTTTGTATATTTTGCAGTTGCCAGACCAATAAA
ATACCTGGTTGAAATACATGGACGAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 652

MPLELTQSRVQKIWVPVDHRPSLPRSCGPKLTNSPTVIVMVGLPARGKTYISKKLTRYLNWIGVPTKVFNVGEYR
REAVKQYSSYNFFRPDNEEAMKVRKQCALAALRDVKSYLAKEGGQIAVFDATNTTRERRHMILHFAKENDFKAFF
IESVCDDPTVVASNIMEVKISSPDYKDCNSAEAMDDFMKRISCYEASYQPLDPDKCDRDLSLIKVIDVGRRFLVN
RVQDHIQSRIVYYLMNIHVQPRTIYLCRHGENEHNLQGRIGGDSGLSSRGKKFASALSKFVEEQNLKDLRVWTSQ
LKSTIQTAEALRLPYEQWKALNEIDAGVCEELTYEEIRDTYPEEYALREQDKYYYRYPTGESYQDLVQRLEPVIM
ELERQENVLVICHQAVLRCLLAYFLDKSAEEMPYLKCPLHTVLKLTPVAYGCRVESIYLNVESVCTHRERSEDAK
KGPNPLMRRNSVTPLASPEPTKKPRINSFEEHVASTSAALPSCLPPEVPTQLPGQNMKGSRSSADSSRKH

FIGURE 653

AGTCGCTGTTTGGGACGCTGGGTGTGCGGTGTTCTGTCTCCGCTCCCGTTTCGCTGTCACAGCCCGTTCCTTCCC
GGAGCCCGGGACAGGCTGGGCGCGCGCCCGTGTGAGTGAGCGGGACTCAGGGCAGAAGTGTCCCCTCACTGCGTT
TTTTTTTCCTTTTATCCAAAGAACGGGGCAGTTAGTACGCTTGCCTTCCTGTCGCCCGGTTGGGAGCGGGGTTGG
TGTGCGGAGTGGTTCGCCTTTTTTTCTTTAGAACTTGTGAGCCTTTTTTTTTTTTTTTTTTCTTTCCTTTTTTT
AGGCTCAGTGCTGTCCGGGCTGGTTTGCCCGGTCCCTGACTAACGGCTTTCTGCCCCTTCTCTCGCCACCCCTGC
CCAAGGTCGCCCCTCTGCCTTCGCCCCTGTCCCGGGAGGGTGGGAAGCTTTGACCCCGCCCTGCCCACTCGCGTC
TCCGCAGCCGTAGCCGCGCCTGTCCCAAT**ATG**AATAGGGTCAACGACCCACTTATTTTTATAAGAGATATTAAGC
CCGGACTGAAAAACTTAAATGTCGTCTTTATTGTCCTGGAGATAGGACGCGTGACCAAAACCAAAGACGGCCATG
AAGTGAGATCGTGCAAAGTAGCAGATAAAACGGGCAGCATCACTATTTCCGTGTGGGATGAGATCGGAGGTCTTA
TACAGCCAGGGGATATTATTCGGTTGACCAGAGGGTATGCATCCATGTGGAAAGGATGTCTGACACTTTATACTG
GAAGGGGTGGTGAACTTCAAAAAATTGGGGATCTAGGTGCGGTGCAGGCAGCCGCAATGCGAGATTCCATACACT
ACTACCCTGGTAATGATCTCCACCCTGACCTGGAGGAGCCATCCTCTCTAGGGGTG**TAA**GATTTTGTATGGTTTA
TTCAGAAGTGCCAAATTTCAGTGAACCCAACCCAGATTATCGAGGACAGCAGAACAAAGGGGCACAGAGTGAACA
GAAGAATAATTCCATGAATAGTAATATGGGTACAGGTACATTTGGACCAGTGGGAAATGGTGTTCACACTGGCCC
TGAATCAAGGGAACACCAGTTTTCACATGCTGGCAGAAGCAATGGCCGGGGACTTATAAATCCACAACTACAAGG
AACAGCTAGTAATCAAACAGTGATGACCACAATAAGTAATGGCAGGGACCCTCGGAGAGCCTTTAAAAGATGACC
TATGCTAAATACTCATGTGTAGTTTTTATACTACATGCCCTACTTGAACACTTATTGCACTTTTATTTATTGTTA
ACTGTGAAAAGTACGTCCTTTATTGGGTTTCCTTTTATATTCTTGGTTTGTTAAGAAGAATGGTTTGTTTTTATA
GCAAAACTGTTAAGCTGCTCGAGTCTCCTGTTGAAGAATGGGAACACTGAAAAGTAGGGGCATTTATTTTTAGAG
TAAAAAGATTATTGGATAGCCTTTAAAAAACCTGCACCCATTTCATGGGTGAGTTACTTAAGACATCAGCTTTAT
AGCCTCTATGAGTCTATCTTCTGTATAAGTTTTGTAATATTTAACATAAGGCTTAATGGGAGATGTTCTTTTGTC
TTGTATTCAGATATTGCCAACTAAAGCAATAACCATCAAAAAACACAAGAACTTGTCAATGCTAGCAGTAATTTT
TGAGTGTTTGTGGCTCTCGGAATGATTGACTTCGTTCAGTGACTACTATTAAGATTTTCCAAGGACTGACTCATC
CCAAATTTTTGTTGTATTACCAAAAAAACAGATTCCTTATCAGAATTTGGAATAGAATGTGATCTCTATTGCAAC
AAGTAATTTTAAAAGAAAGCTACATTTATTTTAGAGTAGTGCTCCTAACATGTATTATCAACTTTGTGGATTACA
TTGGAGGAAAATTTAAAACTGGGGCCTTGAATATTTATTTTTTGAAACTACCATGTTAAATACTGAAGTATAATT
TGGGGGAGTTATAAAGTTATGATAAACATTCATCTGATTATTTTAAACAATAGTTGTGGTAGATAAACATACTGG
AGGTGAGTAAAATTGAATTCATATAGTAACATGCAGTCTGAAGTCCTAGTTACTTAATAGGTACTCAGCCTGGAG
TGAAAATCCTGGGTACTGACTTTGAGAGGAGTGAGTGTGCATGTTGTCAAAGTTTCTGAACACAGTTCACATAGC
CTTATTAGCAAAAGTTTTAAGAAATGGCTCTATCAAAGAAGCAATTGCAGCTTTATTCAGAAATATAAAAGTGGA
ATTTATGTACATGTCATAAGTGGTACCCACTTCCCCTTTTTACTGTAGGGTGGATAACTCTTAGGATTTAACTCT
TTGAATATTATCTCTTGAATAAAGCATGTGTTAATGTTAACAAACCTACGTAATTTTTGCCCTTTCAATGACTTA
CAGTGGAGAGCCAGTACATCTTAACTACTGTTGTAGTGATGGTATCAACCTCATGGTTACTTAGCTCTGCATTTG
TTGCTTTGTTTTTTTTCCACTTCAAATCACAAAATAAGTAGATTTTGTTTTCTGAAAACTCCATAGCATTTGAAT
ACAAAAAGTTGTGCCAGATTGTTTGCCCTAATTCACTGTGTTTAACAAATATTTCAGTACACACTATGTATTAGG
CACTGTGTGGAAAGTGTTAAGGGGTAGACAAGATACCGAATAATCTCCACAAGTTTATTTGTGGTCTATAGTACT
TTTGTAACTGGGGTTACAAAAATTATAGAAATTTTTTTCCTTTGTTCATATGCATATTCATGATTATAATTTGGC
TTTGTTTGTGATTAATGTTTTCTTAAGATTTTCACATTATAGAATACCTCAAAAGAAGTTGTCTAAGGACTGGGA
TAGAGAGTATGTTTCATAAAATTGTAGATGTTTAGAATTTTTAAAAACCCTACAAATTAGTATATGATTGTTTTA
TATAAGTAAGATAGGAGCAACACTTTAAATTATTTGTGGGAGAATACAGCATTAAAGGTGATTTTAAAAGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 654

MNRVNDPLIFIRDIKPGLKNLNVVFIVLEIGRVTKTKDGHEVRSCKVADKTGSITISVWDEIGGLIQPGDIIRLT
RGYASMWKGCLTLYTGRGGELQKIGDLGAVQAAAMRDSIHYYPGNDLHPDLEEPSSLGV

FIGURE 655

CCATCTCAAAACAACAAAAACAACAAAAAAACCACATGCCTGGCGGAGAACAAAGAGATCATTTAGTCCAATCTC
TTCATGGAGATGAGGGCTCCTGGGAGCCCCTCTTCATGTCTCAGGTTCTTAGT**TGA**CTATGTTTATCCAAATGAT
TCCAGATTCCTGTGGAAACAAGGAATCGATGTACAAATGGGGTAGGGTGGCAAGGAAAACTCTTAAGAGAGAAAC
ATCAAGGTTTTCACATTAGGTTAAAGACAAGAAGGTTTCTAGGCAGGTAGTGTAATGTCTAGGTGATTTTGAAGT
GAACTTAAGCCACTAGGTTTGAGGGACAAAGGACAGTAGAAAATGGTGAAGACTGCAGATCACCTGCTATACCTC
AAGGAGCAGCGGACCCAGCAGAATATGGCCCAAAAAGGAGGCAGGTCTCCTGTTGCAAGAGCCTCTGTTTTTTTA
AAGAGAAAACAAAGAATCCTGGTTTTTATGTGAAATCTCTAATTTTAAAATAATAACTCATTAAAAATATTGTAA
TGTCCAAAAGTATCTTTCCATTTAACTTCTAAAAATCTCTTAAATGTTTTTTTTAAATAATTGTAAAGTGAGTTT
TTGTTAAGCTTATAGGAATGGGCCAGTTAACTAAGGTAGACAGATGTAGGAAATTAAATATTTGATTTACTTAGG
GATCTATATGACATCAGTTATCAAAGAATACATTTTAACCCAAAAGTATACCATGCTCATTGTATCTTTGATCGT
TCTTCAAGTATTTCTCAATCTTTTAATCTATCAGGAACATTACTATCAAGAGCAGATTGTTGTAACATAATACTC
AGGATACATGAAATGTATGTGAGAGATAAATAGATAATAGAAAGTTTATTGTTATAAAAATGACCTACAACTTAT
ATAAAAAAATTCTGAAAATGTTGACTTTTTTTGGACTGAAGGCTGCAAAATAAATGGCTTCTCAAAGTAAATTCC
TATTTACTTAAATTGCCTTCTTGATTGTTACACCTGGAAAAATATATTCATCTACTTTTTCCTTTTAATTATGTT
AGTAGACTGAATTAAACCAGCTACATAGACACTCTCTCATTTGAAGCTGTTGGGATCCTTGAGTTGCCTCTTTCA
TTGGTACGTTTTATCCATTGTCACAACTGTGGTCTTCATTAATAACTCATTTTAATGTCTTAGGAGTAGAATGTG
TTTCCTTATTTTTTTTCAAATAAGAGTCAGTTAATTTGAAATGGCAAATTATTTACCTGAATGTGTATCATTGTT
CATTTGCAAGGTTTAAGCTCAGGCAGATCCAATAATTAGGTAAAGGTTGCATCTTTGGTCCTCTTGCACATTTTT
TCTGGTAATCAAATCTGAAGCGACATCTCAGCAAGCAGACTTGGGTTATTTTCCACTAGGATGGGAATGGAAAAC
AGTGCTGGAGACTGGGAAGTGGCTATTTCCTGTGTCTCACTGGGGAATTGCAAGATCAAAGAATGTTGTTACTTT
TATGTGATGAAAAAATAGGGCAAGAAAGATATACCTGAATCATCAGACTGCTTAAAATTTGGGAGGAAAAAAATTC
TATTTTACTACTAACCATAAATCACTTTTGCTAGATAGTACTTTAAAGATTCTGAATTAAATGTATCTTTAAAAA
CAACAATATAATATTACTAAAAAATGCAGACATACTTAAACTTGCTAGAATAAATTCTGTGAGGTCTTCGTTTGG
TATTTTCATAGGATTTCTTACTGTTAAGTTATTGGAAAATGAAAATATAAAGTGCTTTCAGAAGTTATAGTATTT
TCCAATTCATTGAATTACTTTGCTTGTGAAAATATATTAAACATATTTAAATGAGACCTATCCTACATTTAAAAA
CCAGTTTTGTTTATATAAAATTGTATTTGAAAGGTCCTGAACATTAAAAATGTGAAAATTTATAATGTTGATGAT
CAAAAGTAACGTGTTGAGACTCTGAGCTTAATCCATTAAATGGATTTTAGAATCTAGTAGAAGTTA

FIGURE 656

ISKQQKQQKNHMPGGEQRDHLVQSLHGDEGSWEPLFMSQVLS

FIGURE 657

GGGGCGGCCCTGGCCAGAAGCGGAGGAGGTGGCACCCGGGACCGAGCTGGGGTCTTGGAGGAAGAGAGGATGGCG
TCGTCGAGCCCTGACTCCCCATGTTCCTGCGACTGCTTTGTCTCCGTGCCCCCGGCCTCAGCCATCCCGGCTGTG
ATCTTTGCCAAGAACTCGGACCGACCCCGGGACGAGGTGCAGGAGGTGGTGTTTGTCCCCGCAGGCACTCACACT
CCTGGGAGCCGGCTCCAGTGCACCTACATTGAAGTGGAACAGGTGTCGAAGACGCACGCTGTGATTCTGAGCCGT
CCTTCTTGGCTATGGGGGGCTGAGATGGGCGCCAACGAGCATGGTGTCTGCATTGGCAACGAGGCTGTGTGGACG
AAGGAGCCAGTTGGGGAGGGGGAAGCCCTGCTGGGCATGGACCTACTCAGGCTGGCTTTGGAACGGAGCAGCTCT
GCCCAGGAGGCCTTGCATGTGATCACAGGGTTACTGGAGCACTATGGGCAGGGGGGCAACTGCCTGGAGGATGCT
GCGCCATTCTCCTACCATAGCACCTTCCTGCTGGCTGACCGCACTGAGGCGTGGGTGCTGGAGACAGCTGGGAGG
CTCTGGGCTGCACAGAGGATCCAGGAGGGGGCCCGCAACATCTCCAACCAGCTGAGCATTGGCACGGACATCTCG
GCCCAACACCCGGAGCTGCGGACTCATGCCCAGGCCAAGGGCTGGTGGGATGGGCAGGGTGCCTTTGACTTTGCT
CAGATCTTCTCCCTGACCCAGCAGCCTGTGCGCATGGAGGCTGCCAAGGCCCGCTTCCAGGCAGGGCGGGAGCTG
CTGCGGCAACGGCAAGGGGGCATCACGGCAGAGGTGATGATGGGCATCCTCAGAGACAAGGAGAGTGGTATCTGT
ATGGACTCGGGAGGCTTTCGCACCACGGCCAGCATGGTGTCTGTCCTGCCCCAGGATCCCACGCAGCCCTGCGTG
CACTTTCTTACCGCCACGCCAGACCCATCCAGGTCTGTGTTCAAACCTTTCATCTTCGGGGTGGGGGTGGCCCAG
GCCCCCCAGGTGCTGTCCCCCACTTTTGGAGCACAAGACCCTGTTCGGACCCTGCCCCGATTCCAGACTCAGGTA
GATCGTCGGCATACCCTCTACCGTGGACACCAGGCAGCCCTGGGGCTGATGGAGAGAGATCAGGTATCCCCCAGG
GAGTAGGGGCTACCTTGAGGGGATGATAGACCTCCCCCACTCCCAGTGGGACTCTGGAAATATGAAGGAACTAGG
GAGTGGAAGAGATTTCAGAGCTGGGGAGAGGAGTTCCTCCCTTCAAAGCCAGCAACTGCCTTTGGGGAATGTCGG
GGGGTCTCTCCTTTCTCCTGCTTGTGTGAGGTGGTACACAGTCCCCCCTTCACCTGGCGGGAAGCCTGTCCCGGA
CAGACTCATCTCAGCTTTCCCTTGGGGCAGGATCGGGGGCAGCAGCTCCAGCAGAAACAGCAGGATCTGGAGCAG
GAAGGCCTCGAGGCCACACAGGGGCTGCTGGCCGGCGAGTGGGCCCCACCCCTCTGGGAGCTGGGCAGCCTCTTC
CAGGCCTTCGTGAAGAGGGAGAGCCAGGCTTATGCGTAAGCTTCATAGCTTCTGCTGGCCTGGGGTGGACCCAGG
ACCCCTGGGGCCTGGGTGCCCTGAGTGGTGGTAAAGTGGAGCAATCCCTTCACGCTCCTTGGCCATGTTCTGAGC
GGCCAGCTTGGCCTTTGCCTTAATAAATGTGCTTTATTTTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 658

GAALARSGGGGTRDRAGVLEEERMASSSPDSPCSCDCFVSVPPASAIPAVIFAKNSDRPRDEVQEVVFVPAGTHT
PGSRLQCTYIEVEQVSKTHAVILSRPSWLWGAEMGANEHGVCIGNEAVWTKEPVGEGEALLGMDLLRLALERSSS
AQEALHVITGLLEHYGQGGNCLEDAAPFSYHSTFLLADRTEAWVLETAGRLWAAQRIQEGARNISNQLSIGTDIS
AQHPELRTHAQAKGWWDGQGAFDFAQIFSLTQQPVRMEAAKARFQAGRELLRQRQGGITAEVMMGILRDKESGIC
MDSGGFRTTASMVSVLPQDPTQPCVHFLTATPDPSRSVFKPFIFGVGVAQAPQVLSPTFGAQDPVRTLPRFQTQV
DRRHTLYRGHQAALGLMERDQVSPRE

FIGURE 659

GCGGCCGCGCGGCCTCCCGGGCGGGCCTACAGCC**ATG**TCCCGGGACCCGGGGTCGGGCGGCTGGGAGGAGGCCCC
GCGCGCAGCTGCCGCGCTCTGCACCCTGTACCACGAGGCCGGACAGCGGCTGCGCCGCCTGCAGGACCAGCTCGC
TGCCCGCGACGCCCTCATCGCTCGCCTCCGCGCCCGCCTGGCCGCGCTGGAGGGGGACGCCGCGCCGTCCCTAGT
GGACGCGCTGCTGGAGCAGGTTGCGCGCTTCCGGGAGCAGCTGCGAAGGCAGGAGGGCGGCGCCGCCGAGGCCCA
GATGCGCCAGGAAATTGAGAGGCTGACTGAGCGACTAGAAGAAAAAGAGAGGGAGATGCAGCAGCTGCTGAGCCA
GCCCCAACACGAGCGAGAGAAGGAAGTCGTCCTGCTACGGAGGAGCATGGCAGAAGGGGAGCGCGCCCGGGCCGC
CAGTGACGTCCTGTGCCGCTCCTTGGCCAACGAGACCCATCATCTGCGGAGGACGCTGACCGCCACCGCCCACAT
GTGTCAGCATCTGGCCAAGTGTCTGGATGAACGACAGCATGCACAAAGGAATGTGGGGGAGAGAAGTCCTGACCA
GTCGGAACACACAGATGGGCACACCTCTGTCCAGAGTGTTATTGAGAAGTTGCAGGAAGAAAATCGACTGTTAAA
ACAGAAGGTGACTCACGTTGAAGACCTCAATGCCAAGTGGCAGCGCTACAACGCCAGCAGGGACGAATACGTGAG
GGGGCTCCATGCGCAGCTCAGGGGGCTGCAGATCCCCCACGAGCCCGAGCTGATGAGGAAGGAGATCTCCCGGCT
CAACAGACAGTTGGAAGAGAAAATAAATGACTGTGCCGAAGTGAAGCAGGAGCTGGCGGCCTCCAGGACGGCCCG
GGATGCTGCGTTGGAGCGGGTGCAGATGCTGGAACAGCAGATTCTCGCTTACAAGGATGACTTCATGTCAGAAAG
GGCCGATCGGGAACGGGCTCAAAGTAGGATTCAAGAACTGGAGGAAAAGGTCGCCTCTTTGCTGCACCAGGTGTC
CTGGAGACAGGATTCTCGAGAGCCAGACGCCGGCCGGATTCACGCTGGGAGCAAAACTGCCAAGTATTTGGCCGC
CGACGCATTAGAGCTTATGGTGCCTGGTGGCTGGAGGCCTGGGACTGGGTCCCAGCAGCCAGAACCCCCTGCAGA
GGGCGGGCATCCTGGCGCGGCCCAGAGAGGCCAGGGGGACCTTCAGTGCCCTCACTGCCTGCAGTGCTTCAGTGA
CGAGCAAGGGGAAGAGCTCCTCAGGCATGTGGCCGAGTGCTGCCAG**TGA**CCGAGACTCACCCGTGCCCTTGCGGC
CTCCTGGCCCGGTGCAGCTGCCCTCAGGGACAGGGTGGGTGCTCTCAGATGCCATGGGTTGAGCTCTACTGAGAG
CCAAGGCCCCTAGAATAGTTGCGGGGCACTCTGATCGTTCACTTTGGTCCCTTTGGCTATGGAACAGGCTGGGTC
ACAGGGAACTGCCAGTGAGGCTGGAGGCTGGAGGTGGAGATGGGGTCAGGAACATCTGGCAGAGGGAGGTCCCAG
TCTGTGTCTCCATCAGGCTTAAGCCAGAGCTATCTGGTGCTGGTGTGCCAGCCCCTCCCCCAGCCTGCCTAGAAA
GGGGTGGCTGCCTGAGGGAGTCACTTGTATGGTCCCCAGGGTGGGAGCCCCATCCTGTTCTATGGAATAAAGCGT
CGCCTCTCTGCCTCGAACCAGTCAAATGGAGTATTGCGGCTGCACGTCACACTAGGGTGGCCACCCCCGCCATTG
CGAGCCACATGTCTGC

FIGURE 660

MSRDPGSGGWEEAPRAAAALCTLYHEAGQRLRRLQDQLAARDALIARLRARLAALEGDAAPSLVDALLEQVARFR
EQLRRQEGGAAEAQMRQEIERLTERLEEKEREMQQLLSQPQHEREKEVVLLRRSMAEGERARAASDVLCRSLANE
THHLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSPDQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNA
KWQRYNASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDCAEVKQELAASRTARDAALERVQMLE
QQILAYKDDFMSERADRERAQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLAADALELMVPGGW
RPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPHCLQCFSDEQGEELLRHVAECCQ

FIGURE 661

CCTGTTTCTTAATGGCTCTTTTTCAAAGGTTAATGTAAGCTTTTTGGAAATTCACATTGTCTTCCTGACAGTTAT
AGGGCAAAGTAGTATCTACACCCTGGGAACACCTAGCACATCTGTTCTTAGAAGCCCTTAGCAGTTGTTCATGAG
CTTTGATTTTTAAAAAACTCCTTTGGCCTTGCTTTTGATGCCTTGATGTGTTTTTTTCATCACCTTTGGTTATAT
CAGTAAGCATTGAAGCACCCTCTCTGCTGGTACTTGGTGTCTTAGCCTGAAGCTCCCTTTGACGTTCCCTGGAGG
TGGAAAGCACTCTTTTTATTTTG**ATG**TCACCATTTTGTTTTTGCTTTGATGGCATTTGGGCCTGGAATATAGACC
CTCTATTGGCACCGGTAGCCTTTATGTGCCTACGAGGCTCAAAGCCCTGCCTGTGCCCACCGGGCCTGTCTCATA
CCAGGAGGCTATTTCTCTGTCTGTCCTGGGGAAGCCACAGAACCAGTGCAAAGGAGTTGAGGGGTAGTTTTTTAT
TGTTGCTGTTGTTGGGTGCCCTTCTCAATCATTGCCTTTCTAGA**TAG**CCATCTGGATCACCTTTTCTTCCTAAAA
TGTGAAAAGGCCCACACCCCTATGCATTTTATTGTTCCCAAGTATTATATGTTTGTGTCATATATCATATGTATA
TATTCACATATATATATGTTTTTTTTTAACC

FIGURE 662

MSPFCFCFDGIWAWNIDPLLAPVAFMCLRGSKPCLCPPGLSHTRRLFLCLSWGSHRTSAKELRGSFLLLLLLGAL
LNHCLSR

FIGURE 663

GTCCATGGGGAAGCTGCCATTTTCTTGAAAAAGCCAGAATTGCACAGAAAGGAGGTGCTGAAGCA**ATG**TTAGTTG
TCAATAACAGTGTCCTATTTCCTCCCTCAGGTGACAGATCTGAATTTCCTGATGTGAAAATACTGATTGCATTTA
TAAGCTACAAAGACTTTAGAGATATGAACCAGACTCTAGGAGATAACATTACTGTGAAAATGTATTCTCCATCGT
GGCCTAACTTTGATTATACTATGGTGGTTATTTTTGTAATTGCGGTGTTCACTGTGGCATTAGGTGGATACTGGA
GTGGACTAGTTGAATTGGAAAACTTGAAAGCAGTGACAACTGAAGATAGAGAAATGAGGAAAAAGAAGGAAGAAT
ATTTAACTTTTAGTCCTCTTACAGTTGTAATATTTGTGGTCATCTGCTGTGTTATGATGGTCTTACTTTATTTCT
TCTACAAATGGTTGGTTTATGTTATGATAGCAATTTTCTGCATAGCATCAGCAATGAGTCTGTACAACTGTCTTG
CTGCACTAATTCATAAGATACCATATGGACAATGCACGATTGCATGTCGTGGCAAAAACATGGAAGTGAGACTTA
TTTTTCTCTCCGGACTGTGCATAGCAGTAGCTGTTGTTTGGGCTGTGTTTCGAAATGAAGACAGGTGGGCTTGGA
TTTTACAGGATATCTTGGGGATTGCTTTCTGTCTGAATTTAATTAAAACACTGAAGTTGCCCAACTTCAAGTCAT
GTGTGATACTTCTAGGCCTTCTCCTCCTCTATGATGTATTTTTTGTTTTCATAACACCATTCATCACAAAGAATG
GTGAGAGTATCATGGTTGAACTCGCAGCTGGACCTTTTGGAAATAATGAAAAGTTGCCAGTAGTCATCAGAGTAC
CAAAACTGATCTATTTCTCAGTAATGAGTGTGTGCCTCATGCCTGTTTCAATATTGGGTTTTGGAGACATTATTG
TACCAGGCCTGCTGATTGCATACTGTAGAAGATTTGATGTTCAGACTGGTTCTTCTTACATATACTATGTTTCGT
CTACAGTTGCCTATGCTATTGGCATGATACTTACATTTGTTGTTCTGGTGCTGATGAAAAAGGGGCAACCTGCTC
TCCTCTATTTAGTACCTTGCACACTTATTACTGCCTCAGTTGTTGCCTGGAGACGTAAGGAAATGAAAAAGTTCT
GGAAAGGTAACAGCTATCAGATGATGGACCATTTGGATTGTGCAACAAATGAAGAAAACCCTGAGATATCTGGTG
AACAGATTGTCCAGCAA**TAA**TATTATGTGGAACTGCTATAATGTGTCATTGATTTTCTACAAATAGACTTCGACT
TTTTAAATTGACTTTTGAATTGACAATCTGAAAGAGTCTTCAATGATATGCTTGCAAAAATATATTTTTATGAGC
TGGTACTGACAGTTACATCATAAATAACTAAAACGCTTTGCTTTTAATGTTAAAGTTGTGCCTTCACATTAAATA
AAACATATGGTCTGTGTAGTTTCCGAGATGTACTATATACAGTATATTTTTCT

FIGURE 664

MLVVNNSVLFPPSGDRSEFPDVKILIAFISYKDFRDMNQTLGDNITVKMYSPSWPNFDYTMVVIFVIAVFTVALG
GYWSGLVELENLKAVTTEDREMRKKKEEYLTFSPLTVVIFVVICCVMMVLLYFFYKWLVYVMIAIFCIASAMSLY
NCLAALIHKIPYGQCTIACRGKNMEVRLIFLSGLCIAVAVVWAVFRNEDRWAWILQDILGIAFCLNLIKTLKLPN
FKSCVILLGLLLLYDVFFVFITPFITKNGESIMVELAAGPFGNNEKLPVVIRVPKLIYFSVMSVCLMPVSILGFG
DIIVPGLLIAYCRRFDVQTGSSYIYYVSSTVAYAIGMILTFVVLVLMKKGQPALLYLVPCTLITASVVAWRRKEM
KKFWKGNSYQMMDHLDCATNEENPEISGEQIVQQ

FIGURE 665

ATATTCCCCATCTGATTCCACTATGAGCAGTNCCATGCATGCCCTACTAGAACTGTGGATACGCTTTAAAACAAG
TGGAAG**ATG**ATAGGGTGGGACTCATTACGTCTAATCTTGGGGAACACTGATAACGTGTCCAGGAGAGACAGCACA
AGGGGCTCCATCTTCATCACACAACTCATCGCATGCTTCCAGAGATATTCCTGGCGCTGCCACCTAGAGGAAGTA
TTTTGGAAGGTTCAGCAAGCATTTGAAAGTCCGGAGGCAACAGTCCAAATGCCCACCATAGAACGAGTGTCCATG
ACAAGATATTTCTACCTCTTTCCTGGCAAC**TGA**AAATGGTTAAGCATTGAGAGTTGTTGGTGGTGTATGAAATAA
ATGAAAGTGTGATATTGGAGGAAACCACAAGCAGCCCAGCCCTCCTTTATCAACTTCAAGAAACACCTTTACTAG
TACAGATTGAATGCTTAACATTTTGTATTTCAATAAAGGTGAAGACAAATG

FIGURE 666

MIGWDSLRLILGNTDNVSRRDSTRGSIFITQLIACFQRYSWRCHLEEVFWKVQQAFESPEATVQMPTIERVSMTR
YFYLFPGN

FIGURE 667

TTG**ATG**CTTCGCTTTCTGGGTGAAAAAGCTGCAGCAAAGAGACAAGTCCTAAATGCCGACTCAGTGGAACAATCT
TTTGTTGGATTGAAACAGCTAATCAGCTGCAGAAACTGGAGGGCAGCAGTGGACCTGTGCGGACGTCTCCTCACA
GCCCACGGCCAGGGCTACGGCAAGAGCGGGCTGCTCACCAGCCACACGACAGATTCACTGCAGCTCTGGTTTGTC
AGGCTGGCACTACTAGTGAAGTTGGGCCTTTTCCAGAATGCTGAGATGGAATTTGAGCCCGTCGGAAATCTTGAT
CAGCCAGATCTTTATTACGAGTACTACCCGCACGTGTACCCTGGGCGCAGGGGCTCCATGGTCCCCTTCTCGATG
CGCATCTTGCACGCGGATTTGCAGCAGTACCTGGGGAACCCACAGGAGTCGCTGGATAGACTGCACAAGGTGAAG
ACTGTCTGCAGCAAGATCCTGGCCAATTTGGAGCAAGGCTTAGCAGAAGACGGCGGCATGAGCAGCGTGACTCAG
GAGGGCAGACAAGCCTCTATCCGGCTGTGGAGGTCACGTCTGGGCCGGGTGATGTACTCCATGGCAAACTGTCTG
CTCCTGATGAAGGATTATGTGCTGGCCGTGGAGGCGTATCATTCGGTTATCAAGTATTACCCAGAGCAAGAGCCC
CAGCTGCTCAGCGGCATCGGCCGGATTTCCCTCCAGATTGGAGACATAAAAACAGCTGAAAAGTATTTTCAAGAC
GTTGAGAAAGTAACACAGAAATTAGATGGACTACAGGGTAAAATCATGGTTTTGATGAACAGCGCGTTCCTTCAC
CTCGGGCAGAATAACTTTGCAGAAGCCCACAGGTTCTTCACAGAGATCTTAAGGATGGATCCAAGAAACGCAGTG
GCCAACAACAACGCTGCCGTGTGTCTGCTCTACCTGGGCAAGCTCAAGGACTCCCTGCGGCAGCTGGAGGCCATG
GTCCAGCAGGACCCCAGGCACTACCTGCACGAGAGCGTGCTCTTCAACCTGACCACCATGTACGAGCTGGAGTCC
TCACGGAGCATGCAGAAGAAACAGGCCCTGCTGGAGGCTGTCGCCGGCAAGGAGGGGGACAGCTTCAACACACAG
TGCCTCAAGCTGGCC**TAG**CTGCCTCCAACACACTACGTCAGAAGGACCCGGGTCTTTGAAACTGTGTCTTGAAGC
TAATGTATTAATGTGACATGGAGGAACTCAATAAAACTCCTGCTTCACTGGTGAAAAA

FIGURE 668

MLRFLGEKAAAKRQVLNADSVEQSFVGLKQLISCRNWRAAVDLCGRLLTAHGQGYGKSGLLTSHTTDSLQLWFVR
LALLVKLGLFQNAEMEFEPVGNLDQPDLYYEYYPHVYPGRRGSMVPFSMRILHADLQQYLGNPQESLDRLHKVKT
VCSKILANLEQGLAEDGGMSSVTQEGRQASIRLWRSRLGRVMYSMANCLLLMKDYVLAVEAYHSVIKYYPEQEPQ
LLSGIGRISLQIGDIKTAEKYFQDVEKVTQKLDGLQGKIMVLMNSAFLHLGQNNFAEAHRFFTEILRMDPRNAVA
NNNAAVCLLYLGKLKDSLRQLEAMVQQDPRHYLHESVLFNLTTMYELESSRSMQKKQALLEAVAGKEGDSFNTQC
LKLA

FIGURE 669

AATGGAGGAAGACTGGACCTACTGATTCAACTTGGAGATGAGCGGGTCTGTCCTCTTCACGGCGGGAGAGAGGTG
GAGATGCTTTCTGACCCCGTCGAGGTCATCCCTGTACTGGGCCTTACATAATTTCTGCTGTCGGAAAAAATCCAC
TACACCTAAGAAAATTACTCCCAATGTTACTTTTTGTGATGAAAATGCAAAGGAGCCCGAAAATGCACTTGACAA
GCTCTTCTCTTCAGAACAGCAGGCTTCCATCTTGCATGTGTTGAATACAGCATCTACTAAAGAACTTGAAGCTTT
CCGATTGCTTCGTGGAAGAAGGTCCATCAATATCGTAGAGCACAGAGAAAACTTTGGGCCATTTCAGAATTTAGA
GAGTTTAATGAATGTGCCCTTGTTTAAGTATAAAAGTACAGTTCAAGTTTGTAACTCCATACTTTGTCCAAAGAC
TGGACGGGAAAAAAGAAAGTCACCGGAAAACCGGTTCCTGAGAAAGCTCCTCAAACCAGACATAGAAAGAGAAAG
ACTTAAGAATTGCCTGGGCTCACCTTGATCGTAAGTTGACAGTGCTGGACTGGCAGCAAAGTGACCGTTGGAGTT
TA**ATG**AGAGGAATATACTCATCATCAGTCTATTTAGAAGAGATTTCCTCGATCATTTCAAAGATGCCTAAAGCAG
ATTTCTATGTTCTGGAAAAAACAGGACTATCCATTCAGAACTCATCTCTGTTTCCAATACTGTTACATTTTCATA
TCATGGAAGCCATGCTGTATGCCTTATTAAATAAAACTTTTGCCCAGGATGGGCAGCATCAGGTGCTGAGCATGA
ATCGAAATGCAGTGGGGAAGCATTTTGAACTGATGATTGGTGACTCCCGGACTAGTGGAAAAGAGCTAGTGAAGC
AGTTTCTCTTCGATTCTATACTGAAGGCGGATCCTCGGGTGTTCTTCCCATCAGATAAAATAGTTCACTACAGAC
AGATGTTTTTATCTACTGAACTACAAAGAGTAGAAGAGCTTTATGATTCATTATTACAAGCTATTGCCTTCTATG
AATTAGCAGTGTTTGACTCTCAGCCT**TAG**AATTCTGAGGTTAACGTGCTAAAGTATAATTATTAGCTCTAACGTA
ACACCAACTGTTGTGAACATCCATGTTATTGGAAAAGAACACATTTTCAGTGTATTTTAGATGTTTAAATTCTGA
CTTTTGGCTATTAAATGGTTTACACAATAAGCCAAGACCAAATCAATAAACATTTTATGAGAAAAAAAAAAAAAA
AAA

FIGURE 670

MRGIYSSSVYLEEISSIISKMPKADFYVLEKTGLSIQNSSLFPILLHFHIMEAMLYALLNKTFAQDGQHQVLSMN
RNAVGKHFELMIGDSRTSGKELVKQFLFDSILKADPRVFFPSDKIVHYRQMFLSTELQRVEELYDSLLQAIAFYE
LAVFDSQP

FIGURE 671

CCTTCCGGTCGTTAACGCCCACGGGCTCGCGCGGCGCCGCCTCCTGGGCTCAGTTACCGCGGACGCCAGTGCCGG
GCTCCAGGAGACGCAGGGCGACGCCACACGCCGGGGTGGCCGACTGGGTCAGCGCGGGCTGCGCCTCCTCGCCAT
GGGCCCCCTCTCGGCGCGGCTGCTAATGCAGCGCGGGCGCCCCAAGAGCGACCGGCTGGGGAAGATCCGGAGTCT
GGACCTGTCAGGATTGGAGCTGCTTTCCGAGCACCTGGACCCCAAACTCCTGTGCCGCCTGACGCAGCTGCAGGA
GCTTGACCTGTCTAACAACCACCTGGAGACGCTGCCGGACAACCTGGGCCTGTCCCACCTGCGTGTCCTCCGCTG
CGCCAACAACCAGCTGGGGGATGTTACTGCCTTGTGCCAGTTCCCCAAGCTCGAGGAACTCAGCCTGGAGGGCAA
CCCCTTCCTGACGGTCAATGACAACCTGAAAGTCTCCTTTCTCCTGCCCACGCTCCGTAAGGTCAATGGCAAGGA
TGCGTCCTCAACTTACTCTCAGGTGGAGAACCTGAATCGGGAGCTGACCAGCAGGGTCACAGCTCACTGGGAGAA
GTTCATGGCCACACTGGGTCCTGAAGAGGAGGCTGAGAAGGCCCAGGCGGACTTTGTGAAGTCGGCTGTCAGGGA
TGTCCGCTACGGGCCCGAGTCCCTCAGCGAGTTCACCCAGTGGCGGGTGCGGATGATCTCTGAGGAGCTGGTGGC
CGCCAGTAGGACCCAGGTGCAAAAGGCTAACAGCCCAGAGAAGCCCCCAGAAGCTGGAGCTGCCCACAAGCCCAG
GGCCAGACTGGCGGCCTTGAAACGGCCAGACGACGTCCCACTCAGCCTCTCTCCCAGCAAGCGGGCGTGTGCCTC
CCCGTCGGCCCAGGTGGAGGGCAGCCCTGTGGCAGGCTCCGATGGCAGCCAGCCTGCTGTGAAGCTGGAGCCCCT
GCACTTCCTGCAGTGCCACAGCAAGAACAACAGCCCCCAGGACCTCGAGACCCAGCTGTGGGCCTGTGCCTTCGA
GCCGGCCTGGGAGGAGGGGGCCACATCCCAGACCGTGGCCACGTGCGGCGGGGAGGCTGTGTGCGTAATTGATTG
CCAGACGGGCATCGTGCTCCACAAGTACAAGGCACCCGGCGAGGAGTTCTTTTCTGTGGCCTGGACCGCTCTGAT
GGTGGTCACACAGGCTGGCCACAAGAAGCGCTGGAGTGTGCTGGCGGCTGCAGGCCTACGGGGCCTGGTCCGGCT
GCTGCACGTGCGTGCCGGCTTCTGCTGCGGGGTCATCCGAGCCCACAAGAAGGCCATCGCCACCCTGTGCTTCAG
CCCCGCCCACGAGACCCATCTCTTCACGGCCTCCTATGACAAGCGGATCATCCTCTGGGACATCGGGGTGCCCAA
CCAGGACTACGAATTCCAGGCCAGCCAGCTGCTCACACTGGACACCACCTCTATCCCCCTGCGCCTCTGCCCTGT
CGCCTCCTGCCCGGACGCCCGCCTGCTGGCCGGCTGCGAGGGCGGCTGCTGCTGCTGGGACGTGCGGCTGGACCA
GCCCCAAAAGAGGAGGGTGTGTGAAGTGGAATTCGTCTTCTCTGAGGGCTCCGAGGCATCTGGACGGAGAGTGGA
TGGGCTGGCATTTGTGAATGAGGACATCGTGGCCTCCAAGGGGAGCGGCCTGGGCACCATCTGCCTGTGGAGCTG
GAGGCAGACGTGGGGGGGCCGGGGCAGCCAGTCCACAGTGGCAGTGGTGGTCCTGGCGCGGCTGCAATGGTCGTC
CACCGAGTTGGCCTACTTCTCGCTCAGCGCCTGCCCTGATAAGGGGATTGTGCTCTGTGGGGATGAGGAGGGCAA
CGTGTGGCTCTACGACGTCAGCAACATCCTGAAGCAGCCACCCCTGCTGCCGGCAGCCCTGCAGGCCCCCACACA
GATCCTGAAGTGGCCCCAGCCCTGGGCCCTTGGCCAGGTGGTGACCAAGACCATGGTGAACACAGTGGTGGCCAA
TGCCTCCTTCACCTACCTCACCGCCCTGACGGACTCCAACATCGTAGCCATCTGGGGGAGGATGTAGCCTCACAC
CATCGCAAAGGACCAGGGACACAGCTAACTAACTTATTCAGCTTTGGGCCGATGGGGGTGGGGGGGGTCTTTCAG
TGAATATTTTTATTAAACTCTACTGTGGACAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 672

LPVVNAHGLARRRLLGSVTADASAGLQETQGDATRRGGRLGQRGLRLLAMGPLSARLLMQRGRPKSDRLGKIRSL
DLSGLELLSEHLDPKLLCRLTQLQELDLSNNHLETLPDNLGLSHLRVLRCANNQLGDVTALCQFPKLEELSLEGN
PFLTVNDNLKVSFLLPTLRKVNGKDASSTYSQVENLNRELTSRVTAHWEKFMATLGPEEEAEKAQADFVKSAVRD
VRYGPESLSEFTQWRVRMISEELVAASRTQVQKANSPEKPPEAGAAHKPRARLAALKRPDDVPLSLSPSKRACAS
PSAQVEGSPVAGSDGSQPAVKLEPLHFLQCHSKNNSPQDLETQLWACAFEPAWEEGATSQTVATCGGEAVCVIDC
QTGIVLHKYKAPGEEFFSVAWTALMVVTQAGHKKRWSVLAAAGLRGLVRLLHVRAGFCCGVIRAHKKAIATLCFS
PAHETHLFTASYDKRIILWDIGVPNQDYEFQASQLLTLDTTSIPLRLCPVASCPDARLLAGCEGGCCCWDVRLDQ
PQKRRVCEVEFVFSEGSEASGRRVDGLAFVNEDIVASKGSGLGTICLWSWRQTWGGRGSQSTVAVVVLARLQWSS
TELAYFSLSACPDKGIVLCGDEEGNVWLYDVSNILKQPPLLPAALQAPTQILKWPQPWALGQVVTKTMVNTVVAN
ASFTYLTALTDSNIVAIWGRM

FIGURE 673A

GAATTCGGGGGGCGAGTAAGCCAGCGGCAGGACCAGCGGGCGGGGGCCACAACAAAAGCTGGCAGGCTGACAGAG
GCGGCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCCGGATTGTGTGTAGGTGTGAGATC
AACC**ATG**AGTTCCGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGAAGTGGGCTGGTTCCGCAACAAAT
CAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCCTCCAACCTACAAGGATGCCTTCCCTCCACTTCCTGA
GAAAGCTGCTTGCCTGGAAAGTGCCCAGGAACCCGCTGGAGCCTGGGGGAACAAGATCCGACCCATCAAGGCTTC
TGTCATCACTCAGGTGTTCCATGTACCCCTGGAGGAGAGAAAATACAAGGATATGAACCAGTTTGGAGAAGGTGA
ACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAACTGGTGCTCACTTGGAGCTGTCTTTGGCCAAAGACCAAGG
CCTCTCCATCATGGTGTCAGGAAAGCTGGATGCTGTCATGAAAGCTCGGAAGGACATTGTTGCTAGACTGCAGAC
TCAGGCCTCAGCAACTGTTGCCATTCCCAAAGAACACCATCGCTTTGTTATTGGCAAAAATGGAGAGAAACTGCA
AGACTTGGAGCTAAAAACTGCAACCAAAATCCAGATCCCACGCCCAGATGACCCCAGCAATCAGATCAAGATCAC
TGGCACCAAAGAGGGCATCGAGAAAGCTCGCCATGAAGTCTTACTCATCTCTGCCGAGCAGGACAAACGTGCTGT
GGAGAGGCTAGAAGTAGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTATAATAGACTGGTTGGCGAGATCAT
GCAGGAGACAGGCACGCGCATCAACATCCCCCCACCCAGCGTGAACCGGACAGAGATTGTCTTCACTGGAGAGAA
GGAACAGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAGAAAAAGAAGACTACAACCATTGC
AGTGGAAGTGAAGAAATCCCAACACAAGTATGTCATTGGGCCCAAGGGCAATTCATTGCAGGAGATCCTTGAGAG
AACTGGAGTTTCCGTTGAGATCCCACCCTCAGACAGCATCTCTGAGACTGTAATACTTCGAGGCGAACCTGAAAA
GTTAGGTCAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTCTCCTCTGTCGCCGCCCCTTCCTG
GCTTCACCGTTTCATCATTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACTCAGCAGATGCCAAAGGTTCACAT
CGAGTTCACAGAGGGCGAAGACAAGATCACCCTGGAGGGCCCTACAGAGGATGTCAATGTGGCCCAGGAACAGAT
AGAAGGCATGGTCAAAGATTTGATTAACCGGATGGACTATGTGGAGATCAACATCGACCACAAGTTCCACAGGCA
CCTCATTGGGAAGAGCGGTGCCAACATAAACAGAATCAAAGACCAGTACAAGGTGTCCGTGCGCATCCCTCCTGA
CAGTGAGAAGAGCAATTTGATCCGCATCGAGGGGGACCCACAGGGCGTGCAGCAGGCCAAGCGAGAGCTGCTGGA
GCTTGCATCTCGCATGGAAAATGAGCGTACCAAGGATCTAATCATTGAGCAAAGATTTCATCGCACAATCATTGG
GCAGAAGGGTGAACGGATCCGTGAAATTCGTGACAAATTCCCAGAGGTCATCATTAACTTTCCAGACCCAGCACA
AAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCAGAAGATGGT
GGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAATATCATTGGGAA
AGGAGGCGCAAACATTAAAAAGATTCGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAATAGCAATTC
AGAGACCATTATCATCACAGGCAAGCGAGCCAACTGCGAAGCTGCCCGGAGCAGGATTCTGTCTATTCAGAAAGA
CCTGGCCAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAACTCCCTCATTGGCACCAAGGGCCG
TCTGATCCGCTCCATCATGGAGGAGTGCGGCGGGGTCCACATTCACTTTCCCGTGGAAGGTTCAGGAAGCGACAC
CGTTGTTATCAGGGGCCCTTCCTCGGATGTGGAGAAGGCCAAGAAGCAGCTCCTGCATCTGGCGGAGGAGAAGCA
AACCAAGAGTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAATTCCTCATCGGCAAGGGGGGCGGCAA
AATTCGCAAGGTGCGCGACAGCACTGGAGCACGTGTCATCTTCCCTGCGGCTGAGGACAAGGACCAGGACCTGAT
CACCATCATTGGAAAGGAGGACGCCGTCCGAGAGGCACAGAAGGAGCTGGAGGCCTTGATCCAAAACCTGGATAA
TGTGGTGGAAGACTCCATGCTGGTGGACCCCAAGCACCACCGCCACTTCGTCATCCGCAGAGGCCAGGTCTTGCG
GGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCAGCTTCCCACGCTCTGGCACACAGAGCGACAAAGTCACCCT
CAAGGGCGCCAAGGACTGTGTGGAGGCAGCCAAGAAACGCATTCAGGAGATCATTGAGGACCTGGAAGCTCAGGT
GACATTAGAATGTGCTATACCCCAGAAATTCCATCGATCTGTCATGGGCCCCAAAGGTTCCAGAATCCAGCAGAT
TACTCGGGATTTCAGTGTTCAAATTAAATTCCCAGACAGAGAGGAGAACGCAGTTCACAGTACAGAGCCAGTTGT
CCAGGAGAATGGGGACGAAGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGACCCCGGCTCTCCAAGGAGGTGTGA
CATCATCATCATCTCTGGCCGGAAAGAAAAGTGTGAGGCTGCCAAGGAAGCTCTGGAGGCATTGGTTCCTGTCAC
CATTGAAGTAGAGGTGCCCTTTGACCTTCACCGTTACGTTATTGGGCAGAAAGGAAGTGGGATCCGCAAGATGAT
GGATGAGTTTGAGGTGAACATACATGTCCCGGCACCTGAGCTGCAGTCTGACATCATCGCCATCACGGGCCTCGC
TGCAAATTTGGACCGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTACAGGCCGAGCAGGAGGACCGGGC
TTTAAGGAGTTTTAAGCTGAGTGTCACTGTAGACCCCAAATACCATCCCAAGATTATCGGGAGAAAGGGGGCAGT
AATTACCCAAATCCGGTTGGAGCATGACGTGAACATCCAGTTTCCTGATAAGGACGATGGGAACCAGCCCCAGGA
CCAAATTACCATCACAGGGTACGAAAAGAACACAGAAGCTGCCAGGGATGCTATACTGAGAATTGTGGGTGAACT
TGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGCGTTCACGCCCGCATCATTGGTGCCCGCGGCAAAGC

FIGURE 673B

CATTCGCAAAATCATGGACGAATTCAAGGTGGACATTCGCTTCCCACAGAGCGGAGCCCCAGACCCCAACTGCGT
CACTGTGACGGGGCTCCCAGAGAATGTGGAGGAAGCCATCGACCACATCCTCAATCTGGAGGAGGAATACCTAGC
TGACGTGGTGGACAGTGAGGCGCTGCAGGTATACATGAAACCCCCAGCACACGAAGAGGCCAAGGCACCTTCCAG
AGGCTTTGTGGTGCGGGACGCACCCTGGACCGCCAGCAGCAGTGAGAAGGCTCCTGACATGAGCAGCTCTGAGGA
ATTTCCCAGCTTTGGGGCTCAGGTGGCTCCCAAGACCCTCCCTTGGGGCCCCAAACGA**TAA**TGATCAAAAAGAAC
AGAACCCTCTCCAGCCTGCTGACCCGAACCCAACCACACAATGGTTTGTCTCAATCTGACCCAGCGGCTGGACCC
TCCGTAAATTGTTGAGCGCTCTTCCCCTTCCCGAGGTCCGCAGGGAGCCTAGCGCCTGGCTGTGTGTGCGGCCGC
TCCTCCAGGCCTGGCCGTGCCCGCTCAGGACCTGCTCCACTGTTTAACAATAAACCAAGGTCATGAGCATTCGAG
CTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTCAGTCAGCACTCTGGCCTTCATCACGAGAGCTCCG
CAGCCGTGGCTAGGATTCCACTTCCTGTGTCATGACCTCAGGAAATAAACGTCCTTGACTTTATAAAAGCCCCGA
ATTC

FIGURE 674

MSSVAVLTQESFAEHRSGLVPQQIKVATLNSEEESDPPTYKDAFPPLPEKAACLESAQEPAGAWGNKIRPIKASV
ITQVFHVPLEERKYKDMNQFGEGEQAKICLEIMQRTGAHLELSLAKDQGLSIMVSGKLDAVMKARKDIVARLQTQ
ASATVAIPKEHHRFVIGKNGEKLQDLELKTATKIQIPRPDDPSNQIKITGTKEGIEKARHEVLLISAEQDKRAVE
RLEVEKAFHPFIAGPYNRLVGEIMQETGTRINIPPPSVNRTEIVFTGEKEQLAQAVARIKKIYEEKKKKTTTIAV
EVKKSQHKYVIGPKGNSLQEILERTGVSVEIPPSDSISETVILRGEPEKLGQALTEVYAKANSFTVSSVAAPSWL
HRFIIGKKGQNLAKITQQMPKVHIEFTEGEDKITLEGPTEDVNVAQEQIEGMVKDLINRMDYVEINIDHKFHRHL
IGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGVQQAKRELLELASRMENERTKDLIIEQRFHRTIIGQ
KGERIREIRDKFPEVIINFPDPAQKSDIVQLRGPKNEVEKCTKYMQKMVADLVENSYSISVPIFKQFHKNIIGKG
GANIKKIREESNTKIDLPAENSNSETIIITGKRANCEAARSRILSIQKDLANIAEVEVSIPAKLHNSLIGTKGRL
IRSIMEECGGVHIHFPVEGSGSDTVVIRGPSSDVEKAKKQLLHLAEEKQTKSFTVDIRAKPEYHKFLIGKGGGKI
RKVRDSTGARVIFPAAEDKDQDLITIIGKEDAVREAQKELEALIQNLDNVVEDSMLVDPKHHRHFVIRRGQVLRE
IAEEYGGVMVSFPRSGTQSDKVTLKGAKDCVEAAKKRIQEIIEDLEAQVTLECAIPQKFHRSVMGPKGSRIQQIT
RDFSVQIKFPDREENAVHSTEPVVQENGDEAGEGREAKDCDPGSPRRCDIIIISGRKEKCEAAKEALEALVPVTI
EVEVPFDLHRYVIGQKGSGIRKMMDEFEVNIHVPAPELQSDIIAITGLAANLDRAKAGLLERVKELQAEQEDRAL
RSFKLSVTVDPKYHPKIIGRKGAVITQIRLEHDVNIQFPDKDDGNQPQDQITITGYEKNTEAARDAILRIVGELE
QMVSEDVPLDHRVHARIIGARGKAIRKIMDEFKVDIRFPQSGAPDPNCVTVTGLPENVEEAIDHILNLEEEYLAD
VVDSEALQVYMKPPAHEEAKAPSRGFVVRDAPWTASSSEKAPDMSSSEEFPSFGAQVAPKTLPWGPKR

FIGURE 675

AAAATGGTGGTGTTCGGGTATGAGGCTGGGACTAAGCCAAGGGATTCAGGTGTGGTGCCGGTGGGAACTGAGGAA
GCGCCCAAGGAAATGAAACACGATTTCCAAAATGAACTTAATCTTTCATGAGAAACTGAGGATAGAGATGTCAAT
AAGCAGCCACTGTTTCCACCTCCCCACCTGAAGAGCTAGGAGCGCCCAAGCTTTCGGTTCTGAGCTCGGACTAAG
CC**ATG**TGGATTCAGGTGTGGATGACGGTGGGAACTGAGGAAGCGCCCAAGGTTTTCAAGATGGCAGCATCTATGC
ATGGTCAGCCCAGTCCTTCTCTAGAAGATGCAAAACTCAGAAGACCAATGGTCATAGAAATCATAGAAAAAAATT
TTGACTATCTTAGAAAAGAAATGACACAAAATATATATCAAATGGCGACATTTGGAACAACAGCTGGTTTCTCTG
GAATATTCTCAAACTTCCTGTTCAGACGCTGCTTCAAGGTTAAACATGATGCTTTGAAGACATATGCATCATTGG
CTACACTTCCATTTTTGTCTACTGTTGTTACTGACAAGCTTTTTGTAATTGATGCTTTGTATTCAGATAATATAA
GCAAGGAAAACTGTGTTTTCAGAAGCTCACTGATTGGCATAGTTTGTGGTGTTTTCTATCCCAGTTCTTTGGCTT
TTACTAAAAATGGACGCCTGGCAACCAAGTATCATACCGTTCCACTGCCACCAAAAGGAAGGGTTTAATCCATT
GGATGACGCTTTGTCAAACACAAATGAAATTAATGGCGATTCCTCTAGTCTTTCAGATTATGTTTGGAATATTAA
ATGGTCTATACCATTATGCAGTATTTGAAGAGACACTTGAGAAAACTATACATGAAGAG**TAA**CCAAAAAAAATGAA
TGGTTGCTAACTTAGCAAAATGAAGTTTCTATAAAGAGGACTCAGGCATTGCTGAAAGAGTTAAAAGTAACTGTG
AACAAATAATTTGTTCTGTGCCTTTTGCCTGGTATATAGCAAATACTCAAAAAGTATTCAATAATTCAATCAATA
AATATAAGTTTCATCTTACACGTAAGATACAGGTCTTATCTCCTGATGGTGTGTCCATTTTGCCTGGTATATAAC
AGATAATAAATATCCAGTGTCAATAAATGTAACAATAAAAAAAAAAA

FIGURE 676

MWIQVWMTVGTEEAPKVFKMAASMHGQPSPSLEDAKLRRPMVIEIIEKNFDYLRKEMTQNIYQMATFGTTAGFSG
IFSNFLFRRCFKVKHDALKTYASLATLPFLSTVVTDKLFVIDALYSDNISKENCVFRSSLIGIVCGVFYPSSLAF
TKNGRLATKYHTVPLPPKGRVLIHWMTLCQTQMKLMAIPLVFQIMFGILNGLYHYAVFEETLEKTIHEE

FIGURE 677

GGAAAAGATGGCGGCTGCCGCACAATCCCGGGTTGTCCGGGTCCTGTCAATGTCACGTTCTGCCATTACTGCAAT
AGCCACATCTGTGTGTCACGGCCCACCCTGTCGCCAGCTTCATCATGCCCTCATGCCTCATGGGAAAGGTGGACG
TTCCTCAGTCAGTGGGATTGTGGCCACTGTGTTTGGAGCAACAGGATTCCTGGGGCGATATGTTGTCAACCACCT
TGGACGCATGGGGTCACAGGTAATCATACCCTATCGGTGTGATAAATATGACATCATGCACCTTCGTCCCATGGG
TGACCTGGGCCAGCTTCTGTTTCTGGAATGGGACGCGAGAGATAAAGATTCTATCCGACGAGTAGTACAACACAG
CAATGTGGTCATCAATCTTATTGGACGAGACTGGGAAACCAAAAACTTTGATTTTGAGGATGTTTTTGTGAAGAT
TCCCCAAGCAATTGCTCAACTGTCCAAGGAAGCTGGAGTTGAAAAATTCATTCATGTTTCACATCTGAATGCGAA
TATTAAAAGCTCTTCTAGATATTTGAGAAATAAGGCTGTTGGAGAGAAAGTAGTGAGAGATGCATTTCCGGAAGC
CATTATCGTAAAGCCGTCGGACATCTTTGGAAGAGAGGATAGATTCCTTAATTCTTTTGCAAGTATGCATCGGTT
TGGTCCTATACCCCTTGGTTCCTTGGGCTGGAAGACAGTTAAACAACCAGTATATGTCGTAGATGTATCCAAAGG
AATTGTTAATGCAGTTAAGGATCCTGATGCCAATGGGAAAACCTTTGCTTTCGTTGGGCCAAATCGATATCTCCT
CTTTGACCTGGTGAAGTACATCTTTGCTGTGGCTCACAGCAAAGGGGTACTTCCTCCCGTACCCCTTGCCACCTT
TTGCCTATCAGTGGGTAGCAAGAGACTT**TGA**AATAAGCCCATTTGAGTCCTGGACAACAAGGGATAAAGTGGAGC
GTATTCACATCACAGACATGACCTTGTCTCACCTGCCCAGCTTAGAAGACCTTGGTATTCAGGCAACACCACTGG
AACTCAAGGCCATTGAGGTGCTGCGGCTTCATCACACTTACTGCTGGCTGTCTGCTGAAATTGAGGATGTGAAGC
TGGCCAAGACCGTCAACATTTAGTGCCTCCCGAGCAACTCTTGGTTTTGGTGTCTTTTGGGTCAGCCCGTGTGGT
TTGAGCACCCAGCCAGGTGGTCTCTTTAGAGAATCCTGTACACAGTGAATAAGATCCCACCATTAAAACATTTGA
GGTT

FIGURE 678

EKMAAAAQSRVVRVLSMSRSAITAIATSVCHGPPCRQLHHALMPHGKGGRSSVSGIVATVFGATGFLGRYVVNHL
GRMGSQVIIPYRCDKYDIMHLRPMGDLGQLLFLEWDARDKDSIRRVVQHSNVVINLIGRDWETKNFDFEDVFVKI
PQAIAQLSKEAGVEKFIHVSHLNANIKSSSRYLRNKAVGEKVVRDAFPEAIIVKPSDIFGREDRFLNSFASMHRF
GPIPLGSLGWKTVKQPVYVVDVSKGIVNAVKDPDANGKTFAFVGPNRYLLFDLVKYIFAVAHSKGVLPPVPLATF
CLSVGSKRL

FIGURE 679

AGGTTTCGGCGGGGGCTGCACGTGCGCAGGGGTGTGGAAACTTACCGGCTGAGCC**ATG**GATACACCGTTAAGGCG
CAGCCGACGGCTGGGAGGCCTAAGGCCCGAATCCCCCGAGAGCCTCACCTCAGTTTCGCGGACGAGACGGGCCCT
TGTGGAGTTCGAGTCGAACCCAGAAGAAACGAGGGAGCCCGGGTCTCCTCCGAGTGTGCAGCGGGCTGGCCTGGG
GTCCCCCGAAAGGCCGCCGAAGACAAGCCCAGGATCACCCCGTCTGCAGCAGGGTGCAGGCTTGGAGTCACCCCA
AGGGCAGCCAGAGCCAGGCGCAGCGTCCCCCCAGCGTCAGCAAGACCTACACCTGGAGTCGCCTCAAAGACAGCC
AGAGTACAGTCCTGAATCCCCACGATGTCAGCCGAAGCCAAGTGAGGAGGCACCAAAGTGTTCTCAGGACCAGGG
AGTACTGGCCTCGGAGTTGGCCCAGAATAAGGAGGAGCTGACCCCGGGGGCCCCCCAGCATCAGCTACCGCCGGT
CCCAGGATCACCAGAGCCTTACCCCGGTCAGCAAGCTCCCGGTCCGGAGCCCTCTCAGCCACTACTGGAGCTGAC
ACCCAGGGCACCTGGCTCCCCCCGGGGTCAGCATGAGCCGAGCAAGCCACCTCCAGCTGGGGAGACGGTGACAGG
CGGCTTCGGGGCAAAGAAGCGAAAAGGTTCTTCATCCCAGGCCCCAGCGTCCAAGAAGTTGAATAAAGAGGAGCT
TCCTGTAATCCCGAAGGGGAAGCCCAAATCGGGGCGAGTGTGGAAGGACCGCTCCAAGAAAAGATTCTCCCAGAT
GCTTCAGGACAAGCCCCTGCGCACATCGTGGCAGCGGAAGATGAAGGAACGACAGGAGAGGAAGCTGGCCAAGGA
CTTTGCCCGTCACCTGGAGGAGGAGAAGGAGAGGCGCCGCCAGGAGAAGAAACAGCGCCGGGCTGAGAACCTGAA
ACGCCGCCTGGAGAATGAGCGGAAGGCAGAGGTCGTCCAAGTGATCCGAAACCCCGCCAAGCTCAAGCGGGCAAA
GAAGAAGCAGCTGCGCTCCATTGAGAAGCGGGACACCCTGGCCCTGCTGCAGAAGCAGCCGCCCCAGCAGCCGGC
AGCCAAGATC**TGA**GCTCAGGACGGCCCGAGGCCTTCCATGGCCAACGACCATGTCAGACACAGCACCTCAGGCCG
CTGCTCAGATGCCTCTGCTGGAGCTGGCACTCCAAACCCATGGCTCCAGAACGGGGACCCCCACCCCGACCGGGG
CTCCTCGGCCTTTGAAGGCTTCCAGGCAGGTCTGTGTGGGACAGAAGCCCAGAGGGGGCCTGGGACCTGGCAGAG
ATGGGGGCGGGAAGAGATTCAGCTCCCATCCCTCCTTCCTCTCCTTCTCCAAGTGCCTTCAAACCAAGAACTGTA
CATTCTTCTGGTTCCTCAGTGAGCTGGTGACTGGCAGGTGACTCCCTCAGCAGTGTATGCCCTTTCTCAGCATCC
TAGGTCCATCCCAGGCCTGGAGGCTGACAGTTGGGAATCCAGCTTCCCCCACACCTTCCCAAAGGCTGCTCTGAG
CACCTCCACACCCCACTGCCTCTGTCCCCAGCAAACTGAATCCGGTTCCTCTCCACTTTTCAATACTGAAAGATT
AAAATGGGGAGGTTGCAGGGAGCAGAGCTTTTCCCTAGCACCCACTTTCCCAAACCAGTCTCTGCAGAAGCCCCA
GAGAATCTAACTCATGCCTGTCCAGTCTACAGCAAAAATATTTATTGAGTGCCTGTTGCATACAGGCACAATCCT
AGGCACCGGCAAATACAGACAATAGACCAAAGTCCCTGCCCTCGAGGAGCTTTCATTCTGATGGAGAGAAAACAT
AATAAACAAGCAAAATGCAAAAAAAAAAAAAAAAA

FIGURE 680

MDTPLRRSRRLGGLRPESPESLTSVSRTRRALVEFESNPEETREPGSPPSVQRAGLGSPERPPKTSPGSPRLQQG
AGLESPQGQPEPGAASPQRQQDLHLESPQRQPEYSPESPRCQPKPSEEAPKCSQDQGVLASELAQNKEELTPGAP
QHQLPPVPGSPEPYPGQQAPGPEPSQPLLELTPRAPGSPRGQHEPSKPPPAGETVTGGFGAKKRKGSSSQAPASK
KLNKEELPVIPKGKPKSGRVWKDRSKKRFSQMLQDKPLRTSWQRKMKERQERKLAKDFARHLEEEKERRRQEKKQ
RRAENLKRRLENERKAEVVQVIRNPAKLKRAKKKQLRSIEKRDTLALLQKQPPQQPAAKI

FIGURE 681

GTCGACTACCAGAAAATACTTTCAACATAAATGAACTCTCCAACTTATTAAACTTTTATATAGATAGAGGAAGAC
AGCTCTTTCGGGATAACCACCTGATACCTGCAGAAACCCCCAGTCCTGTTATTTTCAGTGATTTTCCATTTATCT
TTAATTCGCTATCCAAAATTAAATTATTGCAAGCTGATTCACATATAAAG**ATG**CAGATGTCAGAAAAGAAAGCAT
ACATGCTTATGCATGAAACAATTCTGCAAAAAAAGGATGAATTTCCTCCATCACCCAGATTTATACTTAGAGTCA
GACGAAGTCGCCTGGTTAAAGATGCTCTGCGTCAATTAAGTCAAGCTGAAGCTACTGACTTCTGCAAAGTATTAG
TGGTTGAATTTATTAATGAAATTTGTCCTGAGTCTGGAGGGGTTAGTTCAGAGTTCTTCCACTGTATGTTTGAAG
AGATGACCAAGCCAGAATATGGAATGTTCATGTATCCTGAAATGTGTTCCTGCATGTGGTTTCCTGCCAAGCCTA
AACCTGAGAAGAAAAGATATTTCCTCTTTGGAATGCTGTGTGGACTCTCCTTATTCAATTTAAATGTTGCTAACC
TTCCTTTCCCACTGGCTCTGTATAAAAAACTTCTGGACCAAAAGCCATCATTGGAAGATTTAAAAGAACTCAGTC
CTCGGTTGGGGAAGAGTTTGCAAGAAGTTCTAGATGATGCTGCTGATGACATTGGAGATGCGCTCTGCATACGCT
TTTCTATACACTGGGACCAAAATGATGTTGACTTAATTCCAAATGGGATCTCCATACCTGTGGACCAAACCAACA
AGAGAGACTATGTTTCTAAGTATATTGATTACATTTTCAACGTCTCTGTAAAAGCAGTTTATGAGGAATTTCAGA
GAGGATTTTATAGAGTCTGTGAGAAGGAGATACTTAGACATTTCTACCCTGAAGAACTAATGACAGCAATCATTG
GAAATACTGATTATGACTGGAAACAGTTTGAACAGAATTCAAAGTATGAGCAAGGATACCAAAAATCACATCCTA
CTATACAGTTGTTTTGGAAGGCTTTCCACAAGCTAACCTTGGATGAAAAGAAAAAATTCCTCTTTTTCCTTACAG
GACGTGATAGGCTGCATGCAAGAGGCATACAGAAAATGGAAATAGTATTTCGCTGTCCTGAAACTTTCAGTGAAA
GAGATCACCCAACATCAATAACTTGTCATAATATTCTCTCCCTCCCTAAGTATTCTACAATGGAAAGAATGGAGG
AAGCACTCCAAGTAGCCATCAACAACAACAGAGGATTTGTCTCACCCATGCTCACACAGTCA**TAA**TCACCTCTGA
GAGACTCAGGGTGGGCTTTCTCACACTTGGATCCTTCTGTTCTTCCTTACACCTAAATAATACAAGAGATTAATG
AATAGTGGTTAGAAGTAGTTGAGGGAGAGATTGGGGGAATGGGGAGATGATGATGATGGTCAAAGGGTGCAAAAT
CTCACACAAGACTGAGGCAGGAGAATAGGGTACAGAGATAGGGATCTAAGGATGACTTGGACACACTCCCTGGCA
CTGAAGAGTCTGAACACTGGCCTGTGATTGGTCCATTCCAGGACCTTCATTTGCATAAGGTATCAAACCACATCA
GCCTCTGATTGGCCATGGGCCAGACCTGCACTCTGGCCAATGATTGGTTCATTCCAGGACATTCATTTGCATAAG
GAGTCAAACCACACCAGTCTTGGATTGGCTGTGAGCCAATTCACCTCAGTCTCTAATTGGCTGTGAGTCAGTCTT
TCATTTACATAGGGTGTAACCATCAAGAAACCTCTACAGGGTACTTAAGCCCCAGAAGATTTTGCTACCAGGGCT
CTTGAGCCACTTGCTCTAGCCCACTCCCACCCTGTGGAATGTACTTTCACTTTTGCTGCTTCACTGCCTTGTGCT
CCAATAAATCCACTCCTTCACCACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 682

MQMSEKKAYMLMHETILQKKDEFPPSPRFILRVRRSRLVKDALRQLSQAEATDFCKVLVVEFINEICPESGGVSS
EFFHCMFEEMTKPEYGMFMYPEMCSCMWFPAKPKPEKKRYFLFGMLCGLSLFNLNVANLPFPLALYKKLLDQKPS
LEDLKELSPRLGKSLQEVLDDAADDIGDALCIRFSIHWDQNDVDLIPNGISIPVDQTNKRDYVSKYIDYIFNVSV
KAVYEEFQRGFYRVCEKEILRHFYPEELMTAIIGNTDYDWKQFEQNSKYEQGYQKSHPTIQLFWKAFHKLTLDEK
KKFLFFLTGRDRLHARGIQKMEIVFRCPETFSERDHPTSITCHNILSLPKYSTMERMEEALQVAINNNRGFVSPM
LTQS

FIGURE 683

TCGAATTCCTAATTTTTGTGGGACTCCTTAAGACCCACAAGTGACTTCTGTCTACACTACAGATGAACTGAATTG
ATCATCTAAAATACGTTTATAGCGTTCATTGTGCCAGTTGCTCATGGTTCTGCTAATTGGCCCAGGACTAGTTGT
GATCTGCAGACTGAAGCCAGAGTAAGTAAGAGAATTCAAGGCACTAAGACAACCAGGAACAGTTTTACCAAGGCA
AGTGGAAGCTGCTAGGCTCAGTGGTTGCATGCCTATAGATGGGGTAAATCATCCTGGTGCAAATATGGTATTCAC
ACCATAAATGTGTAGTGCAAGTTTCCTCTGTGGCCAATCACAGGGCTGCAAGCTGAAGCCCCAGTTTAGCTTATT
CTCCATACATAACTTCAAGGGGACTTTCTGGTGAACTTTTCCAAGAAGCTCCAAGCACAG**ATG**GTTCAAATTTGC
AGTTTGGCTAGACTTTGTGACTGGATGTACATTAAATTAA

FIGURE 684

MVQICSLARLCDWMYIK

FIGURE 685

GGGGGGTGGCTGGGCTGCGCTTGGGTCCGTCGCTGCTTCGGTGTCCCTGTCGGGCTTCCCAGCAGCGGCCTAGCG
GGAAAAGTAAAAG**ATG**TCTGAATATATTCGGGTAACCGAAGATGAGAACGATGAGCCCATTGAAATACCATCGGA
AGACGATGGGACGGTGCTGCTCTCCACGGTTACAGCCCAGTTTCCAGGGGCGTGTGGGCTTCGCTACAGGAATCC
AGTGTCTCAGTGTATGAGAGGTGTCCGGCTGGTAGAAGGAATTCTGCATGCCCCAGATGCTGGCTGGGGAAATCT
GGTGTATGTTGTCAACTATCCAAAAGATAACAAAAGAAAAATGGATGAGACAGATGCTTCATCAGCAGTGAAAGT
GAAAAGAGCAGTCCAGAAAACATCCGATTTAATAGTGTTGGGTCTCCCATGGAAAACAACCGAACAGGACCTGAA
AGAGTATTTTAGTACCTTTGGAGAAGTTCTTATGGTGCAGGTCAAGAAAGATCTTAAGACTGGTCATTCAAAGGG
GTTTGGCTTTGTTCGTTTTACGGAATATGAAACACAAGTGAAAGTAATGTCACAGCGACATATGATAGATGGACG
ATGGTGTGACTGCAAACTTCCTAATTCTAAGCAAAGCCAAGATGAGCCTTTGAGAAGCAGAAAAGTGTTTGTGGG
GCGCTGTACAGAGGACATGACTGAGGATGAGCTGCGGGAGTTCTTCTCTCAGTACGGGGATGTGATGGATGTCTT
CATCCCCAAGCCATTCAGGGCCTTTGCCTTTGTTACATTTGCAGATGATCAGATTGCGCAGTCTCTTTGTGGAGA
GGACTTGATCATTAAAGGAATCAGCGTTCATATATCCAATGCCGAACCTAAGCACAATAGCAATAGACAGTTAGA
AAGAAGTGGAAGATTTGGTGGTAATCCAGGTGGCTTTGGGAATCAGGGTGGATTTGGTAATAGCAGAGGGGGTGG
AGCTGGTTTGGGAAACAATCAAGGTAGTAATATGGGTGGTGGGATGAACTTTGGTGCGTTCAGCATTAATCCAGC
CATGATGGCTGCCGCCCAGGCAGCACTACAGAGCAGTTGGGGTATGATGGGCATGTTAGCCAGCCAGCAGAACCA
GTCAGGCCCATCGGGTAATAACCAAAACCAAGGCAACATGCAGAGGGAGCCAAACCAGGCCTTCGGTTCTGGAAA
TAACTCTTATAGTGGCTCTAATTCTGGTGCAGCAATTGGTTGGGGATCAGCATCCAATGCAGGGTCGGGCAGTGG
TTTTAATGGAGGCTTTGGCTCAAGCATGGATTCTAAGTCTTCTGGCTGGGGAATG**TAG**ACAGTGGGGTTGTGGTT
GGTTGGTATAGAATGGTGGGAATTCAAATTTTTCTAAACTCATGGTAAGTATATTGTAAAATACATATGTACTAA
GAATTTTCAAAATTGGTTTGTTCAGTGTGGAGTATATTCAGCAGTATTTTTGACATTTTTCTTTAGAAAAAGGAA
GAGCTAAAGGAATTTTATAAGTTCTGTTACATGAAAGGTTGAAATATTGAGTGGTTGAAAGTGAACTGCTGTTTG
CCTGATTGGTAAACCAACACACTACAATTGATATCAAAAGGTTTCTCCTGTAATATTTTATCCCTGGACTTGTCA
AGTGAATTCTTTGCATGTTCAAAACGGAAACCATTGATTAGAACTACATTCTTTACCCCTTGTTTTAATTTGAAC
CCCACCATATGGATTTTTTTCCTTAAGAAAATCTCCTTTTAGGAGATCATGGTGTCACAGTGTTTGGTTCTTTTG
TTTTGTTTTTTAACACTTGTCTCCCCTCATACACAAAAGTACAATATGAAGCCTTCATTTAATCTCTGCAGTTCA
TCTCATTTCAAATGTTTATGGAAGAAGCACTTCACTGAAAGTAGTGCTGTAAATATTCTGCCATAGGAATACTGT
CTACATGCTTTCTCATTCAAGAATTCGTCATCACGCATCACAGGCCGCGTCTTTGACGGTGGGTGTCCCATTTTT
ATCCGCTACTCTTTATTTCATGGAGTCGTATCAACGCTATGAACGCAAGGCTGTGATATGGAACCAGAAGGCTGT
CTGAACTTTTGAAACCTTGTGTGGGATTGATGGTGGTGCCGAGGCATGAAAGGCTAGTATGAGCGAGAAAAGGAG
AGAGCGCGTGCAGAGACTTGGTGGTGCATAATGGATATTTTTTAACTTGGCGAGATGTGTCTCTCAATCCTGTGG
CTTTGGTGAGAGAGTGTGCAGAGAGCAATGATAGCAAATAATGTACGAATGTTTTTTGCATTCAAAGGACATCCA
CATCTGTTGGAAGACTTTTAAGTGAGTTTTTGTTCTTAGATAACCCACATTAGATGAATGTGTTAAGTGAAATGA
TACTTGTACTCCCCCTACCCCTTTGTCAACTGCTGTGAATGCTGTATGGTGTGTGTTCTCTTCTGTTACTGATAT
GTAAGTGTGGCAATGTGAACTGAAGCTGATGGGCTGAGAACATGGACTGAGCTTGTGGTGTGCTTTGCAGGAGGA
CTTGAAGCAGAGTTCACCAGTGAGCTCAGGTGTCTCAAAGAAGGGTGGAAGTTCTAATGTCTGTTAGCTACCCAT
AAGAATGCTGTTTGCTGCAGTTCTGTGTCCTGTGCTTGGATGCTTTTTATAAGAGTTGTCATTGTTGGAAATTCT
TAAATAAGACTGATTTAAATAATAAAAAAAAAAAAAAAAAAA

FIGURE 686

MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVV
NYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFV
RFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKP
FRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLG
NNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYS
GSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

FIGURE 687

AAGAGATGATTTCTCCATCCTGAACGTGCAGCGAGCTTGTCAGGAAGATCGGAGGTGCCAAGTAGCAGAGAAAGC
ATCCCCCAGCTCTGACAGGGAGACAGCAC**ATG**TCTAAGGCCCACAAGCCTTGGCCCTACCGGAGGAGAAGTCAAT
TTTCTTCTCGAAAATACCTGAAAAAAGAAATGAATTCCTTCCAGCAACAGCCACCGCCATTCGGCACAGTGCCAC
CACAAATGATGTTTCCTCCAAACTGGCAGGGGGCAGAGAAGGACGCTGCTTTCCTCGCCAAGGACTTCAACTTTC
TCACTTTGAACAATCAGCCACCACCAGGAAACAGGAGCCAACCAAGGGCAATGGGGCCCGAGAACAACCTGTACA
GCCAGTACGAGCAGAAGGTGCGCCCCTGCATTGACCTCATCGACTCCCTGCGGGCTCTGGGTGTGGAGCAGGACC
TGGCCCTGCCAGCCATCGCCGTCATCGGGGACCAGAGCTCGGGCAAGAGCTCTGTGCTGGAGGCACTGTCAGGAG
TCGCGCTTCCCAGAGGCAGCGGAATCGTAACCAGGTGTCCGCTGGTGCTGAAACTGAAAAAGCAGCCCTGTGAGG
CATGGGCCGGAAGGATCAGCTACCGGAACACCGAGCTAGAGCTTCAGGACCCTGGCCAGGTGGAGAAAGAGATAC
ACAAAGCCCAGAACGTCATGGCCGGGAATGGCCGGGGCATCAGCCATGAGCTCATCAGCCTGGAGATCACCTCCC
CTGAGGTTCCAGACCTGACCATCATTGACCTTCCCGGCATCACCAGGGTGGCTGTGGACAACCAGCCCCGAGACA
TCGGACTGCAGATCAAGGCTCTCATCAAGAAGTACATCCAGAGGCAGCAGACGATCAACTTGGTGGTGGTTCCCT
GTAACGTGGACATTGCCACCACGGAGGCGCTGAGCATGGCCCATGAGGTGGACCCGGAAGGGGACAGGACCATCG
GTATCCTGACCAAACCAGATCTAATGGACAGGGGCACTGAGAAAAGCGTCATGAATGTGGTGCGGAACCTCACGT
ACCCCCTCAAGAAGGGCTACATGATTGTGAAGTGCCGGGGCCAGCAGGAGATCACAAACAGGCTGAGCTTGGCAG
AGGCAACCAAGAAAGAAATTACATTCTTTCAAACACATCCATATTTCAGAGTTCTCCTGGAGGAGGGGTCAGCCA
CGGTTCCCCGACTGGCAGAAAGACTTACCACTGAACTCATCATGCATATCCAAAAATCGCTCCCGTTGTTAGAAG
GACAAATAAGGGAGAGCCACCAGAAGGCGACCGAGGAGCTGCGGCGTTGCGGGGCTGACATCCCCAGCCAGGAGG
CCGACAAGATGTTCTTTCTAATTGAGAAAATCAAGATGTTTAATCAGGACATCGAAAAGTTAGTAGAAGGAGAAG
AAGTTGTAAGGGAGAATGAGACCCGTTTATACAACAAAATCAGAGAGGATTTTAAAAACTGGGTAGGCATACTTG
CAACTAATACCCAAAAAGTTAAAAATATTATCCACGAAGAAGTTGAAAAATATGAAAAGCAGTATCGAGGCAAGG
AGCTTCTGGGATTTGTCAACTACAAGACATTTGAGATCATCGTGCATCAGTACATCCAGCAGCTGGTGGAGCCCG
CCCTTAGCATGCTCCAGAAAGCCATGGAAATTATCCAGCAAGCTTTCATTAACGTGGCCAAAAAACATTTTGGCG
AATTTTTCAACCTTAACCAAACTGTTCAGAGCACGATTGAAGACATAAAAGTGAAACACACAGCAAAGGCAGAAA
ACATGATCCAACTTCAGTTCAGAATGGAGCAGATGGTTTTTTGTCAAGATCAGATTTACAGTGTTGTTCTGAAGA
AAGTCCGAGAAGAGATTTTTAACCCTCTGGGGACGCCTTCACAGAATATGAAGTTGAACTCTCATTTTCCCAGTA
ATGAGTCTTCGGTTTCCTCCTTTACTGAAATAGGCATCCACCTGAATGCCTACTTCTTGGAAACCAGCAAACGTC
TCGCCAACCAGATCCCATTTATAATTCAGTATTTTATGCTCCGAGAGAATGGTGACTCCTTGCAGAAAGCCATGA
TGCAGATACTACAGGAAAAAAATCGCTATTCCTGGCTGCTTCAAGAGCAGAGTGAGACCGCTACCAAGAGAAGAA
TCCTTAAGGAGAGAATTTACCGGCTCACTCAGGCGCGACACGCACTCTGTCAATTCTCCAGCAAAGAGATCCAC**T**
GAAGGGCGGCGATGCCTGTGGTTGTTTTCTTGTGCGTACTCATTCATTCTAAGGGGAGTCGGTGCAGGATGCCGC
TTCTGCTTTGGGGCCAAACTCTTCTGTCACTATCAGTGTCCATCTCTACTGTACTCCCTCAGCATCAGAGCATGC
ATCAGGGGTCCACACAGGCTCAGCTCTCTCCACCACCCAGCTCTTCCCTGACCTTCACGAAGGGATGGCTCTCCA
GTCCTTGGGTCCCGTAGCACACAGTTACAGTGTCCTAAGATACTGCTATCATTCTTCGCTAATTTGTATTTGTAT
TCCCTTCCCCCTACAAGATTATGAGACCCCAGAGGGGGAAGGTCTGGGTCAAATTCTTCTTTTGTATGTCCAGTC
TCCTGCACAGCACCTGCAGCATTGTAACTGCTTAATAAATGACATCTCACTGAACGAATGAGTGCTGTGTAAGTG
ATGGAGATACCTGAGGCTATTGCTCAAGCCCAGGCCTTGGACATTTAGTGACTGTTAGCCGGTCCCTTTCAGATC
CAGTGGCCATGCCCCCTGCTTCCCATGGTTCACTGTCATTGTGTTTCCCAGCCTCTCCACTCCCCCGCCAGAAAG
GAGCCTGAGTGATTCTCTTTTCTTCTTGTTTCCCTGATTATGATGAGCTTCCATTGTTCTGTTAAGTCTTGAAGA
GGAATTTAATAAAGCAAAGAAACTTTTTAAAAACGT

FIGURE 688

MSKAHKPWPYRRRSQFSSRKYLKKEMNSFQQQPPPFGTVPPQMMFPPNWQGAEKDAAFLAKDFNFLTLNNQPPPG
NRSQPRAMGPENNLYSQYEQKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEALSGVALPRGSGIV
TRCPLVLKLKKQPCEAWAGRISYRNTELELQDPGQVEKEIHKAQNVMAGNGRGISHELISLEITSPEVPDLTIID
LPGITRVAVDNQPRDIGLQIKALIKKYIQRQQTINLVVVPCNVDIATTEALSMAHEVDPEGDRTIGILTKPDLMD
RGTEKSVMNVVRNLTYPLKKGYMIVKCRGQQEITNRLSLAEATKKEITFFQTHPYFRVLLEEGSATVPRLAERLT
TELIMHIQKSLPLLEGQIRESHQKATEELRRCGADIPSQEADKMFFLIEKIKMFNQDIEKLVEGEEVVRENETRL
YNKIREDFKNWVGILATNTQKVKNIIHEEVEKYEKQYRGKELLGFVNYKTFEIIVHQYIQQLVEPALSMLQKAME
IIQQAFINVAKKHFGEFFNLNQTVQSTIEDIKVKHTAKAENMIQLQFRMEQMVFCQDQIYSVVLKKVREEIFNPL
GTPSQNMKLNSHFPSNESSVSSFTEIGIHLNAYFLETSKRLANQIPFIIQYFMLRENGDSLQKAMMQILQEKNRY
SWLLQEQSETATKRRILKERIYRLTQARHALCQFSSKEIH

FIGURE 689

CGAGCACTAAGTCCTCTGAGTTCCGCAGCGCAGCACCGGAAGCGGCCGAGCGCGCTCAGCCCGGCGACCCCTGCG
GGCTCCAGACCCCTGCGCCGCTGCGCCCCGGGTTTCGCCGCAACCAAGACCCAGCGAGTGCAGCGGCGGCCGCTG
AGGAGGTTCGAAAAC**ATG**GCCAAAAGAAATGCCGAGAAGGAACTGACAGATAGGAATTGGGATCAAGAAGATGAA
GCTGAAGAGGTGGGAACATTCTCCATGGCCAGTGAGGAAGTCTTGAAGAATAGAGCCATAAAGAAAGCAAAGCGC
AGAAATGTTGGATTTGAATCTGACACTGGAGGAGCCTTTAAAGGTTTTAAAGGTTTGGTGGTACCTTCTGGAGGA
GGACGCTTTTCTGGATTTGGTAGTGGCGCTGGAGGGAAGCCTTTGGAAGGACTGTCGAATGGAAACAACATAACC
AGTGCCCCTCCCTTCGCCAGTGCAAAGGCAGCGGCAGATCCCAAGGTAGCCTTTGGTTCTCTTGCTGCAAATGGC
CCTACCACCTTGGTTGATAAAGTTTCAAATCCCAAAACTAATGGGGACAGTCAGCAGCCCTCCTCCTCTGGCCTT
GCTTCCAGTAAAGCTTGTGTCGGAAATGCCTATCACAAGCAGTTGGCCGCCTTGAACTGCTCCGTGCGGGATTGG
ATAGTGAAGCACGTGAATACAAACCCCCTCTGTGATCTGACACCTATCTTTAAAGACTATGAGAAATATTTAGCA
AACATTGAACAGCAACACGGGAACAGTGGCAGGAATTCTGAAAGTGAATCTAACAAAGTGGCAGCTGAAACACAG
TCTCCTTCCCTTTTTGGCTCAACAAAATTACAGCAAGAGTCAAGCTTTTTGTTTCATGGCAACAAAACTGAAGAT
ACACCTGACAAGAAGATGGAGGTGGCATCTGAAAAGAAAACGGACCCATCATCACTAGGAGCGACAAGTGCCTCA
TTTAATTTCGGCAAGAAAGTTGATAGCTCTGTTTTGGGCTCATTAAGCTCTGTCCCCCTGACTGGATTTTCTTTC
TCCCCTGGAAACTCCAGTTTATTTGGCAAAGATACTACCCAGAGTAAACCAGTCTCTTCACCATTTCCCACTAAA
CCATTGGAGGGCCAAGCAGAAGGTGACAGTGGTGAATGCAAAGGTGGAGATGAAGAAGAGAATGATGAGCCACCC
AAAGTAGTAGTTACCGAAGTAAAAGAAGAAGATGCTTTTTACTCCAAAAAGTGTAAACTGTTTTACAAGAAGGAC
AATGAGTTTAAAGAGAAAGGCATAGGTACTCTGCATTTAAAACCTACAGCAAATCAGAAGACACAGCTTTTGGTG
CGGGCAGACACCAATTTAGGCAACATATTGCTGAACGTTCTGATTCCACCCAATATGCCATGTACGCGAACAGGG
AAGAATAACGTTCTTATCGTCTGTGTTCCAAATCCACCAATTGACGAGAAGAATGCCACCATGCCAGTCACCATG
TTGATTCGGGTAAAAACCAGCGAGGATGCAGACGAGTTGCACAAAATTTTACTGGAGAAAAAGGATGCC**TGA**ACA
CGCAAAGTCGGCTGCAGAATTATTGCCAAGTTGCTGCTGCTTCCACCGCCCCTTAAAGTTAGTCAGTTTTTCTTC
TCTTCTTTGACATTCTAAGAACTTATAGATAACTTAAAACTTTTGTGAGGAAGATTAATGTGGCCAATAAAACCT
TTAAATGTTAAGTGTCAAAAAAAAAAAAAAAA

FIGURE 690

MAKRNAEKELTDRNWDQEDEAEEVGTFSMASEEVLKNRAIKKAKRRNVGFESDTGGAFKGFKGLVVPSGGGRFSG
FGSGAGGKPLEGLSNGNNITSAPPFASAKAAADPKVAFGSLAANGPTTLVDKVSNPKTNGDSQQPSSSGLASSKA
CVGNAYHKQLAALNCSVRDWIVKHVNTNPLCDLTPIFKDYEKYLANIEQQHGNSGRNSESESNKVAAETQSPSLF
GSTKLQQESSFLFHGNKTEDTPDKKMEVASEKKTDPSSLGATSASFNFGKKVDSSVLGSLSSVPLTGFSFSPGNS
SLFGKDTTQSKPVSSPFPTKPLEGQAEGDSGECKGGDEEENDEPPKVVVTEVKEEDAFYSKKCKLFYKKDNEFKE
KGIGTLHLKPTANQKTQLLVRADTNLGNILLNVLIPPNMPCTRTGKNNVLIVCVPNPPIDEKNATMPVTMLIRVK
TSEDADELHKILLEKKDA

FIGURE 691

AAGCTTTCCTCTTTGCATTTTGGCATTTGAAAACTCCGAAGAGCGGTTTTTGTTTTTTATTTAAAGAAGATGATA
CATATGTGTACCCGATTCAAAACTAGAGAATAGAATTTAAAACATAATTTTCAAAGTCTTCAAATATGCCTAAAG
GTAACAATGTCATCTTTTAATTGCCAATTTCTCTACCACTTTCAAAAAATTACTTCCAAGGATTTA**ATG**AGCTCC
TTCCTTTCAACAGAAAATGGACTATTTTCCTTTCAGATTTACTATATGCTGTCACTCCAGCTTTATAACCGCATG
TGCATACACAAACATTTCTTTCTCTCTTGCAGGTGGCACAAACCAGGAAGGGGAAATCTGTGGTTTAAATTCTTT
ATGCCTCATCCTCTGAGTGCTGAAGGCTTGCTG**TAG**GCTGTATGCTGTTAATGCTAATCGTGATAGGGGTTTTTG
CCTCCAACTGACTCCTACATATTAGCATTAACAGTGTATGATGCCTGTTACTAGCATTCACATGGAACAAATTGC
TGCCGTGGGAGGATGACAAAGAAGCATGAGTCACCCTGCTGGATAAACTTAGACTTCAGGCTTTATCATTTTTCA
ATCTGTTAATCATAATCTGGTCACTGGGATGTTCAACCTTAAACTAAGTTTTGAAAGTAAGGTTATTTAAAAGAT
TTATCAGTAGTATCCTAAATGCAAACATTTTCATTTAAATGTCAAGCCCATGTTTGTTTTTATCATTAACAGAAA
ATATATTCATGTCATTCTTAATTGCAGGTTTTGGCTTGTTCATTATAATGTTCATAAACACCTTTGATTCAACTG
TTAGAAATGTGGGCTAAACACAAATTTCTATAATATTTTTGTAGTTAAAAATTAGAAGGACTACTAACCTCCAGT
TATATCATGGATTGTCTGGCAACGTTTTTTAAAAGATTTAGAAACTGGTACTTTCCCCCAGGTAACGATTTTCTG
TTCAGGCAACTTCAGTTTAAAATTAATACTTTTATTTGACTCTTAAAGGGAAACTGAAAGGCTATGAAGCTGAAT
TTTTTTAATGAAATATTTTTAACAGTTAGCAGGGTAAATAACATCTGACAGCTAATGAGATATTTTTTCCATACA
AGATAAAAAGATTTAATCAAAAAATTTCATATTTGAAATGAAGTCCCAAATCTAGGTTCAAGTTCAATAGCTTAG
CCACATAATACGGTTGTGCGAGCAGAGAATCTACCTTTCCACTTCTAAGCCTGTTTCTTCCTCCATATGGGGATA
ATACTTTACAAGGTTGTTGTGAGGCTTAGATGAGATAGAGAATTATTCCATAAGATAATCAAGTGCTACATTAAT
GTTATAGTTAGATTAATCCAAGAACTAGTCACCCTACTTTATTAGAGAAGAGAAAAGCTAATGATTTGATTTGCA
GAATATTTAAGGTTTGGATTTCTATGCAGTTTTTCTAAATAACCATCACTTACAAATATGTAACCAAACGTAATT
GTTAGTATATTTAATGTAAACTTGTTTTAACAACTCTTCTCAACATTTTGTCCAGGTTATTCACTGTAACCAAAT
AAATCTCATGAGTCTTTAGTTGATTTAAAAAA

FIGURE 692

MSSFLSTENGLFSFQIYYMLSLQLYNRMCIHKHFFLSCRWHKPGRGNLWFKFFMPHPLSAEGLL

FIGURE 693

GGCACTTTTTAAAAATGTTTATATGAGGAAACAAAGAAGACTTGCTGTGATCCAGCGACATGCCCAG**TGA**GTCGA
AGAGAAGAAACTGGAATTAAGCTATTCTGTGTGCCACTTAGGTCAGGCCCTCCACTACATGGTCCTGCTTCTCTT
GCATGAGTTAGCTACTCATATCATGAGAGCATCCCTTTCTTAATTTTCTGCGCTAGTGGAGCAGAGCCATGTATG
TGCTATGGCCCATATGTTGAAACTTGTTTATCTACAGCTAGCCAGATGGTCTGTAACAGCACACAAAGAAGCCAT
TTGGAAACTTTCAGAGGGTCAGCACGTTTTGAAAACAACTCAGAGTAATGCATATTGTGATGTCATTGCTTACTT
TAAGCTTACAGTGAGGAATATCTTGTTAGGTACTGAATGTGAAACATGCAGACTTTGAGAACCAACTCAGAGGTC
CTAGCCCCCAGAGACAGAAATTTATTTAATTGGATCACCCTTTAGACTTGTTTTGTCTACATGTTCTCTGAAAAA
GGAATATAATGTCTTAATTTAAAATACTTTGTTTTTAAGTTGCTGCTGGGTTAAATACATTTTTTTTAAAGAA
AACCTGCTTATGCAGTACATGTTAACAGATATGATGTGGTCATCAATAAAAATGTAAAATA

FIGURE 694

ALFKNVYMRKQRRLAVIQRHAQ

FIGURE 695

GAGACATTCCTCAATTGCTTAGACATATTCTGAGCCTACAGCAGAGGAACCTCCAGTCTCAGCACC**ATG**AATCAA
ACTGCGATTCTGATTTGCTGCCTTATCTTTCTGACTCTAAGTGGCATTCAAGGAGTACCTCTCTCTAGAACCGTA
CGCTGTACCTGCATCAGCATTAGTAATCAACCTGTTAATCCAAGGTCTTTAGAAAAACTTGAAATTATTCCTGCA
AGCCAATTTTGTCCACGTGTTGAGATCATTGCTACAATGAAAAAGAAGGGTGAGAAGAGATGTCTGAATCCAGAA
TCGAAGGCCATCAAGAATTTACTGAAAGCAGTTAGCAAGGAAATGTCTAAAAGATCTCCT**TAA**AACCAGAGGGGA
GCAAAATCGATGCAGTGCTTCCAAGGATGGACCACACAGAGGCTGCCTCTCCCATCACTTCCCTACATGGAGTAT
ATGTCAAGCCATAATTGTTCTTAGTTTGCAGTTACACTAAAAGGTGACCAATGATGGTCACCAAATCAGCTGCTA
CTACTCCTGTAGGAAGGTTAATGTTCATCATCCTAAGCTATTCAGTAATAACTCTACCCTGGCACTATAATGTAA
GCTCTACTGAGGTGCTATGTTCTTAGTGGATGTTCTGACCCTGCTTCAAATATTTCCCTCACCTTTCCCATCTTC
CAAGGGTACTAAGGAATCTTTCTGCTTTGGGGTTTATCAGAATTCTCAGAATCTCAAATAACTAAAAGGTATGCA
ATCAAATCTGCTTTTTAAAGAATGCTCTTTACTTCATGGACTTCCACTGCCATCCTCCCAAGGGGCCCAAATTCT
TTCAGTGGCTACCTACATACAATTCCAAACACATACAGGAAGGTAGAAATATCTGAAAATGTATGTGTAAGTATT
CTTATTTAATGAAAGACTGTACAAAGTATAAGTCTTAGATGTATATATTTCCTATATTGTTTTCAGTGTACATGG
AATAACATGTAATTAAGTACTATGTATCAATGAGTAACAGGAAAATTTTAAAAATACAGATAGATATATGCTCTG
CATGTTACATAAGATAAATGTGCTGAATGGTTTTCAAATAAAAATGAGGTACTCTCCTGGAAATATTAAGAAAGA
CTATCTAAATGTTGAAAGATCAAAAGGTTAATAAAGTAATTATAACT

FIGURE 696

MNQTAILICCLIFLTLSGIQGVPLSRTVRCTCISISNQPVNPRSLEKLEIIPASQFCPRVEIIATMKKKGEKRCL
NPESKAIKNLLKAVSKEMSKRSP

FIGURE 697

ATGATTGCAACAGTGGATTTAAAAGTCAATGAATATGAGAAAAACCAAAAATGGCTTGAGATCCTAAATAAGATT
GAAAACAAAACATACACGAAGCTCAAAAATGGACATGTGTTTAGGAAGCAGGCACTGATGAGTGAAGAAAGGACT
CTGTTATATGATGGCCTTGTTTACTGGAAAACTGCTACAGGTCGTTTCAAAGATATCCTAGCTCTACTTCTAACT
GATGTGCTGCTCTTTTTACAAGAAAAAGACCAGAAATACATCTTTGCAGCCGTTGATCAGAAGCCATCAGTTATT
TCCCTTCAAAAGCTTATTGCTAGAGAAGTTGCTAATGAGGAGAGAGGAATGTTTCTGATCAGTGCTTCATCTGCT
GGTCCTGAGATGTATGAAATTCACACCAATTCCAAGGAGGAACGCAATAACTGGATGAGACGGATCCAGCAGGCT
GTAGAAAGTTGTCCTGAAGAAAAAGGGGGAAGGACAAGTGAATCTGATGAAGACAAGAGGAAAGCTGAAGCCAGA
GTGGCCAAAATTCAGCAATGTCAAGAAATACTCACTAACCAAGACCAACAAATTTGTGCGTATTTGGAGGAGAAG
CTGCATATCTATGCTGAACTTGGAGAACTGAGCGGATTTGAGGACGTCCATCTAGAGCCCCACCTCCTTATTAAA
CCTGACCCAGGCGAGCCTCCCCAGGCAGCCTCATTACTGGCAGCAGCACTGAAAGAAGCATTAGTCACAGGAGGG
AGAGAAGGAAGAGGCTGTTCGGATGTGGATCCCGGGATCCAGGGTGTGGTAACCGACTTGGCCGTCTCTGATGCA
GGGGAGAAGGTGGAATGTAGAAATTTTCCAGGTTCTTCACAATCAGAGATTATACAAGCCATACAGAATTTAACC
CGTCTCTTATACAGCCTTCAGGCCGCCTTGACCATTCAGGACAGCCACATTGAGATCCACAGGCTGGTTCTCCAG
CAGCAGGAGGGCCTGTCTCTCGGCCACTCTATCCTCCGAGGCGGCCCCTTGCAGGACCAGAAGTCTCGCGACGCG
GACAGGCAGCATGAGGAGCTGGCCAATGTGCACCAGCTTCAGCACCAGCTCCAGCAGGGGCAGCGGCGCTGGCTG
CGCAGGTGTGAGCAGCAGCAGCGGGCGCAGGCGACCAGGGAGAGCTGGCTGCAGGAGCGGGAGCGGGAGTGCCAG
TCGCAGGAGGAGCTGCTGCTGCGGAGCCGGGGCGAGCTGGACCTCCAGCTCCAGGAGTACCAGCACAGCCTGGAG
CGGCTGAGGGAGGGCCAGCGCCTGGTGGAGAGGGAGCAGGCGAGGATGCGGGCCCAGCAGAGCCTGCTGGGCCAC
TGGAAGCACGGCCGGCAGAGGAGCCTGTCCGCGGTGCTCCTTCCGGGTGGCCCCGAGGTAATGGAACTTAATCGA
TCTGAGAGTTTATGTCATGAAAACTCATTCTTCATCAATGAAGCTTTAGTACAAATGTCATTTAACACTTTCAAC
AAACTGAATCCATCAGTTATCCATCAGGATGCCACTTACCCTACAACTCAATCTCATTCTGACTTGGTGAGGACT
AGTGAACATCAAGTAGACCTCAAGGTGGACCCTTCTCAGCCTTCGAATGTCAGTCACAAACTGTGGACAGCCGCT
GGTTCCGGCCATCAGATACTTCCTTTCCATGAAAGCAGCAAGGATTCTTGTAAAAATGGCTCCAGTATGACAAAG
TGCAGTTGTACGTTGACATCTCCCCCGGGACTGTGGACTGGAACCACATCTACTTTGAAGGATTTGGACACCTCC
CACACTGAGTCCCCAACCCCCCATGACTCAAATTCACACCGCCCTCAACTGCAGGCGTTTATAACAGAAGCAAAG
CTAAATCTACCGACAAGGACAATGACCAGACAAGATGGGGAAACTGGAGATGGAGCCAAAGAAAATATTGTTTAC
CTC**TAA**TTGTGTTGTCATTTTTCCAAACAAAACAAAACACTGGCACTTTTGGGAGAAACTTTTTGTCTCCATTCC
TTATGTATGTGTGATTGTCTGTGTCCAAATTGCTTTAAGAATAATATTTAATATTTCCTGGAAGCTCATTTTTTT
GGCATGAGTCTAATTAAATTATTGAAAGCCACCCTGTTTGTATAATCTTTAACTTATCAAATCTAATTTCAGATT
TCTGGAGGAGAAACTAACTTGAATAAGCAGGACTATTTTAAAAGTTGTTTTGACGCTAGAGTAAAATTCCATGTC
ACATTTTCTACCCAATCATCTGGATTTCAAGATTCCTTTTAAGATCTCAATGAAGCAATTTGGATTTAAAGAGTG
GTATTCACAAGGGGTGAACTTTCACAGTCAGGGCAGTTGCCTCAGTGCCCACATAGGCAGAGGAGGATGTGGGAA
AGGGCTTTTCTCAGCTAGTTTTTGTGTGCTCATTTCTTCTGGGAGCATTAAAAGTGGTGATCTGTTACAGTCACT
ATTCAACTGGGCACGTGTTGTGATTGGTCAGTCACTGAGCCAGGGATACAGTCCGGACTTGCTTAGTACCTAAGC
CTAATGCTGGTGGGGTTTCAAGACATGGTTCAGCATCATCTTTTAACAAGGCCCAGAGGCCCAGAGCCCGCATCA
AGTCATTTTGATGTAAATAGTGAACTTTGTTAGAGCCCTCACTTCTATCAATCAGCTGTCCTGTCCCTGCCAGCA
CCTGGAGCACCAACTACCACTCCCTGGAAAGAACCCTTCCCTGCAGTTTTTTAAGGACAAAACTGCCCACTCCTC
ATTAAGTTTGCTGCCTGGATACACTTTTCCACAAAGGAAAACTGGCATATCCTGCCTTCCGAGTAGTATGGGTCT
CTGTGTGAGAAACCAGGAGATATTTTCATCTTGTTCGGAAATACTTGTATGTATTTTGGTGTCAATAAATATCTT
GTACCTCATTAAAAAAAAAAAAAAAAAAA

FIGURE 698

MIATVDLKVNEYEKNQKWLEILNKIENKTYTKLKNGHVFRKQALMSEERTLLYDGLVYWKTATGRFKDILALLLT
DVLLFLQEKDQKYIFAAVDQKPSVISLQKLIAREVANEERGMFLISASSAGPEMYEIHTNSKEERNNWMRRIQQA
VESCPEEKGGRTSESDEDKRKAEARVAKIQQCQEILTNQDQQICAYLEEKLHIYAELGELSGFEDVHLEPHLLIK
PDPGEPPQAASLLAAALKEALVTGGREGRGCSDVDPGIQGVVTDLAVSDAGEKVECRNFPGSSQSEIIQAIQNLT
RLLYSLQAALTIQDSHIEIHRLVLQQQEGLSLGHSILRGGPLQDQKSRDADRQHEELANVHQLQHQLQQGQRRWL
RRCEQQQRAQATRESWLQERERECQSQEELLLRSRGELDLQLQEYQHSLERLREGQRLVEREQARMRAQQSLLGH
WKHGRQRSLSAVLLPGGPEVMELNRSESLCHENSFFINEALVQMSFNTFNKLNPSVIHQDATYPTTQSHSDLVRT
SEHQVDLKVDPSQPSNVSHKLWTAAGSGHQILPFHESSKDSCKNGSSMTKCSCTLTSPPGLWTGTTSTLKDLDTS
HTESPTPHDSNSHRPQLQAFITEAKLNLPTRTMTRQDGETGDGAKENIVYL

FIGURE 699

GCGGCGCTAGGCCTGGGCACGCTGGCGCTGTGCGGGGCGGCGCTGCTCTACCTGGCGCGCTGCGCGGCCGAGCCC
GGGGACCCCAGGGCGATGTCGGGCCGCAGCCCGCCTCCCCCCGCGCCCGCGCGCGCCGCCGCCTTCCTGGCAGTG
CTGGTGGCCAGCGCGCCCCGCGCCGGCCGAGCGCCGCAGCGTGATCCGCAGCACGTGGCTTGCGCGGCGCGGGGC
CCCGGGCGACGTGTGGGCGCGCTTTGCCGTGGGCACGGCCGGCCTGGGCGCCGAGGAGCGGCGCGCCCTGGAGCG
GGAGCAGGCGCGGCACGGGGACCTGCTGCTGCTGCCCGCGCTGCGCGACGCCTACGAAAACCTCACGGCCAAGGT
GCTGGCCATGCTGGCCTGGCTGGACGAGCACGTGGCCTTCGAGTTCGTGCTCAAGGCGGACGACGACTCCTTCGC
GCGGCTGGACGCGCTGCTGGCCGAGCTGCGCGCCCGCGAGCCCGCGCGCCGCCGCCGCTCTACTGGGGCTTCTTC
TCGGGCCGCGGCCGCGTCAAGCCGGGGGGGCGCTGGCGCGAGGCCGCCTGGCAACTCTGCGACTACTACCTGCCC
TACGCGCTGGGCGGCGGCTACGTGCTCTCGGCCGACCTGGTGCACTACCTGCGCCTCAGCCGCGACTACCTGCGC
GCCTGGCACAGCGAGGACGTGTCTCTGGGCGCCTGGCTGGCGCCGGTGGACGTCCAGCGGGAGCACGACCCGCGC
TTCGACACCGAATACCGGTCCCGCGGCTGCAGCAACCAGTACCTGGTGACGCACAAGCAGAGCCTGGAGGACATG
CTGGAGAAGCACGCGACGCTGGCGCGCGAGGGCCGCCTGTGCAAGCGCGAGGTGCAGCTGCGCCTGTCCTACGTG
TACGACTGGTCCGCGCCGCCCTCGCAGTGCTGCCAGAGAAGGGAGGGCATCCCC**TGA**GCCGCCGCGGCCCGGCCC
TCCGGGACACCTGCTTCACCCGGCGGCGCCTTGGGGCAGGTGCCGAGCGGGCGCACTACGCCCGGGCCCCAAGGC
CCCCGTCCCGCAGCCACGCTTGTGGTCGCTGCGTCCCGGTCTGCGTTTGGGAGACCCCTGGGGGTTGCCGGGGCA
GCGCGCCGTGTCCAGGTGGAGGTGCCCGTTCCTGGACCTCAGCGAGCCTGAGCCGGGCCCGGCCGCACGCTGACC
CCCGTGCTGTCCCCGACCGGCTCACGGGGCTGGGCTCCGATCTTCCGTGTCTCTTATCAGTGGCGTTTCTCACGT
CTGCGTCTCAGATCTAACGTGGTTTCACATCAATCCGCTTTCATGGGATTTTGGTCTCTGTCCAGTGACTTCGTG
GTAAATGTAACTCAGTGTTTGCTTGCGACTTATTTATAAATATTGTAAGTTTGTGTCGATGAGTGTAAGTTGGCA
GTGCGCACGTCTCGGTTTTTTTACATGATTTAAGGAAAGACTTTTATGTCAGAACTTGGTGCCTGTACCGTCAAC
CCCGCTGCTGCCCGTGTTTAAACGCAGGAGAACTTTAAAACTGGCCATCTATCTTTTCAGTGTACAAGTCACTGA
ACCCATTGTTTCTTTCTGAAGAGACTTTCCTTTCAAGGCTTCCCATGGGTCCGCGCCACACAGGGCCGGTGCTGC
TTTATTTCAGACTCTGCCCCAGGTTCCAGGAATCCGAACCCCGGAGTGCTGACGCGGTTCCCCAACTTCCGCCTT
AAGAAAACAGGACCAGCCGGCACCAGGCCCGTCTCTCACGTACTTTAACACATCCTTGAAAGCCCCTCGTTTAAT
GAGAAAAGCGAACACTGCGGTCCTTGCCAAAGTAAAATGAAGCTGCCCCAGGACAAGGGGTTACCATGAGCTCCC
TGGAGTCCGACGCGGGTTTTCTCTCTGGGGGACCTGGGTGGTCCCCGCTGTGGTCTTTGTTGTCCCACTTTGGGA
CCGGGTCCAGTCTGGGGTCTAGTCTCGAGCATCAGGGTCAGGCTCGGGGCAGGGCTGGGTTAGGCTCCGGGTCAG
TCTTGCCATGGGTTTGGGAGCAGGTTTGGGTTACTTGCGTTTGAAGGCAGCAGTGGTCTCAGGAGGAAGAAACGG
GGGCGGGAGAGAGTGGTGATCTGTGGTCAGTGGGTCAGTGACCTGCACGGTGATTCTCCCACCTCCAAAAGGTAG
GGGTGGGACTGGAGGCGTCCCTAGGTCAGGCCGTTGAGTTCGAGCTCCGATGGGCCACCTTGAATCCAGGACTGA
CCGCCCGTGTGTGCACAGTTTGTTCTTGGACGAGGACTCGTGAGGATCGAGGGCTGGGGACCCCGGTGTGAGCAG
GATGGGGCCCTGCCCTCCCGTGGGAGTTGTGGACTCGAGCCCAGGGGCTGCCCGTCACAGCGGTGTCCCAGGTCC
CTGCCATCCGATTTTACCTGGGATGTCTTCTCTGGAGTTTGGAATTGCTTGAGGAACCCTGCGTGTGCTTGGAGA
GGCCAGAGGGCTTGCTGAGAACCCCATGGACAGTGGAGAGCGGGATTCGAACCAAGGGCTGGACTCCCACACCTC
TGGCCTGCGTCGCCCAGTTCTTTGTGGCTCTGAAGAATTGGCCGCTGTGGAAAAGAGCAAATGTCCGAGACCCCC
AACAGGAAGAGTCTAAAAATCCAGTTTGCAACCACTTCTGACCTACAAAAAAATGGAAATTTAGTGTTTTTCAGC
CTAAGACATTAAATTTCATATCAGAACAAGAA

FIGURE 700

AALGLGTLALCGAALLYLARCAAEPGDPRAMSGRSPPPPAPARAAAFLAVLVASAPRAGRAPQRDPQHVACAARG
PGRRVGALCRGHGRPGRRGAARPGAGAGAARGPAAAARAARRLRKPHGQGAGHAGLAGRARGLRVRAQGGRRLLR
AAGRAAGRAARPRARAPPPLYWGFFSGRGRVKPGGRWREAAWQLCDYYLPYALGGGYVLSADLVHYLRLSRDYLR
AWHSEDVSLGAWLAPVDVQREHDPRFDTEYRSRGCSNQYLVTHKQSLEDMLEKHATLAREGRLCKREVQLRLSYV
YDWSAPPSQCCQRREGIP

FIGURE 701

CCGAGGCCAAGTCCCGGGCGCTAGCCCACCTCCCACCCGCCTCTTGGCTCCTCTCCTCTAGGCCGTCGCTTTCGG
GTTCTCTCATCGCTTCGTCGTTCGCCAATGTTTGAGGAGAAGGCCAGCAGTCCTTCAGGGAAG**ATG**GGAGGCGAG
GAGAAGCCGATTGGTGCTGGTGAAGAGAAGCAAAAGGAAGGAGGCAAAAAGAAGAACAAAGAAGGATCTGGAGAT
GGAGGTCGAGCTGAGTTGAATCCTTGGCCTGAATATATTTACACACGTCTTGAGATGTATAATATACTAAAAGCA
GAACATGATTCCATTCTGGCAGAAAAGGCAGAAAAAGATAGCAAGCCAATTAAAGTCACTTTGCCTGATGGTAAA
CAGGTTGATGCGGAATCTTGGAAAACTACACCATATCAAATTGCCTGTGGAATTAGTCAAGGCCTGGCCGACAAC
ACCGTTATTGCTAAAGTAAATAATGTTGTGTGGGACCTGGACCGCCCTCTGGAAGAAGATTGTACCTTGGAGCTT
CTCAAGTTTGAGGATGAGGAAGCTCAGGCAGTGTATTGGCACTCTAGTGCTCACATAATGGGTGAAGGCATGGAA
AGAGTCTATGGTGGATGTTTATGCTACGGTCCGCCAATAGAAAATGGATTCTATTATGACATGTACCTCGAAGAA
GGGGGTGTGTCTAGCAATGATTTCTCTTCTCTGGAGGCTTTGTGTAAGAAAATCATTAAAGAAAAACAAGCTTTT
GAAAGACTGGAAGTTAAGAAAGAAACTTTACTGGCAATGTTTAAGTACAACAAGTTCAAATGCCGGATATTGAAT
GAAAAGGTGAATACTCCAACTACCACAGTCTATAGATGTGGCCCTTTGATAGATCTCTGCCGGGGTCCTCATGTT
AGACACACGGGCAAAATTAAGGCTTTAAAAATACACAAAAATTCCTCCACGTACTGGGAAGGCAAAGCAGATATG
GAGACTCTCCAGAGAATTTATGGCATTTCATTCCCAGATCCTAAAATGTTGAAAGAGTGGGAGAAGTTCCAAGAG
GAAGCTAAAAACCGAGATCATAGGAAAATTGGCAGGGACCAAGAACTATATTTCTTTCATGAACTCAGCCCTGGA
AGTTGCTTTTTTCTGCCAAAAGGAGTCTATATTTATAATGCACTTATTGAATTCATTAGGAGCGAATATAGGAAA
AGAGGATTCCAGGAGGTAGTCACCCCAAACATCTTCAACAGCCGACTCTGGATGACCTCGGGCCACTGGCAGCAC
TACAGCGAGAACATGTTCTCCTTTGAGGTGGAGAAGGAGCTGTTTGCCCTGAAACCCATGAACTGCCCAGGACAC
TCCCTTATGTTTGATCATCGGCCAAGGTCCTGGCGAGAACTGCCTCTGCGGCTAGCTGATTTTGGGGGTCTTCAT
AGGAACGAGCTGTCTGGAGCACTCACAGGACTCACCCGGGTACGAAGATTCCAACAGGATGATGCTCACATATTC
TGTGCCATGGAGCAGATTGAAGATGAAATAAAAGGTTGTTTGGATTTTCTACGTACGGTATATAGCGTATTTGGA
TTTTCTTTTAAACTAAACCTTTCTACTCGCCCGGAAAAATTCCTTGGAGATATCGAAGTATGGGATCAAGCTGAG
AAACAACTTGAAAACAGTCTGAATGAATTTGGTGAAAAGTGGGAGTTAAACTCTGGAGATGGAGCTTTCTATGGC
CCAAAGATTGACATACAGATTAAAGATGCGATTGGGCGGTACCACCAGTGTGCAACCATCCAGCTGGATTTCCAG
TTGCCCATCAGATTTAATCTTACTTATGTAAGCCATGATGGTGAGGATAAGAAAAGGCCAGTGATTGTTCATCGA
GCCATCTTGGGATCAGTGGAAAGAATGATTGCTATCCTCACAGAAAACTATGGGGGCAAATTGGCCCCCTTTTGG
CTGTCCCCTCGCCAGGTAATGGTAGTTCCAGTGGGACCAACCTGTGATGAATATGCCCAAAACGTACGACAACAA
TTCCACGATGCCAAATTCATGGCAGACATTGATCTGGATCCAGGCTGTACATTGAATAAAAAGATTCGAAATGCA
CAGTTAGCACAGTATAACTTCATTTTAGTTGTTGGTGAAAAAGAGAAAATCACTGGCACTGTTAATATCCGCACA
AGAGACAATAAGGTCCACGGGGAACGCACCATTTCTGAAACTATCGAGCGGCTACAGCAGCTCAAAGAGTTCCGC
AGCAAACAGGCAGAAGAAGAATTT**TAA**TGAAAAAATTACCCAGATTGGCTCCATGGAAAAGGAGGAACAGCGTTT
CCGTAAAATTGACTTTGTACTCGAAAACGTCAATTTATATTGAACTTGGAGGAGGAGTTTGGCAAAGTCTGAAAT
AGGTCAACCTGCAGGCGTAACTATTTTTGACCTAGTCAGTTTTTAAACAATGTGCATTTGAAGGAGTTAATTAAA
AGAGAGCCAATAAAATGATTTTACTCATTCAGTATCTGAGTACTGGAAGTGAAACATGAGGAATGCTTTAGTGTA
ATGTGGGAGAACTTTTTTGTAAATTTAATGCAATTGAAAAAGTTTTCAAATTCAATTAAGATAACTAGAATTGGT
TATGGTGTAACCCGAATTC

FIGURE 702

MGGEEKPIGAGEEKQKEGGKKKNKEGSGDGGRAELNPWPEYIYTRLEMYNILKAEHDSILAEKAEKDSKPIKVTL
PDGKQVDAESWKTTPYQIACGISQGLADNTVIAKVNNVVWDLDRPLEEDCTLELLKFEDEEAQAVYWHSSAHIMG
EGMERVYGGCLCYGPPIENGFYYDMYLEEGGVSSNDFSSLEALCKKIIKEKQAFERLEVKKETLLAMFKYNKFKC
RILNEKVNTPTTTVYRCGPLIDLCRGPHVRHTGKIKALKIHKNSSTYWEGKADMETLQRIYGISFPDPKMLKEWE
KFQEEAKNRDHRKIGRDQELYFFHELSPGSCFFLPKGVYIYNALIEFIRSEYRKRGFQEVVTPNIFNSRLWMTSG
HWQHYSENMFSFEVEKELFALKPMNCPGHSLMFDHRPRSWRELPLRLADFGGLHRNELSGALTGLTRVRRFQQDD
AHIFCAMEQIEDEIKGCLDFLRTVYSVFGFSFKLNLSTRPEKFLGDIEVWDQAEKQLENSLNEFGEKWELNSGDG
AFYGPKIDIQIKDAIGRYHQCATIQLDFQLPIRFNLTYVSHDGEDKKRPVIVHRAILGSVERMIAILTENYGGKL
APFWLSPRQVMVVPVGPTCDEYAQNVRQQFHDAKFMADIDLDPGCTLNKKIRNAQLAQYNFILVVGEKEKITGTV
NIRTRDNKVHGERTISETIERLQQLKEFRSKQAEEEF

FIGURE 703

ACGTACTCC**ATG**CGCTACCTGCTGCCCAGCGTCGTGCTCCTGGGCACGGCGCCCACCTACGTGTTGGCCTGGGGG
GTCTGGCGGCTGCTCTCCGCCTTCCTGCCCGCCCGCTTCTACCAAGCGCTGGACGACCGGCTCTACTGCGTCTAC
CAGAGCATGGTGCTCTTCTTCTTCGAGAATTACACCGGGGTCCAGATATTGCTATATGGAGATTTGCCAAAAAAT
AAAGAAAATATAATATATTTAGCAAATCATCAAAGCACAGTTGACTGGATTGTTGCTGACATCTTGGCCATCAGG
CAGAATGCGCTAGGACATGTGCGCTACGTGCTGAAAGAAGGGTTAAAATGGCTGCCATTGTATGGGTGTTACTTT
GCTCAGCATGGAGGAATCTATGTAAAGCGCAGTGCCAAATTTAACGAGAAAGAGATGCGAAACAAGGTGCAGAGC
TACGTGGACGCAGGAACTCCAATGTATCTTGTGATTTTTCCAGAAGGTACAAGGTATAATCCAGAGCAAACAAAA
GTCCTTTCAGCTAGTCAGGCATTTGCTGCCCAACGTGGCCTTGCAGTATTAAAACATGTGCTAACACCACGAATA
AAGGCAACTCACGTTGCTTTTGATTGCATGAAGAATTATTTAGATGCAATTTATGATGTTACGGTGGTTTATGAA
GGGAAAGACGATGGAGGGCAGCGAAGAGAGTCACCGACCATGACGGAATTTCTCTGCAAAGAATGTCCAAAAATT
CATATTCACATTGATCGTATCGACAAAAAAGATGTCCCAGAAGAACAAGAACATATGAGAAGATGGCTGCATGAA
CGTTTCGAAATCAAAGATAAGATGCTTATAGAATTTTATGAGTCACCAGATCCAGAAAGAAGAAAAAGATTTCCT
GGGAAAAGTGTTAATTCCAAATTAAGTATCAAGAAGACTTTACCATCAATGTTGATCTTAAGTGGTTTGACTGCA
GGCATGCTTATGACCGATGCTGGAAGGAAGCTGTATGTGAACACCTGGATATATGGAACCCTACTTGGCTGCCTG
TGGGTTACTATTAAAGCA**TAG**ACAAGTAGCTGTCTCCAGACAGTGGGATGTGCTACATTGTCTATTTTTGGCGGC
TGCACATGACATCAAATTGTTTCCTGAATTTATTAAGGAGTGTAAATAAAGCCTTGTTGATTGAAGATTGGATAA
TAGAATTTGTGACGAAAGCTGATATGCAATGGTCTTGGGCAAACATACCTGGTTGTACAACTTTAGCATCGGGGC
TGCTGGAAGGGTAAAAGCTAAATGGAGTTTCTCCTGCTCTGTCCATTTCCTATGAACTAATGACAACTTGAGAAG
GCTGGGAGGATTGTGTATTTTGCAAGTCAGATGGCTGCATTTTTGAGCATTAATTTGCAGCGTATTTCACTTTTT
CTGTTATTTTCAATTTATTACAACTTGACAGCTCCAAGCTCTTATTACTAAAGTATTTAGTATCTTGCAGCTAGT
TAATATTTCATCTTTTGCTTATTTCTACAAGTCAGTGAAATAAATTGTATTTAGGAAGTGTCAGGATGTTCAAAG
GAAAGGGTAAAAAGTGTTCATGGGGAAAAAGCTCTGTTTAGCACATGATTTTATTGTATTGCGTTATTAGCTGAT
TTTACTCATTTTATATTTGCAAAATAAATTTCTAATATTTATTGAAATTGCTTAATTTGCACACCCTGTACACAC
AGAAAATGGTATAAAATATGAGAACGAAGTTTAAAATTGTGACTCTGATTCATTATAGCAGAACTTTAAATTTCC
CAGCTTTTTGAAGATTTAAGCTACGCTATTAGTACTTCCCTTTGTCTGTGCCATAAGTGCTTGAAAACGTTAAGG
TTTTCTGTTTTGTTTTGTTTTTTTAATATCAAAAGAGTCGGTGTGAACCTTGGTTGGACCCCAAGTTCACAAGAT
TTTTAAGGTGATGAGAGCCTGCAGACATTCTGCCTAGATTTACTAGCGTGTGCCTTTTGCCTGCTTCTCTTTGAT
TTCACAGAATATTCATTCAGAAGTCGCGTTTCTGTAGTGTGGTGGATTCCCACTGGGCTCTGGTCCTTCCCTTGG
ATCCCGTCAGTGGTGCTGCTCAGCGGCTTGCACGCAGACTTGCTAGGAAGAAATGCAGAGCCAGCCTGTGCTGCC
CACTTTCAGAGTTGAACTCTTTAAGCCCTTGTGAGTGGGCTTCACCAGCTACTGCAGAGGCATTTTGCATTTGTC
TGTGTCAAGAAGTTCACCTTCTCAAGCCAGTGAAATACAGACTTAATTTGTCATGACTGAACGAATTTGTTTATT
TCCCATTAGGTTTAGTGGAGCTACACATTAATATGTATCGCCTTAGAGCAAGAGCTGTGTTCCAGGAACCAGATC
ACGATTTTTAGCCATGGAACAATATATCCCATGGGAGAAGACCTTTCAGTGTGAACTGTTCTATTTTTGTGTTAT
AATTTAAACTTCGATTTCCTCATAGTCCTTTAAGTTGACATTTCTGCTTACTGCTACTGGATTTTTGCTGCAGAA
ATGTATCAGTGGCCCACATTAAACATACCAGTTGGATCATGATAAGCAAAATGAAAGAAATAATGATTAAGGGAA
AATTAAGTGACTGTGTTACACTGCTTCTCCCATGCCAGAGAATAAACTCTTTCAAGCATCATCTTTGAAGAGTCG
TGTGGTGTGAATTGGTTTGTGTACATTAGAATGTATGCACACATCCATGGACACTCAGGATATAGTTGGCCTAAT
AATCGGGGCATGGGTAAAACTTATGAAAATTTCCTCATGCTGAATTGTAATTTTCTCTTACCTGTAAAGTAAAAT
TTAGATCAATTCCATGTCTTTGTTAAGTACAGGGATTTAATATATTTTGAATATAATGGGTATGTTCTAAATTTG
AACTTTGAGAGGCAATACTGTTGGAATTATGTGGATTCTAACTCATTTTAACAAGGTAGCCTGACCTGCATAAGA
TCACTTGAATGTTAGGTTTCATAGAACTATACTAATCTTCTCACAAAAGGTCTATAAAATACAGTCGTTGAAAAA
AATTTTGTATCAAAATGTTTGGAAAATTAGAAGCTTCTCCTTAACCTGTATTGATACTGACTTGAGTTATTTTCT
AAAATTAAGAGCCGTATACCTACCTGTAAGTCTTTTCACATATCATTTAAACTTTTGTTTGTATTATTACTGATT
TACAGCTTAGTTATTAATTTTTCTTTATAAGAATGCCGTCGATGTGCATGCTTTTATGTTTTTTAGAAAAGGGTG
TGTTTGGATGAAAGTAAAAAAAAAAAATAAAATCTTTCACTGTCTCT

FIGURE 704

MRYLLPSVVLLGTAPTYVLAWGVWRLLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDLPKNKEN
IIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLKWLPLYGCYFAQHGGIYVKRSAKFNEKEMRNKVQSYVD
AGTPMYLVIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATHVAFDCMKNYLDAIYDVTVVYEGKD
DGGQRRESPTMTEFLCKECPKIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPDPERRKRFPGKS
VNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKLYVNTWIYGTLLGCLWVTIKA

FIGURE 705

AGCGGCGAGGGCTGGATCCTGGGCCAAATATATGCCAACAACGACAAGCTCTCCAAGAGGCTGAAGAAAGTGTGG
AAGCCACAGCTGTTTGAGCGAGAGTTCTACAGTGAGATCCTGGACAAGAAGTTCACAGTGACTGTGACC**ATG**CGG
ACCCTGGACCTCATCGATGAGGCTTACGGGCTCGACTTTTACATCCTCAAGACCCCGAAGGAGGACCTGTGCTCC
AAGTTTGGGATGGAGCTGAAGCGAGGGATGCTGCTGCGGCTTGCCCGGCAGGACCCCCAGCTGCACCCCGAGGAC
CCCGAGCGGCGGGCAGCCATCTACGACAAGTACAAGGAATTTGCCATCCCAGAGGAGGAGGCAGAGTGGGTGGGC
CTCACGCTGGAGGAGGCCATTGAGAAGCAGAGACTTTTGGAGGAGAAGGACCCTGTACCCCTGTTCAAGATCTAT
GTGGCGGAGCTGATCCAGCAGCTGCAGCAGCAGGCACTGTCAGAGCCGGCGGTGGTGCAGAAGACAGCCAGTGGC
CAG**TGA**CCACACAGCTCCTCCATGCCTGACCAACAGGCCCAGCTTTCCCTGCCAGGCCCTTTGCACTGAGGACAC
AGATCCCGGGGAGCTGTGAGGGCCACCGGTGGGCAGTGGGTGGATCCTGGTTTCGTGTGCTGCCCATGCACCTTC
CAGCCCGGGGCCAGCTTGGCAGGGATCCCCAGGAGGCCTGGGCCGCCCAGAGGCTCCTCTCAGGCTGGGCCCCGA
CGTTTGCGGCAGTGTTCCTTGTCCCGTGGGGCCGGGAGCGAGTAAAGTCTGGGCCAGGC

FIGURE 706

MRTLDLIDEAYGLDFYILKTPKEDLCSKFGMELKRGMLLRLARQDPQLHPEDPERRAAIYDKYKEFAIPEEEAEW
VGLTLEEAIEKQRLLEEKDPVPLFKIYVAELIQQLQQQALSEPAVVQKTASGQ

FIGURE 707

CCGCTTTGTTGCCTGAGGTGGGTGGCGGTGGAAGTTAAGGGAGTCAGGGGCTATCGCTCCTCGAGACTCGCAGTC
GCGGCCACTGCAGTCACTTCGCCAGTTAGCCCTTAGGGTAGGAGTCGCGCCGGCAGCAGCC**ATG**AGCGGCGGCGT
GTACGGGGGAGATGAAGTTGGAGCCCTTGTTTTTGACATTGGATCCTATACTGTGAGAGCTGGTTATGCTGGTGA
GGACTGCCCCAAGGTGGATTTTCCTACAGCTATTGGTATGGTGGTAGAAAGAGATGACGGAAGCACATTAATGGA
AATAGATGGCGATAAAGGCAAACAAGGCGGTCCCACCTACTACATAGATACTAATGCTCTGCGTGTTCCGAGGGA
GAATATGGAGGCCATTTCACCTCTAAAAAATGGGATGGTTGAAGACTGGGATAGTTTCCAAGCTATTTTGGATCA
TACCTACAAAATGCATGTCAAATCAGAAGCCAGTCTCCATCCTGTTCTCATGTCAGAGGCACCGTGGAATACTAG
AGCAAAGAGAGAGAAACTGACAGAGTTAATGTTTGAACACTACAACATCCCTGCCTTCTTCCTTTGCAAAACTGC
AGTTTTGACAGCATTTGCTAATGGTCGTTCTACTGGGCTGATTTTGGACAGTGGAGCCACTCATACCACTGCAAT
TCCAGTCCACGATGGCTATGTCCTTCAACAAGGCATTGTGAAATCCCCTCTTGCTGGAGACTTTATTACTATGCA
GTGCAGAGAACTCTTCCAAGAAATGAATATTGAATTGGTTCCTCCATATATGATTGCATCAAAAGAAGCTGTTCG
TGAAGGATCTCCAGCAAACTGGAAAAGAAAAGAGAAGTTGCCTCAGGTTACGAGGTCTTGGCACAATTATATGTG
TAATTGTGTTATCCAGGATTTTCAAGCTTCGGTACTTCAAGTGTCAGATTCAACTTATGATGAACAAGTGGCTGC
ACAGATGCCAACTGTTCATTATGAATTCCCCAATGGCTACAATTGTGATTTTGGTGCAGAGCGGCTAAAGATTCC
AGAAGGATTATTTGACCCTTCCAATGTAAAGGGGTTATCAGGAAACACAATGTTAGGAGTCAGTCATGTTGTCAC
CACAAGTGTTGGGATGTGTGATATTGATATCAGACCAGGTCTCTATGGCAGTGTAATAGTGGCAGGAGGAAACAC
ACTAATACAGAGTTTTACTGACAGGTTGAATAGAGAGCTGTCTCAGAAAACTCCTCCAAGTATGCGGTTGAAATT
GATTGCAAATAATACAACAGTGGAACGGAGGTTTAGCTCATGGATTGGCGGCTCCATTCTAGCCTCTTTGGGTAC
CTTTCAACAGATGTGGATTTCCAAGCAAGAATATGAAGAAGGAGGGAAGCAGTGTGTAGAAAGAAAATGCCCT**TG**
AGAAAGAGTTCCCAAGCTTCTACCTTCCTTTTGTCACCTTACGTTTCATAGCTTTAGTATACTCAGGAAAAGAAT
GACCATCTTTTGTAGAATGTTTATACATTTATGCATATTTCAATTTCCACTTAAATTTATTTAAAGCTTTAACTG
GCTCTATAAATTAAGTTTGTGCTTTCCTTGAAATGCACTTATTCTTATTACAAGCATTTTATAATTTTGTATAAA
TGTCTATTTTCTCTAAATATTTTGCTTTCAGTAAAATGCTTTCCAACTCTGTTTAGTGTATTAATTACCAGTGGA
TTGGTAGAACTGCTTTTATTGACTAGTAAAAGTTACTGCCTAGTCTTTTTACCTTAGGCTTACAGAATTAAATAA
AAATTAGCCATTCCAGAAATATAAAAAAAAAAAAAAAAAAA

FIGURE 708

MSGGVYGGDEVGALVFDIGSYTVRAGYAGEDCPKVDFPTAIGMVVERDDGSTLMEIDGDKGKQGGPTYYIDTNAL
RVPRENMEAISPLKNGMVEDWDSFQAILDHTYKMHVKSEASLHPVLMSEAPWNTRAKREKLTELMFEHYNIPAFF
LCKTAVLTAFANGRSTGLILDSGATHTTAIPVHDGYVLQQGIVKSPLAGDFITMQCRELFQEMNIELVPPYMIAS
KEAVREGSPANWKRKEKLPQVTRSWHNYMCNCVIQDFQASVLQVSDSTYDEQVAAQMPTVHYEFPNGYNCDFGAE
RLKIPEGLFDPSNVKGLSGNTMLGVSHVVTTSVGMCDIDIRPGLYGSVIVAGGNTLIQSFTDRLNRELSQKTPPS
MRLKLIANNTTVERRFSSWIGGSILASLGTFQQMWISKQEYEEGGKQCVERKCP

FIGURE 709

AGTGTAAGCAGTGTGCAAACAAGGTGTTACAGCAC**ATG**AAGGCCGTGCAGGCAGATCAGGAGCGGGAGAGGCAGC
GGCGGCTGGAAGTAGAACGTGAGGCAGAGAAGAAGCGTGAGGCTAAGCAGCGAGCTAAGGAAGCTCAGGAGCGGG
AACTGCGGAAGCGGGAGAAGGCGGAAGAGAAGGAGCGCCGGAGAAAGGAGTATGATGCCCTCAAAGCAGCCAAGC
GGGAGCAGGAGAAGAAACCTAAGAAGGAAGCAAATCAGGCCCCGAAATCTAAGTCTGGCTCCCGTCCCCGCAAGC
CACCACCCCGGAAGCACACTCGTTCCTGGGCTGTGCTGAAGCTGCTGCTGCTGCTGCTATTTGGTGTGGCGG
GAGGGCTGGTTGCTTGTCGGGTGACAGAGCTGCAGCAGCAGCCCCTCTGCACCAGCGTGAACACCATCTATGACA
ATGCGGTCCAGGGTCTACGCCGCCATGAGATCCTCCAGTGGGTCCTTCAGACCGACTCTCAGCAG**TGA**GCTTGTT
CCCAGCACCTGCTGCCTCCCAGCCTTGGAGTTTGGATTCCTATGGAATTGGGTTCTGCTGGACACAACCTCTTTT
TAGCATCAGACCTACCTGCCATCATCAAATGGCTGCAGATTGGTACATGAGACCTCCTCTTTGTAGGACTTCTTC
ATTCCTTAGTCAGGGTTCCCTGAAGGAATGAGGAGAAATGGGAGGTGGCGGGGGGGCGTGGGGGGCAGTTACCTG
CATGCCTAAAGGAGTAGGCTTGGGGGTGGGGAGAGAGAAAACATAGCCTTTTCTAGTTGTTATATAAAGCTGTGT
AAAGGCAAGGCTCGTTTCTACTAAATGGTCAGCTGTCACTACATTTATACTTTTGTATGCCACAAACCCTTTCAT
TCCTCCCTGGGAATCAGGGTAGATCAGGAGGAACTGGGGGGGACTAGAACACCACGCTCAGTAAATCCAGTCTAA
ACTGGGAGGTAGGGGTATTCCTGTTTTCTTTAGGACCTCAGAGATGTAAGCATTTTAGCAGCCACACAAAATCTC
TGGCTATGAAAGGGACTTCATGACCATCCAGTCCAATATAACACTTGCAGACAGAGAAACTGAGGTCTTCCATGA
CTTGCCTAGTCTCCCAGCTAGTTTGAGGCAAAACTGGATTCCCACTCTGGTATTCTTTCTTCCCTTTACATCATT
TTCCCTCCTTTATAATGTCCTGAGAGACCAGAACTCACACCAGAATCGATTATTCCTCAGGTGAAGCATAGACTC
TTTCATGGTAGACAGATTTCACGACTCAGAGATAGAAATCTCTTGCTATCATCAGGTCACGGGCAGCTCCTGTGG
AGTCCTGCCCAACTTATGTGGCTTCCATAAAATGGCAACAGTCCAGGCTCCTTGCCTAATTTAGAGCATTAACT
CCCTAATTGCCAGTAAGCAAGGAGGTGGATCTCTGCAAACCTACACTGTCTATGACAGCTCTAGTTGTACTTGGT
GTGACTAAATACCTCAAAGGCAACCTGCTTCTGCAGGTTTTGAAGTGTCAGCTTCATAAGACACTGAGGTTTAGA
ATTGTTTGATTCTAGACCATAACTGAAGGGCATAAATGGAAACAGGATATGAAGGGAAACAAGTAGCATCATGGA
GCTGAAAAGTGGTGCATCACCCAATGGCTAGCACAAACAAGGATCACACTGTCCATTCTCTTGTCTGCTAAATTA
AGCATTTTCTTGCCTCCTTTGCTTCATCTTTTCACAACAGCTGGATAGAGGGATCAGAAATGACTGTGTCATGGT
GCTCATTCACTGCAAACTCCCAGTTGCAAGCTCCTTGGCTCCCCCGGAGGGAGCAAGAATCTCATAGTTCAGAGA
CACAGAGGGCCTTTTAGCCCTAATGACCTTTTGGATGGGACTGCAACTCATGACTATCCTGATATTGGAAGAAAG
GACTTTGTTAATCTTCTCCCCCATAGCTCTGCTGCGTAGGTCTACATCTTACTCAGAATCACTACACATTCCTTT
AGTCTTCCTCCAAGCTCCAGAGCCATTGGTACAAATGCTTTATTGAAACTAAATACATAATACACACAATGAGAT
GAAGACAATATAGAAGTCCGCATAGTCATCATAATCCCGTTCCTTGGCCGGTTGAGGCAGCTCAGTGGCTGAGCC
CAGTCAAGCCAACCCGCAGCTTCACTCACGACTTCAAGATTTGATGCTAATTCTTTTGGATTTCTACAGTTATTA
AATAAGTGTCTGAGTGGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 710

MKAVQADQERERQRRLEVEREAEKKREAKQRAKEAQERELRKREKAEEKERRRKEYDALKAAKREQEKKPKKEAN
QAPKSKSGSRPRKPPPRKHTRSWAVLKLLLLLLLFGVAGGLVACRVTELQQQPLCTSVNTIYDNAVQGLRRHEIL
QWVLQTDSQQ

FIGURE 711

GGGACCCTGGTGACCAAAGTGGCTCCGGTCAGCGCCCCTCCTAAAGTCAGCAGCGGCCCTAGGCTGCCTGCTCCT
CAGATAGTCGCCGTGAAAGCCCCCAACACCACGACAATCCAGTTTCCTGCTAATTTGCAGCTTCCTCCAGGAACC
GTTTTGATTAAAAGTAACAGTGGTCCGTTGATGTTGGTATCTCCTCAGCAAACTGTAACAAGAGCCGAGACCACA
AGTAACATAACCTCAAGGCCAGCAGTACCAGCGAATCCTCAAACAGTCAAAATCTGTACAGTGCCGAACTCTAGC
TCACAATTAATCAAGAAAGTGGCAGTGACACCTGTTAAAAAATTGGCACAAATAGGAACTACTGTGGTAACCACT
GTTCCGAAGCCTTCCTCAGTACAATCTGTGGCTGTGCCAACCAGTGTCGTCACAGTTACTCCTGGAAAGCCATTG
AATACTGTAACTACCCTGAAGCCTTCAAGTTTGGGAGCATCATCCACTCCTTCAAATGAGCCCAATCTTAAAGCA
GAGAACTCAGCAGCTGTTCAGATTAATCTTTCTCCGACAATGCTAGAAAATGTGAAGAAATGCAAGAACTTCCTT
GCAATGTTAATAAAACTAGCATGTAGTGGATCACAGTCCCCTGAAATGGGGCAAAATGTGAAGAAGCTGGTGGAA
CAACTTTTGGATGCAAAAATCGAAGCAGAAGAATTTACTAGGAAACTGTATGTTGAACTCAAGTCTTCACCTCAG
CCTCACCTGGTTCCTTTTCTTAAGAAAAGCGTGGTTGCCTTACGACAACTTCTGCCTAACTCCCAGAGCTTCATC
CAGCAATGTGTTCAGCAGACTTCTAGTGACATGGTCATTGCTACCTGTACTACAACAGTAACAACTTCTCCTGTG
GTGACAACTACAGTGTCCTCAAGCCAGTCTGAAAAGTCAATTATTGTTTCTGGAGCAACAGCACCCAGAACTGTG
TCAGTGCAAACTTTGAACCCACTTGCTGGTCCAGTGGGAGCAAAAGCTGGAGTTGTGACACTTCATTCTGTGGGC
CCAACTGCTGCAACAGGAGGAACAACAGCTGGAACTGGTTTGCTTCAGACTTCAAAACCACTTGTGACATCTGTG
GCAAACACAGTGACCACGGTCTCACTGCAACCTGAAAAGCCAGTTGTCTCTGGAACAGCAGTAACACTGTCCCTT
CCAGCAGTAACTTTTGGAGAAACTTCAGGTGCAGCTATTTGTCTTCCATCTGTGAAACCTGTTGTTTCCTTCTGC
TGGGACCACATCTGCAAGCCTGTTATTGGGACTCCAGTTCAAATCAAACTTGCCCAGCCGGGCCCTGTCCTTTCA
CAACCAGCTGGGATTCCAACAGGCAGTTCAAGCAAGCAACTATTCTCATTGTTTCACGTAGTTCAGCAGCCTTCA
GGAGGCAATGAAAAACAAGTGACCACAATTTCACATTCCTCAACATTGACCATTCAGAAATGTGGACAGAAGACG
ATGCCAGTGAACACCATAATACCTACTAGTCAGTTTCCTCCAGCTTCCATTCTAAAGCAAATTACTCTGCCTGGA
AATAAAATTCTGTCACTTCAAGCATCTCCTACTCAGAAAAATAGAATAAAAGAGAATGTAACATCATGCTTCCGA
GATGAGGATGACATCAATGATGTGACTTCTATGGCAGGGGTCAACCTTAATGAAGAAAATGCCTGCATCTTAGCA
ACAAACTCTGAATTGGTTGGCACACTCATTCAGTCATGTAAAGATGAACCATTTCTTTTTATTGGAGCTCTACAA
AAGAGAATCTTAGACATTGGTAAAAAGCATGACATTACAGAACTTAACTCTGATGCTGTGAACTTGATCTCCCAA
GCAACACAGGAACGACTACGAGGCCTTCTAGAAAAACTGACTGCAATTGCTCAGCATCGAATGACTACTTACAAG
GCAAGTGAAAATTACATCCTGTGTAGTGATACCAGGTCACAGCTCAAATTTCTTGAAAAGCTGGATCAATTGGAG
AAGCAGAGAAAGGATTTGGAAGAAAGAGAAATGTTACTTAAGGCAGCCAAGAGTCGTTCTAATAAAGAAGATCCA
GAACAGCTGAGATTAAAGCAGAAAGCCAAAGAGTTACAGCAATTGGAACTTGCACAGATACAGCATAGAGACGCT
AATCTCACAGCTCTTGCAGCTATTGGACCAAGGAAGAAGAGACCACTAGAATCTGGAATTGAGGGCTTAAAAGAC
AACCTTCTTGCTTCTGGGACATCCAGCCTGACAGCCACCAAACAGTTGCATCGTCCAAGAATCACGAGAATCTGC
CTCAGGGACTTGATATTTTGTATGGAACAGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTG
AAG**TGA**CCACTCCACTCTTCCATCCACATCCTTGCTATTTACTGCCAAAGAAGACACAAAGCATTGTTGCACTGT
CCTGAAATTTCAATTTCTGGAAAATAACACCAACATGAAAGAGCATTGTTTACGATTAGAACTTTATTAACTCTT
ACCTAT

FIGURE 712

GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAETT
SNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPL
NTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVE
QLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV
VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSV
ANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLS
QPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPG
NKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEPFLFIGALQ
KRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLE
KQRKDLEEREMLLKAAKSRSNKEDPEQLRLKQKAKELQQLELAQIQHRDANLTALAAIGPRKKRPLESGIEGLKD
NLLASGTSSLTATKQLHRPRITRICLRDLIFCMEQEREMKYSRALYLALLK

FIGURE 713

ATGGCGGCGGCGGCGGTGGTGGAGTTCCAGAGAGCCCAGTCTCTACTCAGCACCGACCGGGAGGCCTCCATCGAC
ATCCTCCACTCCATCGTGAAGCGTGACATTCAGGAAAACGATGAAGAGGCAGTGCAAGTCAAAGAGCAGAGCATC
CTGGAACTGGGATCTCTCCTGGCAAAGACTGGACAAGCTGCAGAGCTTGGAGGACTCCTGAAGTATGTACGACCC
TTCTTGAATTCCATCAGCAAGGCTAAAGCAGCTCGCCTGGTCCGATCTCTTCTTGATCTGTTTCTTGATATGGAA
GCAGCTACAGGGCAGGAGGTCGAGCTGTGTTTAGAGTCCATCGAATGGGCCAAGTCAGAGAAAAGAACTTTCTTA
CGCCAAGCTTTGGAGGCAAGACTGGTGTCTTTGTACTTTGATACCAAGAGGTACCAGGAAGCATTGCATTTGGGT
TCTCAGCTGCTGCGGGAGTTGAAAAAGATGGACGACAAAGCTCTTTTGGTGGAAGTACAGCTTTTAGAAAGCAAA
ACATACCATGCCCTGAGCAACCTGCCGAAAGCCCGAGCTGCCTTAACTTCTGCTCGAACCACAGCAAATGCCATC
TACTGCCCCCCTAAATTGCAGGCCACCTTGGACATGCAGTCGGGTATTATCCATGCAGCAGAAGAGAAGGACTGG
AAAACTGCGTACTCATACTTCTATGAGGCATTTGAGGGTTATGACTCCATCGACAGCCCCAAGGCCATCACATCT
CTGAAGTACATGTTGCTGTGCAAAATCATGCTCAACACCCCAGAAGATGTCCAGGCTTTGGTGAGCGGGAAGCTT
GCACTTCGGTATGCAGGGAGGCAGACAGAAGCATTAAAATGCGTGGCTCAGGCTAGCAAGAACAGATCACTGGCA
GATTTTGAAAAGGCTCTGACAGATTACCGGGCAGAGCTCCGGGATGACCCAATCATCAGCACACACTTGGCCAAG
TTGTATGATAACTTACTAGAACAGAATCTGATCCGAGTCATTGAGCCTTTTTCCAGAGTACAGATTGAACACATA
TCTAGTCTCATCAAACTCTCCAAGGCCGACGTGGAAAGGAAATTATCACAGATGATTCTTGACAAGAAATTTCAT
GGGATTTTGGACCAGGGGGAGGGTGTCCTGATTATTTTCGATGAACCCCCAGTAGATAAAACTTACGAAGCTGCT
CTGGAAACAATTCAGAACATGAGCAAAGTAGTGGATTCCCTCTACAACAAAGCCAAGAAACTGACA**TAG**

FIGURE 714

MAAAAVVEFQRAQSLLSTDREASIDILHSIVKRDIQENDEEAVQVKEQSILELGSLLAKTGQAAELGGLLKYVRP
FLNSISKAKAARLVRSLLDLFLDMEAATGQEVELCLESIEWAKSEKRTFLRQALEARLVSLYFDTKRYQEALHLG
SQLLRELKKMDDKALLVEVQLLESKTYHALSNLPKARAALTSARTTANAIYCPPKLQATLDMQSGIIHAAEEKDW
KTAYSYFYEAFEGYDSIDSPKAITSLKYMLLCKIMLNTPEDVQALVSGKLALRYAGRQTEALKCVAQASKNRSLA
DFEKALTDYRAELRDDPIISTHLAKLYDNLLEQNLIRVIEPFSRVQIEHISSLIKLSKADVERKLSQMILDKKFH
GILDQGEGVLIIFDEPPVDKTYEAALETIQNMSKVVDSLYNKAKKLT

FIGURE 715

GAGATGGTGATTAAATCCGGGACTTTTAGCATATGGAACAGACCAAGAGGGATTGTTTCAGAGAGGGCATCTCAT
GTGCAGAAAAACAGGTTG**TGA**AGTCAAACGCAGCTCAGATTCTCACCAGCTGTGCGTATACCCTGACGAGTCCCC
TCACCATTCTGGGCCTTAGTCCCCTCTGAAAAATGGGACATGGGCACCAGAGAGACTCCTGAGAGCTCCCTTAGT
GCTCTTAGAGGAGACAGGGGAGGTCTCCTTTATCTTTGACCCCTAACCCCTCAGACTTCCAGAGGCGGGAACTGC
AGCGATGATACAAATGGTGTGGTGGAAAGAATGCCGTTTTGGAGTCAGGACACCTGGGTTTGAATCCACTTGCAG
CCACTTGCAGGCTGCTTGACCTTGAACGTATCGTGTCGTATCGTTTCACCTTGGGATCTGTACCTGTGAAGTGGG
TGAAAGTTAAAGAGATAATAAAGTAACAGTCGTGAAAAAA

FIGURE 716

EMVIKSGTFSIWNRPRGIVSERASHVQKNRL

FIGURE 717

GATCCGGAAGTCGGAGCCTAGCTGCGCGAGAGTTTCTGCTCGCTCAACCGAGTTGTCGTGTTGCCCTCGCTTCTC
AGATCCCCGCCGGAAGTGAAGAGAGCAAGCAGATTTGAACCTATCTGCTTTCAAGCTGGTCATC**ATG**ATGAAACT
TAGACACAAAAATAAAAAGCCAGGTGAAGGTTCCAAGGGCCACAAGAAGATAAGTTGGCCCTACCCTCAGCCTGC
AAAGCAAAATGGGAAGAAAGCAACCTCCAAAGTGCCCTCTGCACCTCATTTTGTTCACCCCAATGATCATGCCAA
TCGAGAGGCTGAATTAAAGAAGAAGTGGGTTGAGGAGATGAGGGAGAAGCAGCAAGCCGCCCGGGAGCAAGAAAG
ACAAAAACGCAGGACCATTGAGAGCTACTGTCAGGATGTCCTAAGACGCCAGGAGGAGTTTGAGCATAAGGAGGA
AGTTTTGCAGGAATTAAATATGTTTCCTCAGCTGGATGACGAGGCCACGAGGAAGGCTTATTACAAGGAGTTCCG
TAAGGTGGTGGAATACTCTGATGTGATTCTGGAAGTCCTGGATGCCAGAGACCCATTAGGCTGCCGCTGCTTCCA
AATGGAGGAGGCTGTCCTGCGAGCACAAGGCAACAAGAAGCTGGTCCTGGTCTTGAACAAGATTGACCTGGTCCC
CAAGGAGGTTGTGGAGAAATGGCTGGATTACCTTCGGAATGAGTTGCCAACCGTGGCTTTCAAGGCCAGTACCCA
GCATCAGGTCAAAAACCTGAATCGTTGCAGTGTGCCAGTAGATCAGGCCTCTGAGTCACTGCTGAAAAGCAAAGC
CTGCTTTGGAGCTGAAAACCTCATGAGGGTTCTGGGGAACTATTGCCGCCTTGGTGAAGTGCGCACCCACATTCG
TGTGGGTGTTGTGGGTCTTCCCAATGTTGGGAAGAGCAGCCTGATCAATAGCCTGAAGCGCAGCCGCGCATGCAG
CGTGGGAGCTGTTCCTGGAATTACCAAATTCATGCAGGAGGTCTACCTGGACAAGTTCATCCGGCTCTTGGATGC
TCCAGGCATTGTCCCAGGGCCCAACTCAGAGGTGGGCACCATCCTGCGTAACTGCGTCCACGTGCAGAAGCTGGC
AGACCCTGTGACCCCAGTGGAGACCATCCTGCAGCGCTGCAACCTGGAGGAGATTTCCAACTATTATGGCGTCTC
TGGGTTCCAGACCACTGAGCACTTTCTGACGGCAGTGGCCCACCGTTTGGGGAAGAAGAAGAAGGGAGGCTTATA
TAGTCAGGAACAGGCGGCCAAAGCTGTCCTAGCTGACTGGGTGAGCGGGAAGATCAGCTTCTATATACCACCACC
AGCCACTCACACTCTGCCCACCCATCTCAGTGCTGAGATCGTTAAGGAAATGACCGAGGTCTTTGACATCGAGGA
TACTGAGCAGGCCAATGAAGACACCATGGAATGCTTGGCCACCGGAGAATCTGATGAGCTGTTGGGTGACACGGA
CCCACTTGAAATGGAGATCAAGTTGCTCCATTCTCCGATGACGAAAATAGCAGATGCCATTGAAAATAAAACCAC
CGTGTATAAGATTGGAGATCTCACTGGGTATTGCACCAATCCAAACCGTCATCAGATGGGGTGGGCTAAACGCAA
TGTGGACCACCGCCCTAAGAGCAACAGTATGGTGGATGTCTGCTCAGTGGACCGCCGCTCAGTGCTGCAGAGGAT
CATGGAGACGGACCCCCTGCAACAGGGCCAGGCTCTGGCATCTGCCCTGAAAAATAAGAAGAAGATGCAGAAACG
TGCAGATAAAATCGCCAGCAAGCTGTCTGATTCCATGATGTCTGCTCTCGACCTCTCTGGCAATGCTGATGATGG
TGTTGGTGAC**TAA**TCGACTGATCTCACTTCCCTTCCGCTCCAAGCACCAGTTCCGGTGGTACGGGGGAATACCAG
TGAAATAGTTTGGTTCTCCCTGAAGCATCTGCATATTGAAAGAACGCTTTCCCCACTGTGTGTCTTCTCCCCCTC
CTCCAGTAAAAACAGTCCCGGCTGGGTGCTGTGGCTCACGTCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGG
CGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGGCCAACATGGTGAGGCCCCGTCTCTACTAAAAATACAAA
AAAATTTAGCCGTGCTTGGTGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCCTGAACCT
GGGAGACTAAGGCAGGAGAATCGCCTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCCAGACGGCACCATTGCACT
CTAGCCTGGGCAACAACACGAAACTCCGTCCC

FIGURE 718

MMKLRHKNKKPGEGSKGHKKISWPYPQPAKQNGKKATSKVPSAPHFVHPNDHANREAELKKKWVEEMREKQQAAR
EQERQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRKAYYKEFRKVVEYSDVILEVLDARDPLGC
RCFQMEEAVLRAQGNKKLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNLNRCSVPVDQASESLL
KSKACFGAENLMRVLGNYCRLGEVRTHIRVGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKFIR
LLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRCNLEEISNYYGVSGFQTTEHFLTAVAHRLGKKKK
GGLYSQEQAAKAVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDTEQANEDTMECLATGESDELL
GDTDPLEMEIKLLHSPMTKIADAIENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVCSVDRRSV
LQRIMETDPLQQGQALASALKNKKKMQKRADKIASKLSDSMMSALDLSGNADDGVGD

FIGURE 719

GGGTGCTTTACTCCTTCTGTGCTTGGAGGCTTACCCAACTGAAAGGAGATGGAGGGCAGGAGAGGCCGATGCCTA
GCGTGCCTGCTGCTTACAGGGGTGGTGTCACAGGTCACCATTATTCATTAAAATTTTACTTTTTTGATCCCCTAC
CACATGCTCAACATGGTATTGAGTCCTCAAGAATA**TAA**AAAGAAAATACAACAGGAACCAGTAGTCATTAACTGT
TTGTTCTGGACTTTAATAAAAGTACAGAGGGTCTTGGAGTACAAAGGCAAAGACATTTAGCTGTGTATAGAATGG
GTGGGGGAATGTGTTCCATGGTTTGGCATTCAGTTCAGCAACATTCCTGAGAGAAATCAACTAGCCCCCTTATAG
AGAAGAGGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGGAATTTCTTTTTTATAGTATTGGATAAAG
TTTGGTGTTTTTACAGAGGAGAAGCAATGGGTCTTAGCTCTTTCTCTATTATGTTATCATCCTCCCTTTTTTGTA
CAATATGTTGTTTACCTGAAAGGAAGGTTTCTATTCGTTGGTTGTGGACCTGGACAAAGTCCAAGTCTGTGGAAC
TTAAAACCTTGAAGGTCTGTCATAGGACTCTGGACAATCTCACACCTTAGCTATTCCCAGGGAACCCCAGGGGGC
AACTGACATTGCTCACAAGATGTTCTCCTGATGTAGCTTGAGATATAAAGGAAAGGCCTGCACAGGTGGCTGTTT
CTTGTCTGTTATGTC

FIGURE 720

VLYSFCAWRLTQLKGDGGQERPMPSVPAAYRGGVTGHHYSLKFYFFDPLPHAQHGIESSRI

FIGURE 721

GAGACATACAGGACAGAGC**ATG**GCTCGCCTACAGACTGCACTCCTGGTTGTCCTCGTCCTCCTTGCTGTGGCGCT
TCAAGCAACTGAGGCAGGCCCCTACGGCGCCAACATGGAAGACAGCGTCTGCTGCCGTGATTACGTCCGTTACCG
TCTGCCCCTGCGCGTGGTGAAACACTTCTACTGGACCTCAGACTCCTGCCCGAGGCCTGGCGTGGTGTTGCTAAC
CTTCAGGGATAAGGAGATCTGTGCCGATCCCAGAGTGCCCTGGGTGAAGATGATTCTCAATAAGCTGAGCCAA**TG**
AAGAGCCTACTCTGATGACCGTGGCCTTGGCTCCTCCAGGAAGGCTCAGGAGCCCTACCTCCCTGCCATTATAGC
TGCTCCCCGCCAGAAGCCTGTGCCAACTCTCTGCATTCCCTGATCTCCATCCCTGTGGCTGTCACCCTTGGTCAC
CTCCGTGCTGTCACTGCCATCTCCCCCCTGACCCCTCTAACCCATCCTCTGCCTCCCTCCCTGCAGTCAGAGGGT
CCTGTTCCCATCAGCGATTCCCCTGCTTAAACCCTTCCATGACTCCCCACTGCCCTAAGCTGAGGTCAGTCTCCC
AAGCCTGGCATGTGGCCCTCTGGATCTGGGTTCCATCTCTGTCTCCAGCCTGCCCACTTCCCTTCATGAATGTTG
GGTTCTAGCTCCCTGTTCTCCAAACCCATACTACACATCCCACTTCTGGGTCTTTGCCTGGGATGTTGCTGACAC
TCAGAAAGTCCCACCACCTGCACATGTGTAGCCCCACCAGCCCTCCAAGGCATTGCTCGCCCAAGCAGCTGGTAA
TTCCATTTCATGTATTAGATGTCCCCTGGCCCTCTGTCCCCTCTTAATAACCCTAGTCACAGTCTCCGCAGATTC
TTGGGATTTGGGGGTTTTCTCCCCCACCTCTCCACTAGTTGGACCAAGGTTTCTAGCTAAGTTACTCTAGTCTCC
AAGCCTCTAGCATAGAGCACTGCAGACAGGCCCTGGCTCAGAATCAGAGCCCAGAAAGTGGCTGCAGACAAAATC
AATAAAACTAATGTCCCTCCCCTCTCCCTGCCAAAAGGCAGTTACATATCAATACAGAGACTCAAGGTCACTAGA
AATGGGCCAGCTGGGTCAATGTGAAGCCCCAAATTTGCCCAGATTCACCTTTCTTCCCCCACTCCCTTTTTTTT
TTTTTTTTTTTGAGATGGAGTTTCGCTCTTGTCACCCACGCTGGAGTGCAATGGTGTGGTCTTGGCTTATTGAAG
CCTCTGCCTCCTGGGTTCAAGTGATTCTCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTTCCTGCTACCA
CGCCCAGCTAATTTTTGTATTTTTAGTAGAGACGAGGCTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGTC
CTCAGGTAATCCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACAGTGCCTGGCCTCTTCC
CTCTCCCCACTGCCCCCCCCAACTTTTTTTTTTTTTTTATGGCAGGGTCTCACTCTGTCGCCCAGGCTGGAGTGC
AGTGGCGTGATCTCGGCTCACTACAACCTCGACCTCCTGGGTTCAAGTGATTCTCCCACCCCAGCCTCCCAAGTA
GCTGGGATTACAGGTGTGTGCCACTACGGCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGTTTCACCATATTG
GCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCCACCTTCCTTGTGCTCCCAAAGTGCTGAGATTACAGGCG
TGAGCTATCACACCCAGCCTCCCCCTTTTTTTCCTAATAGGAGACTCCTGTACCTTTCTTCGTTTTACCTATGTG
TCGTGTCTGCTTACATTTCCTTCTCCCCTCAGGCTTTTTTTGGGTGGTCCTCCAACCTCCAATACCCAGGCCTGG
CCTCTTCAGAGTACCCCCCATTCCACTTTCCCTGCCTCCTTCCTTAAATAGCTGACAATCAAATTCATGCTATGG
TGTGAAAGACTACCTTTGACTTGGTATTATAAGCTGGAGTTATATATGTATTTGAAAACAGAGTAAATACTTAAG
AGGCCAAATAGATGAATGGAAGAATTTTAGGAACTGTGAGAGGGGGACAAGGTGAAGCTTTCCTGGCCCTGGGAG
GAAGCTGGCTGTGGTAGCGTAGCGCTCTCTCTCTCTGTCTGTGGCAGGAGCCAAAGAGTAGGGTGTAATTGAGTG
AAGGAATCCTGGGTAGAGACCATTCTCAGGTGGTTGGGCCAGGCTAAAGACTGGGAGTTGGGTCTATCTATGCCT
TTCTGGCTGATTTTTGTAGAGACGGGGTTTTGCCATGTTACCCAGGCTGGTCTCAAACTCCTGGGCTCAAGCGAT
CCTCCTGGCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAATCACTGCGCCTGGCTTCCTCTTCCTCTTGAG
AAATATTCTTTTCATACAGCAAGTATGGGACAGCAGTGTCCCAGGTAAAGGACATAAATGTTACAAGTGTCTGGT
CCTTTCTGAGGGAGGCTGGTGCCGCTCTGCAGGGTATTTGAACCTGTGGAATTGGAGGAGGCCATTTCACTCCCT
GAACCCAGCCTGACAAATCACAGTGAGAATGTTCACCTTATAGGCTTGCTGTGGGGCTCAGGTTGAAAGTGTGGG
GAGTGACACTGCCTAGGCATCCAGCTCAGTGTCATCCAGGGCCTGTGTCCCTCCCGAACCCAGGGTCAACCTGCC
TGCCACAGGCACTAGAAGGACGAATCTGCCTACTGCCCATGAACGGGGCCCTCAAGCGTCCTGGGATCTCCTTCT
CCCTCCTGTCCTGTCCTTGCCCCTCAGGACTGCTGGAAAATAAATCCTTTAAAATAGTAAAAAAAAAAAAAA

FIGURE 722

MARLQTALLVVLVLLAVALQATEAGPYGANMEDSVCCRDYVRYRLPLRVVKHFYWTSDSCPRPGVVLLTFRDKEI
CADPRVPWVKMILNKLSQ

FIGURE 723

GGCAGGCGCGTGGCCGGGCCGCGGCGCG**ATG**AGTGGGGCCCGGGCGGCGCCCGGGGCCGCGGGCAACGGCGCGGT
CCGGGGGCTGCGGGTGGACGGGCTGCCCCCGCTGCCAAAGAGCTTGAGCGGGCTGCTGCACTCGGCGTCGGGCGG
CGGCGCGTCTGGGGGCTGGCGGCACCTGGAGCGGCTGTACGCGCAGAAGTCGCGCATCCAGGACGAGCTGAGCCG
CGGGGGCCCGGGCGGCGGCGGGGCCCGGGCGGCAGCGCTGCCCGCCAAGCCTCCCAACCTGGACGCCGCTCTGGC
GCTGCTCCGCAAAGAGATGGTTGGTCTCCGCCAGCTGGACATGTCCTTGCTCTGCCAACTGTACAGCCTCTACGA
GTCGATTCAGGAGTACAAGGGGGCATGCCAGGCAGCCTCCAGCCCAGACTGCACTTACGCTCTGGAGAACGGCTT
CTTCGATGAAGAGGAGGAATATTTCCAGGAGCAGAACTCCCTGCACGACAGGAGGGACCGAGGCCCTCCTCGGGA
CTTGTCACTGCCTGTCTCCTCCCTCTCCAGCAGCGACTGGATTCTGGAGTCCATC**TAG**AGGGTCTTGGGAGGGAT
GTGACTGTTGGGAAGCCCTTCCTACTGGACACGCTGTCATCATTTGCTGCTTCTCTTGCAAGAAAGCACCTCCGT
TGTGGACGGTCCTCGGGCACAGGGGATGAGCGCTACCAGTTTCATTTGTAGGCAGGGAGTTCTCCGCGGATGCAT
GGTGGCAGTCTGCTTTGATGGCAGCAGTTATCTGCTTAGGTGACCTAGAGGTCCTCAGCAGTATCCTCCACACCT
ATTTATTGAGGTGCACCTGCTGGGGATTCATAATGAGAATATAACAAGAGGATCTCGGTGAAAGGCCTTAGTGGG
TGTTTTGTGTGAGGTGGCTTGTAGCTAGCTACTTCCTTACAGATGGTAGAGTATTCCAATCCTCTTTGTGTTAGG
GTTCTTGCTTCCAGTTTGGGATGTATTAAAACCACCATTTCACTGCTTCCCTTCCTCAATATGCTCTGCAGCTTT
TCTTGCTGTTTAAACCTCTCGCCTCAGCTTTATTTATTTGTAAGCTGCATTACTAACTGCCCAGTGATTCGGTGA
AAGCTTTTTACTGAAAAAGTTAACATTTCTAGTCATCCCAATCAACTGGCTTTTTTCAACCAAAATTTTATATCA
TTCTTTGTCTATCAGATACGAGAGGAAGGAAGATAATACGAAGACATGTTGAATAGTGAAAAAAAAAAAAAAAAA
A

FIGURE 724

MSGARAAPGAAGNGAVRGLRVDGLPPLPKSLSGLLHSASGGGASGGWRHLERLYAQKSRIQDELSRGGPGGGAR
AAALPAKPPNLDAALALLRKEMVGLRQLDMSLLCQLYSLYESIQEYKGACQAASSPDCTYALENGFFDEEEEYFQ
EQNSLHDRRDRGPPRDLSLPVSSLSSSDWILESI

FIGURE 725

AAATGCAGAGAAGAATGGGCAAAGACCAAAGACCCAACTGCTGCCCTCAGAAAACTACCTGTCAAAAGGTGTGTG
GAAGGGCAGCTGCTTCGAGGACTTTCAAAATATGGA**ATG**AAGAATATAGTCTCTGCATTTGGCATAATACCCAGA
AATAATCGCTTAATGTATATTCATAGCTACCAAAGCTATGTGTGGAATAACATGGTAAGCAAGAGGATAGAAGAC
TATGGACTAAAACCTGTTCCAGGGGACCTCGTTCTCAAAGGAGCCACAGCCACCTATATTGAGGAAGATGATGTT
AATAATTACTCTATCCATGATGTGGTAATGCCCTTGCCTGGTTTCGATGTTATCTACCCAAAGCATAAAATTCAA
GAAGCCTACAGGGAAATGCTCACAGCTGACAATCTTGATATTGACAACATGAGACACAAAATTCGAGATTATTCC
TTGTCAGGGGCCTACCGAAAGATCATTATTCGTCCTCAGAATGTTAGCTGGGAAGTCGTTGCATATGATGATCCC
AAAATTCCACTTTTCAACACAGATGTGGACAACCTAGAAGGGAAGACACCACCAGTTTTTGCTTCTGAAGGCAAA
TACAGGGCTCTGAAAATGGATTTTTCTCTACCCCCTTCTACTTACGCCACCATGGCCATTCGAGAAGTGCTAAAA
ATGGATACCAGTATCAAGAACCAGACGCAGCTGAATACAACCTGGCTTCGC**TGA**GCAGTACCTTGTCCACAGATT
AGAAAACGTACACAAGTGTTTGCTTCCTGGCTCCCTGTGCATTTTTGTCTTAGTTCAGACTCATATATGGATTTC
AAATCTTTGTAATAAAAATTATTTGTATTTTTAAGTTTTTATTAGCTTAAAGAAATAATTTGCAATATTTGTACA
TGTACACAAATCCTGAGGTTCTTAATTTTAGCTCAGAATATAAATTAGTCAAAATACACTTCAGGTGCTTAAATC
AGAGTAAAATGTCAGCTTTACAATAATAAAAAAAGGACTTTGGTTTAAAGTAGCAGGTTTAGGTTTTGCTACATT
CTCAAAAGACAGCAGGAGTATTTGACACATCTGTGATGGAGTATACAACAATGCATTTTAAGAGCAAATGCAACA
AAACAAATCTGGACTATGGATAAATAATTTGAGAGCTGCCACCCACAAATATAAATACAGTACTCATGCTGACTG
AAATAATAAGACATCTACAAATTTATAAACAAAAAGTGATTGTCATTATCCTGCTTATGTACTAGATTCAGGCAA
GCATTATAGACTTTTTGGTTGCGGTGGCTTTTGCATTTATATTATCAATGCCTTGCAGGAACGTTGCATTGATAG
GCCCATTTTATTTTTTTATTTTTTTTTTCGAGACAGGATCTCACTCTGTAGCACAGGCTGGATTGCAGTGCAATC
CTGCAATTCTCAATCTTGCACTGCAGCCTCGACCTCCCAGGCTCCAGTGACTCTCCCACCTCAGCCTCCTAAGTA
GCTGGGAGTACAGGCGCGCACCACCACGCCTAGCTGATTTTTGTATTTTTTTGTAGAGACGGGGGTTTGGCCATG
TTGCCGAGGCTAACTCCTGGGATTACAGGCATGAGCTGTGCTGGCCGGGTTTTTTTTTCTTGATGTAAACGTGTA
CAGCTGTTTTATTAGTTAAGGTCTAATTTTTACTCTAGGTGCCTTTTATGTTCAGAACTCTTTCCACTGGACTGG
TATTTGCTCAAAAATAAATAATGGTAGAGAAGAAAACTATAAAAATGGACAAGGCTTTCTTCTATCAGTAGCGTT
TACCCTTTGTCACCAGTGGCTTTGGTATTTCCATGTCTGGCATTGCATAAACTTCTCTGGTGTGAAAGGATAAAT
ATGCCTTTCTAAAGTTGTATATCAAAATTGTATCAATTTTTATTTTCTATGATTTCTAGAAACAAATGTAATAAA
TATTTTTAAAATCTCCTTTCTACTGGTTATGTAAATAAATCAAATAAATATATCAAAAAAAAAAAAAAAAA

FIGURE 726

MKNIVSAFGIIPRNNRLMYIHSYQSYVWNNMVSKRIEDYGLKPVPGDLVLKGATATYIEEDDVNNYSIHDVVMPL
PGFDVIYPKHKIQEAYREMLTADNLDIDNMRHKIRDYSLSGAYRKIIIRPQNVSWEVVAYDDPKIPLFNTDVDNL
EGKTPPVFASEGKYRALKMDFSLPPSTYATMAIREVLKMDTSIKNQTQLNTTWLR

FIGURE 727

ATGGCAGTGACAACTCGTTTGACATGGTTGCACGAAAAGATCCTGCAAAATCATTTTGGAGGGAAGCGGCTTAGC
CTTCTCTATAAGGGTAGTGTCCATGGATTCCGTAATGGAGTTTTGCTTGACAGATGTTGTAATCAAGGGCCTACT
CTAACAGTGATTTATAGTGAAGATCATATTATTGGAGCATATGCAGAAGAGAGTTACCAGGAAGGAAAGTATGCT
TCCATCATCCTTTTTGCACTTCAAGATACTAAAATTTCAGAATGGAAACTAGGACTATGTACACCAGAAACACTG
TTTTGTTGTGATGTTACAAAATATAACTCCCCAACTAATTTCCAGATAGATGGAAGAAATAGAAAAGTGATTATG
GACTTAAAGACAATGGAAAATCTTGGACTTGCTCAAAATTGTACTATCTCTATTCAGGATTATGAAGTTTTTCGA
TGCGAAGATTCACTGGATGAAAGAAAGATAAAAGGGGTCATTGAGCTCAGGAAGAGCTTACTGTCTGCCTTGAGA
ACTTATGAACCATATGGATCCCTGGTTCAACAAATACGAATTCTCCTCCTGGGTCCAATTGGAGCTCCCAAGTCC
AGCTTTTTCAACTCAGTGAGGTCTGTTTTCCAAGGGCATGTAACGCATCAGGCTTTGGTGGGCACTAATACAACT
GGGATATCTGAGAAGTATAGGACATACTCTATTAGAGACGGGAAAGATGGCAAATACCTGCCGTTTATTCTGTGT
GACTCACTGGGGCTGAGTGAGAAAGAAGGCGGCCTGTGCAGGGATGACATATTCTATATCTTGAACGGTAACATT
CGTGATAGATACCAGTTTAATCCCATGGAATCAATCAAATTAAATCATCATGACTACATTGATTCCCCATCGCTG
AAGGACAGAATTCATTGTGTGGCATTTGTATTTGATGCCAGCTCTATTCAATACTTCTCCTCTCAGATGATAGTA
AAGATCAAAAGAATTCAAAGGGAGTTGGTAAACGCTGGTGTGGTACATGTGGCTTTGCTCACTCATGTGGATAGC
ATGGATTTGATTACAAAAGGTGACCTTATAGAAATAGAGAGATGTGAGCCTGTGAGGTCCAAGCTAGAGGAAGTC
CAAAGAAAACTTGGATTTGCTCTTTCTGACATCTCGGTGGTTAGCAATTATTCCTCTGAGTGGGAGCTGGACCCT
GTAAAGGATGTTCTAATTCTTTCTGCTCTGAGACGAATGCTATGGGCTGCAGATGACTTCTTAGAGGATTTGCCT
TTTGAGCAAATAGGGAATCTAAGGGAGGAAATTATCAACTGTGCACAAGGAAAAAAA**TAG**

FIGURE 728

MAVTTRLTWLHEKILQNHFGGKRLSLLYKGSVHGFRNGVLLDRCCNQGPTLTVIYSEDHIIGAYAEESYQEGKYA
SIILFALQDTKISEWKLGLCTPETLFCCDVTKYNSPTNFQIDGRNRKVIMDLKTMENLGLAQNCTISIQDYEVFR
CEDSLDERKIKGVIELRKSLLSALRTYEPYGSLVQQIRILLLGPIGAPKSSFFNSVRSVFQGHVTHQALVGTNTT
GISEKYRTYSIRDGKDGKYLPFILCDSLGLSEKEGGLCRDDIFYILNGNIRDRYQFNPMESIKLNHHDYIDSPSL
KDRIHCVAFVFDASSIQYFSSQMIVKIKRIQRELVNAGVVHVALLTHVDSMDLITKGDLIEIERCEPVRSKLEEV
QRKLGFALSDISVVSNYSSEWELDPVKDVLILSALRRMLWAADDFLEDLPFEQIGNLREEIINCAQGKK

FIGURE 729

GCAGACGCTGCCGTGGAATCCTTGACTCTAGTTCTCTGAGTCGATTGTGATC**ATG**GCTGCTGAGTCTGATGTTCT
GCATTTCCAGTTTGAACAGCAAGGAGATGTGGTCTTGCAGAAAATGAATCTTTTGAGACAGCAGAATTTATTTTG
TGATGTATCAATTTACATTAATGACACTGAGTTCCAGGGGCACAAGGTGATTTTGGCTGCTTGCTCCACTTTTAT
GAGAGATCAGTTTTTACTCACACAGTCAAAACATGTCAGAATCACCATCTTACAGAGTGCAGAAGTTGGCAGAAA
ATTGTTACTGTCTTGCTATACTGGAGCACTTGAAGTTAAAAGGAAAGAGCTTTTGAAATACTTGACTGCTGCCAG
TTACCTTCAGATGGTTCACATTGTGGAAAAGTGCACAGAAGCTTTGTCAAAGTATCTGGAAATTGATCTTTCTAT
GAAAAACAACAACCAACACACTGACCTGTGTCAGTCTTCTGATCCTGATGTTAAGAATGAAGATGAAAATTCTGA
TAAAGACTGTGAGATAATTGAAATTTCAGAAGATAGTCCTGTAAACATAGATTTCCATGTTAAAGAAGAGGAAAG
CAATGCTTTGCAGTCTACAGTAGAGAGTCTGACATCAGAGAGAAAGGAAATGAAGTCACCAGAGCTGTCTACAGT
AGACATAGGTTTTAAAGACAATGAAATTTGTATCCTTCATGTAGAATCCATCAGTACAGCTGGTGTCGAAAATGG
GCAGTTTTCACAGCCTTGTACCTCTTCAAAAGCAAGCATGTATTTCTCTGAAACACAGCATTCATTGATCAATTC
TACAGTTGAGAGCAGAGTGGCTGAAGTTCCTGGGAATCAAGATCAGGGCTTATTTTGTGAGAATACTGAAGGAAG
TTATGGTACAGTGAGTGAGATTCAGAATCTGGAGGAAGGTTATTCACTGAGGCACCAGTGCCCCAGGTGTCCTCG
AGGCTTTCTTCATGTTGAAAACTATCTGCGCCACCTTAAAATGCATAAACTATTCTTATGCTTACAGTGCGGAAA
AACATTTACACAGAAGAAAAATCTCAACCGACACATCCGAGGACACATGGGCATACGGCCCTTTCAGTGTACTGT
GTGCTTGAAGACATTTACTGCCAAAAGCACACTTCAGGACCACTTGAACATACACAGTGGGGATCGGCCATACAA
ATGCCACTGTTGTGATATGGATTTCAAGCACAAGTCTGCTCTCAAAAAGCACTTAACCTCTGTCCATGGCAGAAG
CAGTGGTGAAAAACTATCTAGGCCTGATCTCAAAAGGCAAAGTCTACTA**TAA**TTATAATCACAGACTTGTTATAT
AAMGTTTGTATTATTCTATTACGCAAGTCTTTCTGTAGAGATGCAGCATTTGTAATATTTCATCCCCCCAATCTT
TGTTTCTTATATTTTGTCGGCTTACACATAATCATTCTTTCTGAACTTCTAACAGTTCCAAAGTTATGGGAGGCA
CAGTAAAGCTGATGGGATTCTGTCTCATCTCATACCTTACATATAAGTCTCAGTAGTATCCCTAGAGAAATAGTG
TTCCTCTCTTATATATTCTTGATTCTAGTGACAAAGGATCCAGCAGTATTTGCAGATTCCGATTTGGAGTCTCTA
GGTAATTGATTTAAGTATAAAATCCAATCATATAAAAACTTTAATGAATTAGGATAACAAGAAGAGAAAATAAAG
GTAAAAACACTATTACCTGTTTCTAGTCACTTTAGAACAGATGGCACTAAAAAAATTTTTTTTAACTTTTTACC
AGCTGTTCTTGGATTCCAAACTAAACACCAAGATACTTTTCATTTTAAAATGTATAAAGTAACAATTCAGATTCA
CTTGGGAATAGCAGAATTTTTTTATACAGGGTTAATAATCCTTAAAATACTTTTATTTCCATGCCTTATTAGTAT
ACATACTTAAGAAATGGTTCATTGGGCCCGAGTTTCTTGATTTTATTTAATACAATCGGATTTAATAATTTTGTG
GCCAGTAAAATTATACCATTGGCATGAAGCTGTGAAAAATGAGAAATTCTACCTTTACCAGGGATATCTGTTCTA
CTGTTTTAAAAGTTCCTCTCTATTTTATTTTTTATTTAACATGAAGTAAAATTGAAATTTCTTCTTGGTGTATAG
TTCTGTGAATTTTAACAGAAAGATTTGTGCACCACTACTGCAGTCGGTACAGAACAGTTCCTTCACTCCCAATAG
CTCTCTTATGCTGTCCCTTTGTAGTCAGCTCCTTCTAGCTCTAATCCTGGCAACAGTTCTCCGTCACTATTATTT
TGCCTTTTCTGGACTGTCATATAAACAGAATCTTATAGTACGTTCCCTCTTGAAATGCTTTTTCACCCAGCATAA
TGACTTTGAGGTTCATCCATGTCATTTTAAATTTTGAATTGGCAATATATATTCTAGCTGTTACTAGATGAGCAA
TTTAAAAAGGTGTAGCTATTAGTGTTGTATTTTTTCATTTACATTAATGTAATTTCCATTCACTATGTGTTGATA
AAAATCTTAACCATCCCTAGAGTTTTATATTTCCAAAAATATGCCAAAAGGAAAACTATGACTGTATGATTATTT
TAGCGAGAGTCATATTTGAGATGGTGTTCTGAGCCATAGTTCTCTAACATCTCCGTCTACATATAACACAAAACT
TTTATAAATTATTTTAACAAAGATTAAAATATACTGCAGGGCAAATAATATTCTCTAAAACACAGGAACTGCTTT
TCGTAAAGAAGACTGACTAGATGCATCTTTCTTTGAAGCTGTTCTAGTCCTCCTCTAGTTAACTTAGCTTTATGT
AGAATYTCTACTGTATTTAATTTYTATTGAAGCCCTTCTGTATTTTAAAATGTAATATACTTTGTACCATTTATA
AAAATTGTGTGATGAATGAATCACATGTTCGTTGTTATAAGTGTTAACCTTTTTTTGACAATTTTGTGGGAAAGA
CATTCTCCACTGAATTTTAACTTTCCTTGAGACTTTCAAGAATGCAGGTCTCGTTTGATGAAAAAACCGACTTCA
TAACCYAATGTTACTAGTTAGCGACATTGTGCTGAATTCTCCTTGAACTTTTAACTTTATATGTAAAATAACTT
TGATCTTGGTCATTTGAAAGATCATTTCCAGGTCTAAAATTCCATGATTTTGTATTTAATTCTYCCTGAGAACAG
AAGAGGGGAAAGCAAGAGAGGACGGTTTTGTGTCTTTATGAACTTTGTTACTTAAGTACTCCATTGGAGACATAA
TTTTTCTAATTAGTGGATCTTTTTCCACTGGAAAGTGTGATAGCTCATTGCTAATTTTTCATTCATAGTTCATTG
CTTCCATTTGACCTAAGATTGGCCATTTGTTGGTGTGAAAATATTTTCTTTTCAGAAATAGTTTACTAGTGATTG
AAGTACTTTTCTTATTTTTGCTTCCTATTATAAAATGGCGTGGGG

FIGURE 730

MAAESDVLHFQFEQQGDVVLQKMNLLRQQNLFCDVSIYINDTEFQGHKVILAACSTFMRDQFLLTQSKHVRITIL
QSAEVGRKLLLSCYTGALEVKRKELLKYLTAASYLQMVHIVEKCTEALSKYLEIDLSMKNNNQHTDLCQSSDPDV
KNEDENSDKDCEIIEISEDSPVNIDFHVKEEESNALQSTVESLTSERKEMKSPELSTVDIGFKDNEICILHVESI
STAGVENGQFSQPCTSSKASMYFSETQHSLINSTVESRVAEVPGNQDQGLFCENTEGSYGTVSEIQNLEEGYSLR
HQCPRCPRGFLHVENYLRHLKMHKLFLCLQCGKTFTQKKNLNRHIRGHMGIRPFQCTVCLKTFTAKSTLQDHLNI
HSGDRPYKCHCCDMDFKHKSALKKHLTSVHGRSSGEKLSRPDLKRQSLL

FIGURE 731

ATGGCGGTAGCGGCGGCGGCGGCGGCTGGGCCGGCTGGCGCGGAGGCGGCCGGGCGCAGCGGAGCGGGCTG
CTGGAAGTTTTGGTGCGGGATCGCTGGCACAAAGTTCTGGTGAACTTGAGCGAGGACGCCCTGGTTCTGAGCAGC
GAGGAGGGCGCTGCGGCGTACAACGGCATCGGGACCGCCACCAATGGCTCGTTCTGCAGGGGCGCCGGGGCTGGG
CACCCGGGCGCGGGCGGCGCGCAGCCCCCGGACTCGCCCGCCGGGGTCCGCACCGCTTTCACCGACCTGCCCGAG
CAGGTGCCCGAGTCCATCTCGAACCAGAAGCGTGGCGTGAAGGTGCTGAAGCAGGAGCTGGGCGGGCTGGGGATC
AGCATCAAGGGGGGCAAGGAGAACAAGATGCCCATCCTCATCAGCAAGATCTTCAAGGGGCTGGCGGCGGACCAG
ACCCAAGCCCTGTACGTGGGCGACGCCATCCTGTCGGTGAACGGAGCCGACCTGCGGGACGCCACCCACGACGAG
GCGGTGCAGGCGTTGAAGCGCGCGGGCAAGGAAGTGCTGCTGGAAGTGAAGTACATGCGAGAAGCCACGCCCTAT
GTGAAGAAAGGATCCCCAGTATCCGAGATTGGGTGGAAACACCTCCGCCTGAATCCCCTCGGTTAGGGGGCAGC
ACCTCAGACCCCCCGTCATCGCAGTCCTTCTCCTTCCACAGAGACCGGAAAAGCATCCCCCTCAAAATGTGCTAC
GTCACTCGGAGTATGGCCTTGGCCGACCCTGAGAACAGGCAGCTTGAAATCCACTCTCCAGATGCTAAGCACACG
GTGATCCTAAGGAGCAAGGACTCAGCCACGGCCCAGGCATGGTTCAGTGCCATCCATTCCAACGTTAATGACCTG
CTGACCCGAGTGATTGCTGAGGTCAGAGAGCAGCTGGGGAAAACAGGCATTGCTGGGAGCCGAGAGATTAGGCAT
CTTGGCTGGCTTGCAGAAAAGGTGCCAGGGGAGAGCAAGAAACAGTGGAAACCAGCCCTGGTTGTGCTGACTGAG
AAAGACCTTTTAATCTATGACAGCATGCCACGGAGGAAGGAAGCCTGGTTCAGCCCAGTTCACACATACCCTCTT
CTTGCCACCAGGCTGGTCCATTCAGGTCCAGGAAAGGGATCACCCCAGGCTGGTGTGGATCTGTCCTTTGCAACG
CGAACTGGTACCAGGCAAGGGATTGAAACACATCTCTTCAGAGCAGAGACCAGCAGGGACCTCTCCCACTGGACA
AGGAGCATAGTACAGGGTTGCCACAATTCTGCTGAACTCATTGCTGAAATCAGCACTGCTTGCACCTACAAAAAC
CAGGAGTGCCGTTTGACCATACATTATGAGAATGGATTTTCTATTACCACTGAACCACAGGAGGGTGCCTTTCCC
AAGACCATCATACAGTCTCCTTATGAAAAGCTCAAAATGTCTTCAGATGATGGAATCAGGATGCTGTATTTAGAT
TTTGGAGGCAAAGATGGAGAGATTCAACTGGACCTTCATTCCTGCCCCAAGCCAATTGTTTTCATCATTCATTCC
TTCCTGTCAGCTAAGATTACAAGACTGGGCTTGGTGGCC**TGA**

FIGURE 732

MAVAAAAAAAGPAGAGGGRAQRSGLLEVLVRDRWHKVLVNLSEDALVLSSEEGAAAYNGIGTATNGSFCRGAGAG
HPGAGGAQPPDSPAGVRTAFTDLPEQVPESISNQKRGVKVLKQELGGLGISIKGGKENKMPILISKIFKGLAADQ
TQALYVGDAILSVNGADLRDATHDEAVQALKRAGKEVLLEVKYMREATPYVKKGSPVSEIGWETPPPESPRLGGS
TSDPPSSQSFSFHRDRKSIPLKMCYVTRSMALADPENRQLEIHSPDAKHTVILRSKDSATAQAWFSAIHSNVNDL
LTRVIAEVREQLGKTGIAGSREIRHLGWLAEKVPGESKKQWKPALVVLTEKDLLIYDSMPRRKEAWFSPVHTYPL
LATRLVHSGPGKGSPQAGVDLSFATRTGTRQGIETHLFRAETSRDLSHWTRSIVQGCHNSAELIAEISTACTYKN
QECRLTIHYENGFSITTEPQEGAFPKTIIQSPYEKLKMSSDDGIRMLYLDFGGKDGEIQLDLHSCPKPIVFIIHS
FLSAKITRLGLVA

FIGURE 733

GTTTCATAATACAGCATGGTCTGGTAGTTTGCAAAATGGTGTGCTTTTGGGGAGATACACTAGCAATTTTTTTAA
AAAATGGAACAGTGTGATAGGAAGCCTGCTGGATGATTTCTTAAATATTCTAAAATGTAAGTCAAATATGTTT**TA**
ATAACAAAGACTTAAATGGCTTTTCTCCCTAGAGACTGAAACTAGTATTCATTGTGTTCAGAACTTAATTGGGCT
TGAACTGAGATTTAAATCTAATAAACAAGTTAATAAATGTGTATGTTTTGTTGTGGGTTTGGTAGTGATCTGTGG
TTCTATAGGGTTTAATAGGAATTGCTTTTGATTTGTTTCTGGCTTTAGAATGTGAGGCAAATTTTACATTCTTGG
TTCTATTAAGATTTTCTTAGGCATGCTAACATGCCAACAAAAAGCCATGTAAGTATTGTATAAAAAGATTCACAT
TGTTAATTTAGCCATTTTGAAATTCAGATGAGTGAGCAAGTTGATAATGGCCTCATCTCTGACCTGAGAAAAAAC
AACTTTGACCCTTGTTCTTAAAATGCTTTAACCTTGAAGTTGCTTGAGACTTAAGAGGTCATGTTGCTTTAGGTT
TAATAAATAGCCTTAACTATTTGGAGGGGAAAAAATGGGTCCACTTTTTTTTTTTTTTGGCGTTTGCATGTACAA
CTTTCTATTTTTAGCCTATATTTGGAAAGAAAGCACTTAACATTTTAGGAATTCTTTTTAAAGCTGCTTGCAAAG
TGTTGGTGATTTTACTGAAAACTTTTGAGATCTTCATTTTACAGGCAGACCTGTCTAACTACAAGCCAGACTTGG
GTTTTCTCCTGTAGTTTGAAGACACACTGACTCCTGACAAAATGCAGCCTGCAACTTCCTGGAGAACAACTCAGT
GTCACATTAAAGTTTATTATGTATTTAATGATACACTGTTTAATTGACAGTTTTGCATAGTTTGTCTAACTTTAG
AGAATTAAGAGCCTCTCAACTGAGCAGTAAAGGTAAGGAGAGCTCAATCTGCACAGAGCCAGTTTTTAGTGTTTG
ATGGAAATAAGATCATCATGCCCACTTGAGACTTCAGATTATTCTTTAGCTTAGTGGTTGTATGAGTTACATCTT
ATTAAAGTCGAAATTAATGTAGTTTTCTGCCTTGATAACATTTCATATGTGGTATTAGTTTTAAAGGGTCATTAG
GAAAATGCACATATTCCATGAATTTTAAGACCCATAGAAAAGTTGAAGAATGCTTAATTTTCTTATCCAGTAATG
TAAACACAGAGACAGAACATTGAGATGTGCCTAGTTCTGTATTTACAGTTTGGTCTGGCTGTTTGAGTTCTAGCG
CATTTAATGTTAATAAATAAAATACTGAATTTTAAAGCTGTTAAGAAATTGTCCAGAACGAGAATATTGAAATAA
AAACTTCAAGGTTATTATCGCAGTTTTTATGGCGTTTTTGTTTTGTCACTACAG GGTCTAAAGGTTACTTATT
AATTAATTGGGGAAGTGGAGACAAGGACCAAAGTTTATCTGGATTTTCTTATTTAATCTTCATTACCTGTGAAAT
ATGTATTTGTATTCTTACTTTACATATGAGATCAGAAGTTCATTTTCAAGCAGANTGGAAAGGTGGTAAATGGAC
TCTGAATTAAAATATGTCAGTATTTTAAAAGGTTATCTTCTGCCTAGTATTTTTATGGAATCTGACAAGTTCTCA
GATCACACTTGTTTCCTTAAATCTTGGTAAGTCTGAAGCATTCTTCATTTTGTTTATATTATACACGTTAGTAAG
GTGGGAGTTCTTTTGTTTTTTGTGTNTTTTGGCCAGTTGATAACATGAAAGTTTAAGAGAGGAGGCC

FIGURE 734

FHNTAWSGSLQNGVLLGRYTSNFFKKWNSVIGSLLDDFLNILKCKSNMF

FIGURE 735

GTGCGGTTGGGAACGCGGAGCGGACGGATTCGATTCAACGGGGTTCCGGACCGCGCTGCGCT**ATG**GAGCAGGTCA
ATGAGCTGAAGGAGAAAGGCAACAAGGCCCTGAGCGTGGGTAACATCGATGATGCCTTACAGTGCTACTCCGAAG
CTATTAAGCTGGATCCCCACAACCACGTGCTGTACAGCAACCGTTCTGCTGCCTATGCCAAGAAAGGAGACTACC
AGAAGGCTTATGAGGATGGCTGCAAGACTGTCGACCTAAAGCCTGACTGGGGCAAGGGCTATTCACGAAAAGCAG
CAGCTCTAGAGTTCTTAAACCGCTTTGAAGAAGCCAAGCGAACCTATGAGGAGGGCTTAAAACACGAGGCAAATA
ACCCTCAACTGAAAGAGGGTTTACAGAATATGGAGGCCAGGTTGGCAGAGAGAAAATTCATGAACCCTTTCAACA
TGCCTAATCTGTATCAGAAGTTGGAGAGTGATCCCAGGACAAGGACACTACTCAGTGATCCTACCTACCGGGAGC
TGATAGAGCAGCTACGAAACAAGCCTTCTGACCTGGGCACGAAACTACAAGATCCCCGGATCATGACCACTCTCA
GCGTCCTCCTTGGGGTCGATCTGGGCAGTATGGATGAGGAGGAAGAGATTGCAACACCTCCACCACCACCCCCTC
CCAAAAAGGAGACCAAGCCAGAGCCAATGGAAGAAGATCTTCCAGAGAATAAGAAGCAGGCACTGAAAGAAAAAG
AGCTGGGGAACGATGCCTACAAGAAGAAAGACTTTGACACAGCCTTGAAGCATTACGACAAAGCCAAGGAGCTGG
ACCCCACTAACATGACTTACATTACCAATCAAGCAGCGGTATACTTTGAAAAGGGCGACTACAATAAGTGCCGGG
AGCTTTGTGAGAAGGCCATTGAAGTGGGGAGAGAAAACCGAGAAGACTATCGACAGATTGCCAAAGCATATGCTC
GAATTGGCAACTCCTACTTCAAAGAAGAAAAGTACAAGGATGCCATCCATTTCTATAACAAGTCTCTGGCAGAGC
ACCGAACCCCAGATGTGCTCAAGAAATGCCAGCAGGCAGAGAAAATCCTGAAGGAGCAAGAGCGGCTGGCCTACA
TAAACCCCGACCTGGCTTTGGAGGAGAAGAACAAAGGCAACGAGTGTTTTCAGAAAGGGGACTATCCCCAGGCCA
TGAAGCATTATACAGAAGCCATCAAAAGGAACCCGAAAGATGCCAAATTATACAGCAATCGAGCTGCCTGCTACA
CCAAACTCCTGGAGTTCCAGCTGGCACTCAAGGACTGTGAGGAATGTATCCAGCTGGAGCCGACCTTCATCAAGG
GTTATACACGGAAAGCCGCTGCGCTGGAAGCGATGAAGGACTACACCAAAGCCATGGATGTGTACCAGAAGGCGC
TAGACCTGGACTCCAGCTGTAAGGAGGCGGCAGACGGCTACCAGCGCTGTATGATGGCGCAGTACAACCGGCACG
ACAGCCCCGAAGATGTGAAGCGACGAGCCATGGCCGACCCTGAGGTGCAGCAGATCATGAGTGACCCAGCCATGC
GCCTTATCCTGGAACAGATGCAGAAGGACCCCCAGGCACTCAGCGAACACTTAAAGAATCCTGTAATAGCACAGA
AGATCCAGAAGCTGATGGATGTGGGTCTGATTGCAATTCGG**TGA**TGACTTGTTCATCCCCCCTTCCCTTCGCCCT
CATGTGGAAAGAGGAGCTGGGACCGCGGCGAGCAGCACGGAGCGGAAGGGAGAGCAGGGGAGAGAAGGCCTCATC
TCTCTATATTTATACATAACCCCGGGGAAGACACAGAGACTCGTACCTGCGCTGTTTGTGCCGCCGCTGCCTCTG
GGCCCTCCCAGCACACGCATGGTCTCTTCACCGCTGCCCTCGAGTTCCATGTCTCTTTCCCCTGCCCCTAGTTGC
TGTCTCGGCTGCTCTCCCATAGTTGGTTTTTTTTTTATTTGGGGCAGTGGGCATGTTATGGGGAGGGGAGGGGGT
TCTTCCAGCCTCAGGTCCCAGCTGTCTCACGTTGTTTATTCTGCGTCCCCTTCTCCAATAAAACAAGCCAGTTGG
GCGTGGTTATAAC

FIGURE 736

MEQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYEDGCKTVDLKPDWGKGY
SRKAAALEFLNRFEEAKRTYEEGLKHEANNPQLKEGLQNMEARLAERKFMNPFNMPNLYQKLESDPRTRTLLSDP
TYRELIEQLRNKPSDLGTKLQDPRIMTTLSVLLGVDLGSMDEEEEIATPPPPPPPKKETKPEPMEEDLPENKKQA
LKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAVYFEKGDYNKCRELCEKAIEVGRENREDYRQIA
KAYARIGNSYFKEEKYKDAIHFYNKSLAEHRTPDVLKKCQQAEKILKEQERLAYINPDLALEEKNKGNECFQKGD
YPQAMKHYTEAIKRNPKDAKLYSNRAACYTKLLEFQLALKDCEECIQLEPTFIKGYTRKAAALEAMKDYTKAMDV
YQKALDLDSSCKEAADGYQRCMMAQYNRHDSPEDVKRRAMADPEVQQIMSDPAMRLILEQMQKDPQALSEHLKNP
VIAQKIQKLMDVGLIAIR

FIGURE 737A

GCGCGGCCCGGGCGCGGGGCGGCGGCAGCGGCGGCGCGCGGGGAGGCGGGGAGGCGGGGGGCCCGGCCGGACGCC
CCTGCGCCCCCTCCCCGCGCCCCGGCCGAGGGCGGAGCGCGCTGGCCCTGCAGCCTCCGGCCCGCCCCCGGCCCG
CCGCCTCCCCCGGGACGTGGGACGCGGGCGCAGGCGGGGTCCGCGCGGCGGGCGGCGGGGGACGGGCGGAGTCAA
AAGTCTATTGAAAAAGCAGAGAGAGAATGCCTCGGTGTGTAAGTGGAGTGATGAGGACCTGATCTCTGGGCCGTG
TGGGAACACTGGCTGCCATTTCATCACAGTCAACCTGGACTCACAGAATTTCAAGAGCTTGTCGGTTGGGTCAAG
AATGAACCTACGCATGACGGCGTGCTGATCCTGGGTTTCTAGTCATCCTTTTTAAGCTGCAAAGAAGCATTTGCA
GACGTTGTCTCATGGGTACCGCTTGCCAACTTTGGAGGATGTGAAGCCGGTAGAGAAATAAAGCATCGCCCCTCT
GCGCGCCCCTCCCCGTCTGCTAGA**<u>ATG</u>**TTTCTCATGAACGCTTCTCCAGTGGTTGCTCTCCAGTCCAAATGGGAG
GCCTTTGGCCCGCCAGGGAGCTGTAGGTTCCCCAGGTGCTTCTCGGAGGCTGACGAGGGCGTGGAGAGCGCGTCG
GTGAGCGCCCGGGTGCAGATGCTTATCAGCACTCTGCAGCGCGACGGGGCTGCTCGGGGCACCAGCGATGAGCGC
GCCGCACAGAGGGGCCACAGGGCAGAGGGATGCCACGACGCCAGGCCGGCTGCCAAGCCCACCGTGCACAAGGAG
CCACCCGCGTTGGCTGTCTGTGGTCTCGTTGCTGACTTTGACCCCATGGGGGAGGAGGAAACTACAGACTTTGGC
CCGTTGGTGCTAGATTCAGACAGTGATGATTCCGTGGACAGGGACATTGAGGAGGCCATCCAGGAGTACCTGAAG
GCAAAGAGTGGAGCCGCACAGCCCGGGGCCGGCGGGGCCCAGCCAGGTGCAGCCCAGCCTTCCAGGGCCGCAGGC
GGAGGCAGTAGATGTAAGCCGGAACCGGCTCACGGCAGTGCCCCGACTGCCCTGTGTCCCCCAAAACTTGTACCT
GGATCAGGTGGTGGCCCCGGCAGCCAGGTGGGATCCAGCAAGGACCAGGGCTCCGCCTCCCCGGTCAGTGTGAGC
AGCGATGACTCCTTCGAGCAGAGCATCAGGGCGGAAATAGAACAGTTTCTGAATGAGAAGAGACAGCATGAGACC
CAAAAATGTGATGGGTCAGTGGAGAAGAAACCAGACACAAATGAAAATTCCGCCAAGTCACTCTTGAAATCCCAC
CAAGAGCCGCCTACAAAGGTGGTGCATCGGCAGGGCCTGCTGGGCGTCCAGAAGGAGTTTGCCTTCCGCAAACCT
CCCCGGTTAGCGAAGATGAACGTCCAGCCCAGAAGCCTCAGGTCCAAGGTCACAACCACGCAGGAGAACGAGGGC
AGCACGAAGCCGGCAACCCCCTGCCGCCCTTCAGAAGCAGCACAGAATAAAGGTGGGATCAAAAGGAGCGCCAGC
GCTGCAAGGAGGGGAAAGCGAGTCATGAGTGCGGCACAGGCGTCCGAGGCGTCCGACTCCAGCAGCGACGATGGC
ATTGAGGAGGCCATCCAGCTGTACCAGCTGCAGAAAACACGCAAGGAGGCCGACGGGGACCTGCCCCAGAGGGTC
CAACTCCGAGAGGAGAGAGCGCCTGACCCTCCCGCACACAGCACAAGCAGTGCCACAAAAAGTGCCTTGCCCGAG
ACCCACAGGAAAACACCCAGCAAGAAGAAGCTAGTGGCCACCAAGACCATGGACCCTGGTCCAGGGGGCCTGGAC
ACTGACCATGCCCCCAAGCTCCTGAAGGAAACCAAAGCTCCACCTCCAGCGAGCCCTGCTTCCAGGAGTGAGTTT
GTGGAACGGTCCTCGTGCCGGGCGGACACATCTGCTGAGCTGATGTGTGCAGAAGCAATCCTGGACATCTCCAAG
ACGATCCTGCCGGCCCCTGTAGAGGGCAGTGACGGGTCCCTGTCCGCAAGCCCACTCTTCTACTCCCCGAACGTG
CCTTCCCGCTCTGACGGCGACAGTAGCTCCGTGGACAGCGATGACAGCATCGAGCAGGAAATCCGGACATTTTTG
GCCCTAAAGGCGCAGTCAGGGAGTTTGCTGGCCAGAGGTGAGAGCTGCCCGCAGGCTGCCCAGGGTCCACTTTTG
CCGCCTGGCCTCAACAGCCAGACCGGCGGCCACAAGACCCCTCTCTCTAAAACACCAGACCCACTGCTGGGCTGC
AAAAGGAAGCGTAGAGGTGGTGGCCATGTGAGGCCATCCACGCCCAAGAAAATGCAGGAGGTGGTGAAAGACGGT
AGCCAGGATGCCGACCACAGCCAGGGGAGAGCTGAGCCCGGCCATGAGAGGCGAGACCTGCCCATCCAGGGCAAA
GCCAGTGAGGCCCTGGGAGGGGAGGGCACCGCCAGGGGCCCTGGCGACACTCGCATGTCACAGGGCCAGGGTAAG
ACAGACGAGGCAAGGCGCCTAGACGAGAAAGAGAGCTCTGAAGACAAAAGCAGCTCCCTGGACAGTGACGAGGAC
CTGGACACAGCCATCAAGGACTTGTTAAGGTCCAAGCGAAAGCTCAAGAAGAGGTGCAGGGAGCCCAGGGCTGCG
TGCAGGAAGAAGGTCAGGTTCAGCACAGCCCAGACGCACTTCTTGGAGCAGCTGGGCGGGCTCCGGAGAGACTGG
AAAGACAGGGGCCCGCCAGTGCTGAAGAGCTGCCTCTCCAAGTCCAAGAGAGACAGTGGCGAGGGTCCTGGGAAG
AAACCCCCCAGTGTCTTTGGCAGCACGGCAGAGAGGATGAGGCAGGAGGGTGCCGCGAGCCAGGACGCGGCCCTG
GCCTTCCGGGTGAGGAGACCCGCCTCCGCCTCTGCCTCCGAAGGGAATCCATTCCCCAGGGAGTCCCAGGGCCCA
GCTCCCAGCCCCGGCTCCCTGTCTGATGACAGCAGTTCAGTGGACAGCGACGACAGCATCGAACTGGAGATTAGG
AAGTTTTTGGCGGAAAAGGCCAAGGAGTCAGTGAGCAGTTCAGAAGTTCAGGCAGAGGGCCCCACCGCTCTTGGG
ACAGGGGGCCCAGCCAGGCCAGAGGTGCTGTGCAGGAAGGAGCCGGCCCCACCGCCTGGCGTGTGCACACGCAGC
CAGAGGGCCAGGGGGGTCCCACATCTGGCCGAAGGGCTTCGAGGCACAGAGAGCGCAGGAGCACAGGGCACAGCT
GGTCTGTTCAGCCAGGGCGGGAAGGGGCTCCCTGCTGCTCCTGCCCGAGGGGATCCGGTGCCGCCCAGGAGCACC
AGCGGCGGTGTCTCCGCCAAGGGGCTCTCAGTGAGCAGGAGAAATGTTTACGTTCACAAAGACCAGAGCCCACGA
GGGGCTGAGCCTGCTGCCAAAAGTGCTTTTGGTCAGCTGCCCAGCTGTGCCACAGCGGGCACCGAGGCAGGAGGC
GCCAGAGGAACCTTTCACATGGGCTGCGGGAGCCCGAGCTTCCTGACCCCCAGCCCGGGAGCGGAGAGGGACGCT

FIGURE 737B

GGAGCCCAGGCCGACCGCACACCGCCCTGGAGCGACTTCGCCCACCAGAGTCGGCTGCCCAGCCCGTGGGTGCTG
CGCTCCGAAGGCAGAGATGCAGTGTGGAGGGGGGGCGTCGGGAGCGAGAGAGACAAGGGGTCCGAGGGCCCCGCC
CGGGGCCTGCCCAGCCTGCCCCTTGCGGGCTTCTCGCCGCTGCTGTCCACCCAGCTCTTCCACTTTGGAAAGGGT
GTCTCCTGGGGGGGCAGGCAGGCTGGCCTCTTCAGCCCCCACCTGGGGCTGCCTCTGCAGGGCCCCTCCTTCTCG
GCCTTCAGGGAGGCCCAGGCCGGACCCAGCCCTGTCTTTGGAAGCCCACACTTGCTGGCAAAGAAGGACGGCGGC
CCCTGGCCAACCAGGAAGGCACAGGCAGGGCTGAGTTTGCATGACAGGAGGAGCTCGGGCTCGGAGGAAAGCATT
TTAGACCTGAGGTATCGACGAAGGGTCAACAGGGATGACCAGGAGCAGGACGCCTTGGGCAGTGACGCCAGTGAC
TTCAGCGACACCTCCACGGAGGACAGTGGCGGCAGCTCAGTAGTGAAGGTC**TAA**GCCCTCGAGCTGTGGGTTCGC
GTCCTGGGTTGCGTGCATTCGTGGAAAGCGGCGTAGCCGTGCGTGTGTGTGATGGTTCCGTGGCTGCAAGGAAGG
GAAACAGTCTATTATACATAGCCCTGTATATATGTACACCAACATGAAACTTTATTTAACAGACGTGTCCTGGT
AAATATGATTTTTGTAGCTTTTTGTAAATTATTTAAAGTGATGTAAAAGATATTTTTGGAAAATACTGTTGTTCA
ATTTTGTAGGGTGTTCCTAACTGCAGTTTTCTGTGTTCTGCATACAAGTCTTAGCTTAGGAAACATTTGGTTCTT
ACCATCACAGCCAGGTTCACAGAGGCTCTGATGCTTTTTGGTTGATTGCTGGTGAGAATGGCCGGCGGTGGCTGC
AGTGGTAGCCTGAGGAAGGCCAAGCTGCCCTCCCTGGGAATCACTCAGATGCCCCAAGATGTCCGTTGGGAAGCT
CCCAGGACAGCACTTTTTATACAGAGGACACCGCCTCGGCCCCACGTCCTTAGAGGCCAGAGCACATCTGAAAAC
TGCAATCACAGCCGTCCGCTGGAAAAACGTTTCGAAGCACAGTGGCCAGCGAGCGAGCACGTGGCTACTCCCTGT
TGCATGTCAAATCCACACAGATGTCAGCGGCAGCTGCTCGGCAGCCCAGCCCTGGGCCTGGGTGGGTTCATGTCC
AATCTTGTTCGATCACTAGATGATTCTAACATCGAAATAAACCTCTTTTTATATGGC

FIGURE 738

MFLMNASPVVALQSKWEAFGPPGSCRFPRCFSEADEGVESASVSARVQMLISTLQRDGAARGTSDERAAQRGHRA
EGCHDARPAAKPTVHKEPPALAVCGLVADFDPMGEEETTDFGPLVLDSDSDDSVDRDIEEAIQEYLKAKSGAAQP
GAGGAQPGAAQPSRAAGGGSRCKPEPAHGSAPTALCPPKLVPGSGGGPGSQVGSSKDQGSASPVSVSSDDSFEQS
IRAEIEQFLNEKRQHETQKCDGSVEKKPDTNENSAKSLLKSHQEPPTKVVHRQGLLGVQKEFAFRKPPRLAKMNV
QPRSLRSKVTTTQENEGSTKPATPCRPSEAAQNKGGIKRSASAARRGKRVMSAAQASEASDSSSDDGIEEAIQLY
QLQKTRKEADGDLPQRVQLREERAPDPPAHSTSSATKSALPETHRKTPSKKKLVATKTMDPGPGGLDTDHAPKLL
KETKAPPPASPASRSEFVERSSCRADTSAELMCAEAILDISKTILPAPVEGSDGSLSASPLFYSPNVPSRSDGDS
SSVDSDDSIEQEIRTFLALKAQSGSLLARGESCPQAAQGPLLPPGLNSQTGGHKTPLSKTPDPLLGCKRKRRGGG
HVRPSTPKKMQEVVKDGSQDADHSQGRAEPGHERRDLPIQGKASEALGGEGTARGPGDTRMSQGQGKTDEARRLD
EKESSEDKSSSLDSDEDLDTAIKDLLRSKRKLKKRCREPRAACRKKVRFSTAQTHFLEQLGGLRRDWKDRGPPVL
KSCLSKSKRDSGEGPGKKPPSVFGSTAERMRQEGAASQDAALAFRVRRPASASASEGNPFPRESQGPAPSPGSLS
DDSSSVDSDDSIELEIRKFLAEKAKESVSSSEVQAEGPTALGTGGPARPEVLCRKEPAPPPGVCTRSQRARGVPH
LAEGLRGTESAGAQGTAGLFSQGGKGLPAAPARGDPVPPRSTSGGVSAKGLSVSRRNVYVHKDQSPRGAEPAAKS
AFGQLPSCATAGTEAGGARGTFHMGCGSPSFLTPSPGAERDAGAQADRTPPWSDFAHQSRLPSPWVLRSEGRDAV
WRGGVGSERDKGSEGPARGLPSLPLAGFSPLLSTQLFHFGKGVSWGGRQAGLFSPHLGLPLQGPSFSAFREAQAG
PSPVFGSPHLLAKKDGGPWPTRKAQAGLSLHDRRSSGSEESILDLRYRRRVNRDDQEQDALGSDASDFSDTSTED
SGGSSVVKV

FIGURE 739

ATTTTGACTGGCAAAATGTGGCAGATTTCAGGGATGCAGGTGGATCCTTAACTGAGGTCAAGGTGGAAGAGGAAG
AAAGGGATCCGCAGAGTCCTGAATTTGAAATTGAGGAGGAGGAAGAA**ATG**TTGTCATCCGTCATACCAGATTCCA
GGAGAGAAAATGAACTTCCCGATTTCCCCCACATTGATGAGTTTTTTACCCTTAACTCAACACCATCTAGATCTG
CATATGATGAGCCTCATTTGCTCGTAAATATTGAGAAACAGAAACTAGAGTTGGAAAAAACGACGACTGGATATCG
AGGCCGAAAGGCTGCAGGTAGAAAAGGAACGCCTACAAATCGAGAAAGAGAGGCTGCGGCATTTAGACATGGAAC
ATGAGCGGCTTCAGCTAGAGAAGGAGCGGCTGCAGATTGAAAGAGAAAAGTTGAGGTTACAGATAGTCAATTCAG
AGAAACCGTCCTTGGAAAATGAACTTGGTCAAGGAGAAAAATCCATGCTTCAACCACAGGACATAGAAACAGAGA
AGTTAAAACTTGAGCGAGAACGCTTGCAACTGGAAAAGGATAGGCTGCAGTTTTTGAAGTTTGAATCTGAGAAGC
TGCAGATTGAAAAGGAACGCTTACAGGTAGAGAAAGACAGACTTCGAATTCAGAAAGAAGGACACTTGCAG**TGA**T
TTTTCCAGGCTTCCATTTAGCAAATGTTTGAAAACTCTAGATTTTTCTCATATCAGGTGATATAATGATGGTTGC
TGGATTAGCTGTGGTTTCTTGTCTAATGTCAGTGTTCAGTAGGAAAAAGTTATATGTGGATAACTGTATGCCTAA
GTAGTATATAAAAGCTGTGCCCTAGCGTAAACAGTATAGCAGAAACTTACTGTGCTGGACTCTTTACCTTATAAT
ATTACATAGAGTCTTGTATTGTCTGTGTACCCAGAGTTTACAATTATGTCCATATAAAATTCTAGCCCAGAAGTT
CTCATCTGGGGTAGATTTTGGCCTTCAGAAGACCAATTTGGTGATGTCTGGAGACATGTTGGGTTGTCAAAACTG
GGGTGGGGAAAAGGTTGCTACTGTGCAATGCATACCTCCTCAACACCCCCCCACACTCAGTAAAGAATTTTCCAA
CCCAAAATATCATTAGTCCTGAGGTTGAGAAACCCTGTCCTAGCCTAACTGTATACCTCTATAGCTATGTTTTAT
AGTTTTAGAATATTAAAACCTCAGATATTTATGTGGGTAGGTACTTAAATGGCCAAAAACTTTAACTATGAAATG
TTACTGTGTAGTATATTGAATATAGGAAGTGATGAAGATTATAGGTATTTTATTCCCATGTTTCCATCTATAAAT
AGCCTTCTCAGATTCAGAAAACAATACAGAGAACATCAGAAATTTTCTAAAATGGGTCACTTTGAAAAGAATTCT
TTTTCTCACTATTAATGCTTTAGAAGCAAGACGCAATTTTAAAGCTTTAGTTCCTTTTCTTTCAGTCATTGTCTT
AGTTTGGGTACAAAAATGTCATTTCAGTAATGTACTGAAATCTTATAAGTGAATAGTTGAAGCTAGTAAAAATGA
TACCAGTATAAAAATGGTACTTGTAGTCCATGAGCTTGAACCCAATGACTGATTGTTTGACTTTTAAAATAAGTA
ATAGCAGCCATTTGGGAGTAGGGGGTAGGTGGGGAAGATGTACTCCGTATCAAATAATAATGATGTTGAAATAAT
GATAGTAGGTATGTATTATGGATTGGAGAAGCACTTATTACACTATCTAACCTAATATGTAGAACAATTCTTGAG
AGTTGTATCTGTCGTTATTTCTGAATGTGAAGCTCAGAGAAGTGACACAGAGTAAATGGCTGATCTTCTATATTG
TAGTATATTTTGTCCTTCCCTCTTCCCTGAGGAACAAAGCACGTATCTTTAGTCTCTTTGATATTTATTCTGAGA
CCAAGGGCTTGCTTGACCTGATGATTTTCCTTCAGCTCTCTGAAGGTGCTTTTTCCACAATCCAAGTGATTCTGA
TACACACTAAAGTTGAGAATCACTGCACTAGATCACTTTGTGTTTTCTGATTTTCAAGGTTGATACGTAGCTTTA
ATACAGCTCCTCTGTTGACAGTTATTACTTTAATTTGCATTTGTTCCTTGTAAGAATGGCTGGAAACTGTGTGT
TGACATTTGAGGATGGGTATGCAAGGAAAAAATATACTTCTGTTTACTTACTCTGACTTTGAAATAGTGTTATTT
TTCTATATCTGAAATAAATGCTTCTACCATAGAAAT

FIGURE 740

MLSSVIPDSRRENELPDFPHIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAERLQVEKERLQIEK
ERLRHLDMEHERLQLEKERLQIEREKLRLQIVNSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRL
QFLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ

FIGURE 741

TGCGGGCGCGAGGTTCCCAGCAGGATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGC
CCGCCCGGGGCAGG**ATG**ACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCTGC
TGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCTCTAGGCCGCACACGG
GGCCGCCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACGGCCGACTCCGATGTCGACGAGTTTCTGG
ACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGA
GCATGGAGGAGAGCGTGAGAGGCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGC
AGGCGGAGCGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCAT
TCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTGCTACGTGC
CCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCTGCTGCACCGCGGTGCGCCCT
ACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGC
GCCGCTACGGGAAGCTCTCCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCG
ACCCCTTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCG
CCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGCGCGAGGCCTTCCGCGCTGGCC
TCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCTGGCGCCCTTCAACGAGC
ACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGG
ACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCCGAGCTACCGGAACA
GGACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCT
ACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCCGAGAC**TGA**AAGCTTTCGCGTTGCT
TTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCCAGTTTTTTATGACCTACGATTTTGCAATCTGGGCTT
CTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTTTTTAAGATTAATATATTTCAGGTAT
TTAATACGAAAAAAAAAAAAAAAAAAA

FIGURE 742

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTADSDVDEFLDKFLS
AGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERAFDDIP
NSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGK
LSRHLMKVKLKKYTKFLFVRDPFVRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSF
ANFIQYLLDPHTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDRQLRFPPSYRNRTASS
WEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD